

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1243:

AAAATATGCC	TGCTCACATT	CAGGGGAAGT	AAGGTGGATA	TGATTTTGTG	TAATCCACCC	60
TATTTCAAGG	TGAATCCTTA	TTCTAATCTG	AACGAGAGTG	AACATTATCT	CTTGGCTCGA	120
CACGAAATCA	CGACTAATTT	GGAAGAAATC	TGTCGTAGTG	CCCAGAGTAT	TCTCAAGTCT	180
AATGGGCGTT	TGGCCATGGT	TCATCGTCCT	GATCGACTTC	TGGATATTTT	GGATACGTTA	240
AAACGACATA	ATCTAGCCCC	TAAGCGCCTG	CAGTTTGTTT	ATCCAAAAAG	AGAAAAGGAA	300
GCCAATATGC	TTTTGATTGA	GGCGATCAAG	GATGGCTCAA	CAAGTGGCTT	TAAGGTCTTA	360
CCTCCTTTGA	TTGTCCACAA	TGATGATGGC	TCTTATACGC	CCGAAATCGA	AGAGATTTAT	420
TATGGATCAT	AA					432

(2) INFORMATION FOR SEQ ID NO:1244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1244:

GTTTTTGCCG	ATGTAGAGAA	AACAAACGAA	TCAACGCAAT	CAGAGAATCA	AAGTTTTGAC	60
AAGACTACTT	TTTCAGAAGA	ATCGATTACT	TCTGAAACTA	CAGAATCTCA	AAGTGAGGCT	120
TCTACTAATA	AAAGGCAAGA	AGAAAATAAG	ACAAGTGAGA	CCTCAGAAGT	AGCTGAACAA	180
ACGTCTGATA	GCACTGAAGC	GGCACTGGCA	AGAGCTGTTT	CAGCGGATGG	GTACAGCGAA	240
GCTGCCACAA	CAGAAGAACT	GGCGCAGCTT	CTCGCAGACG	AATCAGTAAC	TAAGATCCGA	300
CTGATTACAG	CTTTGACTTT	AGACAGGGAA	TTAGAGATCA	AACGAGATAT	CGTTATTGAT	360
TTTGGTGGAT	TCGCTCACAA	TTTCGGCACA	CACCATATTT	AT		402

(2) INFORMATION FOR SEQ ID NO:1245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1245:

GAAGGTGCCG	ATCTGTTTGC	CTTGAGGAAA	CCAGGGAACA	TTTATACTCG	TATCACCAAT	60
CCTACAACAG	CTGCCCTTGA	AGGTGGTGT	GAAGCGCTAG	CAACAGCATC	AGGTATGACT	120
GCAGTGA	CTT	GGCGCTTGCC	CATGCTGGTG	AGCATGTAGT	GGCTGCTTCG	180
ACTATTTACG	GTGGAACCTT	CAATCTTTTG	AAAGAACCCC	TTCCCTCGTTA	TGGTATCACA	240
ACAACCTTTG	TCGATGTTGA	TAATTTGGAG	GAAGTAGAAG	CAGCTATCAA	AGACAATACC	300
AAGCTTGTCT	TGATTGAAAC	CCTGGGTAAAC	CCCTTGATTA	ATATTCCAGA	CCTGGAAAAA	360
CTGGCAGAGA	TTGCTCATAA	ACATCAAATC	CCACTTGTGT	CAGACAATAC	TTTTGCAACA	420
CCTTATTTGA	TTAACGTCCT	CTCTCATGGC	GTTGACATTG	CCATTCACCTC	TGCGACTAAG	480
TTTATCGGTG	GGCATGGTAC	AACTATTGGA	GGAATAATTG	TCGATAGTGG	TCGTTTTTGAC	540
TGGACGGCTT	CAGGGAAATT	CCCTCAAATTT	GTTGACGAGA	GTCCAAGCTG	CCACAATTTG	600
AGCTATACTC	ATGATGTGGG	TGCAGCAGCC	TTTATTATAG	CTGTTTCGAGT	TCAATTGCGT	660
CGTGATACAG	GTGCAGCCTT	GTCACCATTG	AATGCTTTCC	TCTTGCTACA	AAGACTTGAA	720
ACCCTTTCAC	TTCGTGTGGA	ACGCCATGTA	CAAAATGCTG	AGACAATTGT	TGATTTTCTT	780
GTCAACCATC	CTAAGGTAGA	AAAGGTAAAT	TATCCAAAAC	TTGCAGATAG	TCCTTATTAT	840
GCCTTGGCTG	AGAAATACTT	GCCAAAAGGT	GTCGGTTCAA	TCTTTACCTT	CCACGTCAAA	900
GGTGACGAGG	AGGAAGCACG	CAAGGTCATT	GATAATTTAG	AAATCTTTTC	TGACCTTGCA	960
AACGCGGCAG	ATGCTAAATC	GCTTGTTGTC	CATCCAGCAA	CAATCACTCA	CGGTCAATTG	1020
TCAGAAAAAG	ACCTAGAAGC	AGCAGGTGTC	ACACCAAATC	AAATCCACTT	GTCTATCGGT	1080
CTTGAAAAATG	TAGAAGATTT	GATTGAAGAC	TTACGCTTGG	CCTTGAAAAA	AATTTAA	1137

(2) INFORMATION FOR SEQ ID NO:1246:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1953 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1246:

AAGACTTACG	ATTATCTTGA	ATGCCTTAGG	GAAACATGCT	ATACTACTTG	TATGATTATT	60
TTACAAGCTA	ATAAAATTGA	ACGTTCTTTT	GCAGGAGAGG	TTCTTTTCGA	TAATATCAAC	120
CTGCAGGTTG	ATGAACGAGA	TCGGATTGCC	CTTGTTGGGA	AAAATGGTGC	AGGTAAGTCT	180
ACTCTTTTGA	AGATTTTAGT	AGGAGAAGAG	GAGCCAACTA	GTGGAGAAAT	CAATAAGAAA	240
AAAGATATTT	CTCTGTCTTA	CCTAGCTCAA	GATAGCCGTT	TTGAGTCTGA	AAATACCATC	300

TATGATGAGA	TGCTTCATGT	CTTTGATGAC	TTACGTCGGA	CAGATAAACA	ACTGCGTCAG	360
ATGGAGCTGG	AGATGGGTGA	AAAGTCTGGT	GAGGATTTGG	ATAAACTGAT	GTCAGATTAT	420
GACCGCTTAT	CTGAAAATTT	TCGCCAAGCA	GGTGGCTTTA	CCTATGAAGC	TGATATTCTGA	480
GCGATTTTGA	ATGGATTCAA	GTTTGACGAG	TCTATGTGGC	AGATGAAAAT	TGCTGAGCTT	540
TCTGGTGGTC	AAAATACTCG	TTTGGCTCTA	GCTAAAATGC	TCCTTGAAAA	GCCCAATCTC	600
TTGGTCTTGG	ACGAGCCAAC	TAACCACTTG	GATATTGAAA	CCATCTCCTG	GCTAGAGAAT	660
TACTTGGTAA	ACTATAGCGG	TGCCCTCAT	ATCGTCAGCC	ACGACCGTTA	TTTCTTGGAC	720
AAGGTTGCGA	CAATTACGCT	AGATTTGACC	AAGCATTCCT	TGGATCGCTA	TGTGGGGAAT	780
TACTCTCGTT	TTGTTGAGTT	GAAGGAGCAA	AAGCTAGCTA	CTGAGGCAAA	AAACTATGAA	840
AAGCAACAGA	AGGAAATCGC	TGCTCTGGAA	GACTTTGTCA	ATCGCAATCT	AGTTCGTGCT	900
TCAACGACTA	AACGTGCTCA	ATCTCGCCGT	AAACAAC TAG	AAAAAATGGA	GCGTTTGGAC	960
AAGCCTGAAG	CTGGCAAGAA	AGCAGCCAAC	ATGACCTTCC	AGTCTGAAAA	AACGTCGGGC	1020
AATGTTGTTT	TGACTGTTGA	AAATGCAGCT	GTTGGCTATG	ACGGGGAAGT	CTTGTCACAA	1080
CCTATCAACC	TAGATCTTCG	TAAGATGAAT	GCTGTCGCTA	TCGTTGGTCC	AAATGGTATC	1140
GGCAAGTCAA	CCTTTATCAA	GTCTATTGTG	GACCAGATTC	CTTTTATCAA	GGGAGAAAAG	1200
CGCTTTGGCG	CTAATGTTGA	GGTTGGTTAC	TATGACCAAA	CCCAAAGCAA	GCTGACACCA	1260
AGTAATACGG	TGCTGGATGA	ACTCTGGAAT	GATTTCAAAC	TGACACCAGA	AGTTGAAATC	1320
CGCAACCGTC	TTGGAGCCTT	CCTTTTCTCA	GGAGATGATG	TAAAAAATC	AGTCGGCATG	1380
CTATCTGGTG	GCGAAAAAGC	TCGTTTGCTT	TTAGCTAAAT	TGTCTATGGA	AAACAATAAC	1440
TTTTTGATTG	TGGATGAGCC	GACCAACCAC	TTGGATATTG	ATAGTAAGGA	AGTGCTAGAA	1500
AATGCCTTGA	TTGACTTTGA	TGGTACCTTG	CTTTTGTGCA	GTCATGATCG	TTACTTTATC	1560
AATCGTGTGG	CAACTCATGT	TTTGGAATTG	TCTGAGAATG	GTTCAACTCT	CTACCTTGGA	1620
GATTACGACT	ACTATGTTGA	GAAGAAAGCA	ACAGCAGAAA	TGAGTCAGAC	TGAGGAAGCT	1680
TCAACTAGCA	ATCAAGCAAA	GGAAGCAAGT	CCAGTCAATG	ACTATCAGGC	CCAGAAAGAA	1740
AGTCAAAAAG	AAGTTCGCAA	ACTCATGCGA	CAAATCGAAA	GTCTAGAAGC	TGAAATTGAA	1800
GAGCTAGAAA	GTCAAAGCCA	AGCCATTTCT	GAACAAATGT	TGGAAACAAA	CGATGCCGAC	1860
AAACTCATGG	AATTACAGGC	TGAGCTGGAC	AAAATCAGCC	ATCGTCAGGA	AGAAGCTATG	1920
CTTGAGTGGG	AAGAATTATC	AGATCAGGTG	TAA			1953

(2) INFORMATION FOR SEQ ID NO:1247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1247:

TCAAACAACG	ATTTGGCGAA	ATGTAACAAA	TATGAGGAGT	TCGGACTCGA	CTCTCTCCTT	60
CAAGAAACAC	GTGGTGGTCG	TAACCATGCA	TATATGACAG	TTGAGGAAGA	GAAAGCCTTT	120
CTTGCTCGCC	ATTTGAAGGC	TACAGAGGCA	GGAGAATTTG	TTACAATTGA	TGCCTTATTT	180
CAGGCTTATA	AAAAGGAGTT	AGGTCGTTCC	TACACACGTG	ATGCCTTCTA	TCAACTGTTG	240
AAGCACCATG	GTTGGCGAAA	TATTATGCCA	CGTCCAGAAC	ATCCTAGGAA	AGCAGACGCT	300

CAAACCATTG TCGCGTCTAA AAATAAAATC TCAATTCAAG AAGGCAAGAA AGCGCTTTAA

360

(2) INFORMATION FOR SEQ ID NO:1248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1248:

GCATGCAACG AACAAATTACC TGATGAAATG ACATTAGCTA AACAGTTTGC CTGTAGTCGA	60
ATGACGATCA AAAAAGCTTT AGACTTGTTA GTTCTGAGG GCTTAATTTT TAGAAAACGT	120
GGGCAGGGAT CCTTTGTTCT CTCTCGTGGC AGCTCAAAAA GAAAATTAAT CGTTCCAGAA	180
AGAGATATCC GGGGACTGAC AAAAATATCT GAAGATGCTC ATTCTACAAT TGACTCGAGG	240
ATTATTCACT TCAAATTAGA ATTTGCAAAT GAATTTTGTAG CAGAAAAACT ACAGGTCGCT	300
TTGCAGAGTC CAGTTTATAA TATTTACCGC CTGCGTATTA TTGACGGTAA ACCTTATGTT	360
CTGGAACAAA CTTATATGAG TACCGATGTT ATTCCAGGTA TTAGTGAAGA TATTTTACAA	420
AAATCGATTT ACAATTACAT TGAAGGAAAAG TTAGGATTGC ATATTGCCAG TGCTACAAAA	480
ATCTTACGAG CTTCTTCTAG TTCAGAAAAAT GAGCAACATT ACTTGCAGCT CCTTCCAACG	540
GAACCGGTAT TTGAAGTAGA ACAAGTGGCT TATTTGGATA ACGGAACTCC GTTTGAGTAC	600
TCGATTAGTC GTCATCGCTA TGATTTATTT GAATTTAATT CTTTTCATT ACACATTCT	660
TCCTAG	666

(2) INFORMATION FOR SEQ ID NO:1249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...1392

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1249:

TTCAAAAACG	AATTAAAAAT	AGAAAAGGAT	TTTATAACAA	TGGGTAAATA	TTTTGGGACT	60
GATGGAGTCC	GTGGAGAAGC	TAACCTAGAA	CTAACACCAG	AATTAGCCTT	TAAACTAGGA	120
CGTTTTTGGAG	GCTATGTTCT	TAGTCAACAT	GAAACGGAAG	CGCCGAAAGT	CTTTGTAGGA	180
CGTGACACAC	GTATTTTCAGG	GGAAATGCTG	GAATCGGCCCT	TGGTGGCAGG	TCTCCTTTCA	240
GTAGGGATTTC	ACGTATACAA	ACTTGGTGTG	CTTGCAACAC	CAGCAGTAGC	TTACTTGGTT	300
GAAACTGAAG	GAGCAAGTGC	CGGTGTCATG	ATTTCTGCTA	GCCACAACCC	AGCCCTTGAT	360
AACGGAATCA	AGTTCTTTGG	CGGTGATGGC	TTCAAAC TAG	ATGATGAAAA	AGAAGCAGAA	420
ATTGAAGCCT	TGCTAGATGC	TGAGGAAGAC	ACTCTTCCTC	GTCCAAGTGC	AGAAGGCTTA	480
GGAAATTTTGG	TAGATTATCC	AGAAGGCTTG	CGTAAGTATG	AAGGATACCG	TGTGTCAACT	540
GGAACCTCCTC	TTGATGGAAT	GAAGGTTGCC	TTGGATACAG	CTAATGGAGC	AGCTTCTACC	600
AGTGCCCGTC	AAATCTTTGC	AGACCTTGGT	GCCCAATTGA	CGGTTATCGG	GGAAACACCA	660
GACGGTCTTA	ACATCAACCT	TAATGTTGGT	TCAACACATC	CAGAAGCCCT	TCAAGAAGTG	720
GTCAAAGAAA	GTGGGTCAGC	TATTGGTFTG	GCCTTTGATG	GAGACAGTGA	CCGCTTGATT	780
GCTGTTGATG	AGAATGGTGA	CATCGTCGAT	GGTGACAAGA	TTATGTACAT	CATCGGAAAA	840
TACCTTTCTG	AAAAAGGACA	ATTGGCTCAA	AATACAATTG	TGACAACTGT	TATGTCTAAC	900
CTTGGTTTCC	ACAAGGCCCT	GAATCGCGAA	GGTATTAACA	AGGCAGTTAC	TGCAGTTGGT	960
GACCGCTACG	TTGTTGAAGA	AATGAGAAAA	TCAGGCTACA	ACCTTGGTGG	TGAACAGTCT	1020
GGTCACGTTA	TCATTGATGGA	TTACAATACC	ACAGGTGATG	GTCAATTATC	AGCAGTTCAA	1080
TTGACTAAAA	TCATGAAGGA	AACTGGTAAG	AGCTTATCAG	AGTTGGCGGC	AGAAGTAACG	1140
ATTTATCCAC	AAAAATTAGT	TAATATCCGA	GTGGAAAACG	TCATGAAGGA	AAAGGCCATG	1200
GAAGTGCCAG	CTATCAAGGC	CATCATCGAG	AAGATGGAAG	AAGAAATGGC	GGGGAACGGC	1260
CGTATCCTTG	TTCGTCCAAG	TGGAACAGAG	CCCCTCTTGC	GTGTTATGGC	AGAAGCGCCT	1320
ACAACAGAAG	AAGTGGACTA	CTATGTTGAT	ACCATCACAG	ATGTAGTTTC	TGCTGAAATT	1380
GGGATTGACT	AA					1392

(2) INFORMATION FOR SEQ ID NO:1250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1008 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1250:

NGTGAAGACG	ATTTGATTAA	AACGGACAAC	AGAACAAGTT	ATACCGTACA	GTATGGTGAT	60
ACTTTGAGCA	CCATTGCAGA	AGCCTTGGGT	G TAGATGTCA	CAGTGCTTGC	GAATCTGAAC	120
AAAATCACTA	ATATGGACTT	GATTTTCCCA	GAAACTGTTT	TGACAACGAC	TGTCAATGAA	180
GCAGAAGAAG	TAACAGAAGT	TGAAATCCAA	ACACCTCAAG	CAGACTCTAG	TGAAGAAGTG	240
ACAAC TGCGA	CAGCAGATTT	GACCACTAAT	CAAGTGACCG	TTGATGATCA	AAC TGTTTCAG	300

GTTGCAGACC	TTTCTCAACC	AATTGCAGAA	GTTACAAAGA	CAGTGATTGC	TTCTGAAGAA	360
GTGGCACCAT	CTACGGGCAC	TTCTGTCCCA	GAGGAGCAAA	CGACCGAAAC	AACTCGCCCA	420
GTTGAAGAAG	CAACTCCTCA	GGAAACGACT	CCAGCTGAGA	AGCAGGAAAC	ACAAGCAAGC	480
CCTCAAGCTG	CATCAGCAGT	GGAAGTAACT	ACAACAAGTT	CAGAAGCAAA	AGAAGTAGCA	540
TCATCAAATG	GAGCTACAGC	AGCAGTTTCT	ACTTATCAAC	CAGAAGAGAC	GAAAATAATT	600
TCAACAACCTT	ACGAGGCTCC	AGCTGCGCCC	GATTATGCTG	GACTTGCAGT	AGCAAAATCT	660
GAAAATGCAG	GTCTTCAACC	ACAAAACAGCT	GCCTTTAAAG	AAGAAATTGC	TAACTTGTTT	720
GGCATTACAT	CCTTTAGTGG	TTATCGTCCA	GGAGACAGTG	GAGATCACGG	AAAAGGTTTG	780
GCTATCGACT	TTATGGTACC	AGAACGTTCA	GAATTAGGGG	ATAAGATTGC	GGAATATGCT	840
ATTCAAAATA	TGGCCAGCCG	TGGCATTAGT	TACATCATCT	GGAAACAACG	TTTCTATGCT	900
CCATTCGATA	GCAAATATGG	GCCAGCTAAC	ACTTGGAACC	CAATGCCAGA	CCGTGGTAGT	960
GTGACAGAAA	ATCACTATGA	TCACGTTTAC	GTTTCAATGA	ATGGATAA		1008

(2) INFORMATION FOR SEQ ID NO:1251:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...198
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1251:

GCTCAGGACG	ATCAGGAAGA	TTTGACAGCG	ATTGTACGAG	ACCATTTTTTC	AGACATGGGG	60
GAAATTGCGA	CCCTCTATGT	TCAAGTCTAT	GAAAGCAGTC	TAGAGAGCTT	GCTTGGTGGC	120
GTTATTTTTG	AGGATGGCCG	TCATTATACC	TTTGTCTATG	AAAATGAAGA	CCTAGTCTAT	180
GAGGAGGAAG	TCTTATGA					198

(2) INFORMATION FOR SEQ ID NO:1252:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1252:

AGAATTTGCG AGATATGTTT AAAGCAAGAG AAGCAGCTTC TGTAAAAATT GCTACCTTGT	60
TGGATAAACC AAGAAGGACG TGTTGTAGAA ATTGAGGCAG ACTATACCTG CTTTACTATC	120
CCAAATGAGT TTGTAGTAGG TTATGGTTTA GACTACAAAG AAAATTATCG TAATCTTCCT	180
TATATTGGAG TATTGAAAGA GGAAGTGTAT TCAAATTAG	219

(2) INFORMATION FOR SEQ ID NO:1253:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1253:

ACTTTCTGCG AAACAAAAAT ACAACACAAT AAAACTATGA ATGATGAAGC AAGTAAACAA	60
TTAAGAGATA GCCGTTTCAA GAGCCTTGCA GGTGTTTCAGC GCACGACTTT TGAAGAGATG	120
TTAGCCGTGC TAAAAACAAC TTATCAACGT AAACACGCAA AAGGTGGACG AAAAACCAAA	180
TTAAGCCTAG ACGATCTCCT CATGGTAACT ATTCAATACA TGCGAGAATA G	231

(2) INFORMATION FOR SEQ ID NO:1254:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 939 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1254:

AGTCTACGCG	AGACAACAGA	TTACGTGGAA	GTGTCAAAAA	ACATTCAAGA	GCGTGTGCGC	60
TTTAGCTGTG	AAAAACCAGC	TTGGAATTAC	TGCTCAGACT	GTAAATGTCT	ACATTCAAAA	120
TATCAAAGTT	GTAGGAGAAT	AACCGTGTCA	AAAATTACTA	CTAGCTTATT	TCAAGAAATG	180
GTGCAGGCTG	CATCAACTCG	CTTGAATAAG	CAAGCTGAAT	ATGTCAATTC	ATTAAACGTC	240
TTTCCAGTTC	CAGATGGAGA	TACTGGGACA	AATATGGGAA	TGACCATTGA	AAATGGTGCT	300
AAAGAAGTTG	CAGACAAGCC	AGCTTCTACA	GTTGGAGAAG	TAGCGAGCAT	TCCTGCCAAA	360
GGGCTTTTGA	TGGGTGCGCG	TGGGAACTCA	GGAGTGATTA	CGTCTCAGCT	TTTCCGTGGA	420
TTTTCCCAAG	CTATCAAGGA	TAAAGACGAG	TTAACAGGTC	AAGACTTGGC	TCTGGCCTTC	480
CAATCAGGTG	TGGAAGTTGC	CTATAAGGCA	GTGATGAAAC	CTGTTGAAGG	AACGATTTTA	540
ACAGTTTCTC	GTGGAGCTGC	TATCGGTGCT	AAGAAAAAAG	CTGAGCAAAC	AGATGACGCT	600
GTTGAAGTCA	TGCGCGCAGC	CTTGGAAGGT	GCTAAAACAG	CTCTAGCTAA	AACACCAGAC	660
ATGCTTCCAG	TATTGAAAAG	AGTTGGCGTT	GTGGACTCAG	GTGGTCAAGG	ATTGGTCTTC	720
ATCTACGAAG	GTTTCCTTTC	AGCCCTTACT	GGCGAATATA	TTGCATCTGA	GGACTTTGTA	780
GCGACTCCTG	CCAACATGAG	TGAGATGATC	ACTGTAGAGC	ATCATAAGTC	TGTAGCTGGT	840
CACGTAGCGA	CTGAGGACAT	CACGTTTTGT	TACTGTACTG	AAATCATGGT	AGCTCTTAAG	900
CAAGGTCCAA	CCTATGCTAA	AGATTTTGAC	TACGAATGA			939

(2) INFORMATION FOR SEQ ID NO:1255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1653 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1653

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1255:

GGAGAAAGCG	AAAGAAGTAA	AAAAAGCTTC	GGAAGAGAAC	AAGCTGCAAA	TCTGAAATAT	60
CAACAAGAGT	TGGTTAAATA	TATTAAATAT	ACACGTGAAA	ATAATTCAAC	AAAAAGAACT	120
GAAGCTGAGA	AAGTAATGAC	TGCAGCTAAG	AAAGAGCATG	AGAAAAAACA	AACAGAACTT	180
GCTAAAGTTC	TCGCAAAGGT	AATTCCTAGC	GCGGAAGAAT	TAGAAAATAC	TAGACAAAAA	240
GCAGAGAAAG	CTAAAGAAAA	AGAACCAGAG	CTTACTAAAA	AACTAGAAGA	AGCTAAAGCA	300
AAATCAGAAG	AAGCTGAGAA	AAAAGCTACT	GAAGCCAAAC	AAAAAGTGGA	TGCAGAACAT	360
GCTGAAGAAG	TCGTTCCCTCA	AGCTAAAATC	GCTGAGTTGG	AAAATGAAGT	TCAGAAACTA	420
GAAAAAGATC	TCAAAGAGAT	TGATGAATCT	GACTCAGAAG	ATTATGTTAA	AGAAGGTCTC	480
CGTGCTCCTC	TTCAATCTGA	ATTGGATGCC	AAACAAGCTA	AACTATCAAA	ACTTGAAGAG	540
TTGAGTGATA	AGATTGATGA	GTTAGACGCT	GAAATTGCAA	AACTTGAAAA	AAATGTAGAA	600
GATTTCAAAA	ACTCAAACGG	TGAGCAAGCT	GAACAATACC	GTGCTGCAGC	TGAAGAAGAC	660

TTAGCTGCTA	AACAAGCTGA	ATTAGAAAAA	ACTGAAGCTG	ACCTTAAGAA	AGCAGTTAAT	720
GAGCCAGAAA	AACCAGCTCC	AGCTCCAGAA	ACTCCAGCCC	CAGAAGCACC	AGCTGAACAA	780
CCAAAACCAG	CGCCGGCTCC	TCAACCAGCT	CCCGCACCAA	AACCAGAGAA	GCCAGCTGAA	840
CAACCAAAAG	CAGAAAAACC	AGCTGATCAA	CAAGCTGAAG	AAGACTATGA	TCGTAGATCA	900
GAAGAAGAA	ATAACCGCTT	GACCCAACAG	CAACCGCCAA	AAGCAGAAAA	ACCAGCTCCT	960
GCACCACAAC	CAGAGCAACC	AGCTCCTGCA	CCAAAAACAG	GCTGGAAACA	AGAAAAACGGT	1020
ATGTGGTACT	TCTACAATAC	TGATGGTTCA	ATGGCGACAG	GATGGCTCCA	AAACAACGGT	1080
TCATGGTACT	ACCTCAACAG	CAATGGTGCT	ATGGCAACAG	GTTGGCTCCA	AAACAATGGA	1140
TCATGGTATT	ACCTAAATGC	TAACGGTGCT	ATGGCAACAG	GTTGGCTCCA	AAACAATGGT	1200
TCATGGTACT	ACCTCAACAG	CAATGGCGCT	ATGGCGACAG	GATGGCTCCA	ATACAATGGC	1260
TCATGGTACT	ATCTAAACGC	TAGCGGCGCT	ATGGCAACAG	GTTGGGCTAA	AGTCAACGGT	1320
TCATGGTACT	ACCTCAACGC	TAACGGTTCA	ATGGCAACAG	GATGGCTCCA	ATACAACGGT	1380
TCATGGTACT	ACCTCAACGC	TAACGGTGCT	ATGGCAACAG	GTTGGGCTAA	AGTCAACGGA	1440
TCATGGTACT	ACCTCAACGC	TAACGGTTCA	ATGGCAACAG	GTTGGGTGAA	AGATGGAGAT	1500
ACCTGGTACT	ATCTTGAAGC	ATCAGGTGCT	ATGAAAGCAA	GCCAATGGTT	CAAAGTATCA	1560
GATAAATGGT	ACTATGTCAA	TGGCTTAGGT	GCCCTTGCG	TCAACACAAC	TGTAGATGGC	1620
TATGAAGTCA	ATGCCAATGG	TGAATGGGTT	TAA			1653

(2) INFORMATION FOR SEQ ID NO:1256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1256:

AGAGGAAGCG	ATGTAATGGC	TAGAGAAGGC	TTTTTTTACAG	GTCTAGATAT	TGGAACAAGC	60
TCTGTCAAGG	TGCTTGTGGC	CGAGCAGAGA	AATGGTGAAT	TAAATGTAAT	TGGCGTGAGT	120
AATGCCAAAA	GTAAAGGTGT	AAAGGATGGA	ATTATTGTTG	ATATTGATAC	AGCAGCAACT	180
GCTATCAAGT	CAGCCATTTC	CCAAGCGGAA	GAAAAGGCAG	GCATTTTCGAT	TAAATCAGTG	240
AATGTCGGCT	TGCCTGGTAA	TCTTTTGCAG	GTAGAACCAA	CTCAGGGGAT	GATTCCAGTA	300
ACATCTGATA	CTAAGGAAAT	TACGGATCAA	GATGTTGAAA	ATGTTGTCAA	ATCAGCTTTG	360
ACAAAGAGTA	TGACACCTGA	CCGTGAAGTC	ATTACCTTTA	TTCCTGAAGA	ATTTATTGTG	420
GATGGTTTCC	AAGGGATTTC	TGACCCACGT	GGTATGATGG	GGGTTTCGCCT	TGAAATGCGT	480
GGTTTGCTTT	ATACAGGACC	TCGTACTATC	TTGCACAAAT	TGCGTAAGAC	GGTTGAGCGT	540
GCAGGTGTTT	AGGTTGAAAA	TGTTATCATT	TCACCACTAG	CAATGGTTCA	GTCTGTTTTG	600
AATGAAGGGG	AACGTGAATT	TGGTGCTACA	GTGATTGATA	TGGGGGCAGG	TCAAACGACT	660
GTCGCTACAA	TCCGTAATCA	AGAACTCCAG	TTCACACATA	TTCTCCAAGA	AGGTGGAGAT	720
TATGTAAC TA	AAGATATCTC	CAAGGTTTTG	AAAACCTCTC	GCAAATTAGC	GGAAGGCTTG	780
AAACTGAATT	ACGGGGGAAGC	CTATCCGCCCT	CTTGCAAGCA	AAGAAACCTT	CCAAGTAGAG	840
GTTATTGGAG	AAGTGGAAGC	AGTCGAAGTG	ACGGAAGCCT	ACTTGTCAGA	AATTATTTCT	900
GCACGAATCA	AGCACATCCT	TGAACAAATC	AAGCAAGAAT	TAGATAGAAG	GCGTCTATTG	960

GACCTCCCTG	GTGGTATTGT	CTTAATCGGT	GGGAATGCCA	TTTTACCAGG	TATGGTTGAG	1020
CTTGCTCAGG	AAGTCTTTGG	CGTCCGTGTC	AAGCTTTATG	TTCCAAATCA	AGTTGGTATC	1080
CGTAATCCAG	CCTTTGCGCA	TGTGATTAGT	TTATCAGAAT	TTGCGGGTCA	ATTAACAGAA	1140
GTTAATCTTT	TGGCTCAGGG	AGCGATAAAA	GGTGAGAATG	ACTTAAGTCA	TCAGCCAATT	1200
AGTTTTGGTG	GGATGCTGCA	AAAAACAGCT	CAGTTTGTAC	AATCAACGCC	TGTTCAACCA	1260
GCTCCTGCTC	CAGAAGTAGA	GCCGGTGGCG	CCTACAGAAC	CAATGGCGGA	TTCCAACAA	1320
GCTTCACAAA	ATAAACCGAA	ATTAGCAGAT	CGTTTCCGTG	GCTTGATCGG	AAGCATGTTT	1380
GACGAATAA						1389

(2) INFORMATION FOR SEQ ID NO:1257:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...213
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1257:

TGGGTAGGCG	AAAAGTTACA	ATCTGGAGAG	TACGAAATTC	GTACTCTCTT	TTTTGATGTT	60
CAAAGTCATC	AAAATCCGTT	TTTAAAAATT	GTTAAAGTTC	CGGAAACCAA	AGGCTTTGCA	120
CTTGATAACC	TTAATCAAAT	TATTGGTCGC	TTCAAGTTTA	GCGTTGGAAT	AAGGCAGCTT	180
AAGTGCGTTG	ATAATCTTAT	CTCTATCCCT	TAA			213

(2) INFORMATION FOR SEQ ID NO:1258:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 222 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1258:

TTTCTGGGCG	ACCAAAGGTC	ACTCAGTAGA	CCATCAGTAA	GTTTGGTTCC	TGTAAATGAC	60
CCAACCTCTT	TGTGGATCAA	CTCTGGGGTA	GCAACCCTTA	AGAAATACTT	TGACGGGACC	120
ATTATCCCTG	AAAATCCACG	TATTACCAAT	GCCCCAAAAG	CTATCCGTAC	TAACGACATC	180
GAAAACGTAG	GGCAAGACTG	CGCGTCACCA	TACCATGTTT	GA		222

(2) INFORMATION FOR SEQ ID NO:1259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1259:

AGAAACAGCC	TTTGTCTTGA	ACTATTTTGG	TGTGGAAGCA	CACGTGTTAT	CACTTCTGCC	60
AAAGCAGAGG	GGGCAGAGCA	AGTTATCTTG	ACTGACCACA	ATGAATTCCA	ACAATCTGTA	120
TCAGATATCG	CTGAAGTAGA	AGTTTACGGT	GTTGTAGACC	ACCACCGTGT	GCTAACTTTG	180
AAACTGCAAG	CCCACTTTAC	ATGCGTTTGG	AGCCAGTTGG	ATCAGCGTCT	TCAATCGTTT	240
ACCGTATGTT	CAAAGAACAT	GGTGTAG				267

(2) INFORMATION FOR SEQ ID NO:1260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1260:

TTTTCCTTTAG	AAAATATTAT	CAGAAGAAAAG	TTGAGAAAAA	TGGCAGAAAA	AACATATCCT	60
ATGACCCCTTG	AGGAAAAGGA	AAAACCTGAA	AAAGAATTAG	AAGAATTGAA	ATTGGTTCGT	120
CGACCAGAAG	TGGTAGAACG	CATTAAGATT	GCCCCGTTTCAT	ACGGTGACCT	TTCAGAAAAAC	180
AGTGAGTACG	AAGCAGCTAA	GGATGAACAA	GCCTTTGTCTG	AAGGACAAAT	CTCTAGCTTA	240
GAAACAAAAA	TCCGCTATGC	TGAAATCGTC	AATAGCGACG	CAGTTGCCCA	GGACGAAAGTA	300
GCGATTGGTA	AAACAGTCAC	CATCCAAGAA	ATTGGTGAGG	ACGAAGAAGA	AGTTTATATT	360
ATCGTAGGTT	CAGCTGGTGC	GGATGCCTTT	GCAGGTAAGG	TTTCAAATGA	AAGCCCAATT	420
GGGCAGGCCT	TGATTGGCAA	GAAAACAGGT	GATACAGCAA	CCATTGAAAC	GCCTGTTGGT	480
AGCTATGATG	TAAAAATCTT	GAAGGTTGAA	AAAACAGCCT	AA		522

(2) INFORMATION FOR SEQ ID NO:1261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1261:

AGTATGTTAG	AAAATGGCGA	TTTGATTTTT	GTGAGAGATG	GGTCAGACAT	GGGACAGGCC	60
ATCCAGACTT	CCACAGGTAA	CTATAGCCAT	GTTGCCATTT	ATTTGGATGG	GATGATTTAT	120
CATGCTAGTG	GACAGGCTGG	TGTTGTCTGT	CAAGAACCGG	CAGACTTCTT	TGAGTCCAAT	180
CATTTATACG	ACCTCTATGT	TTACCCAGAA	ATGGATATCC	AGTCGGTGAA	GGAAAAGAGCT	240
TGCAGACATC	TTGGAGCACC	CTACAATGCT	TCTTTCTATC	CAGATGCAGC	TGGTTTCTAC	300
TGCTCCCAGT	ATATAGCAGA	AATCCTACCT	ATTTTTGAAA	CTATTCCTAT	GAAAATTTGGA	360
GATGGGGAAC	AGGAGATTAG	TGATTTTTTG	AGGGAGTATT	ACATAGAACT	AGGTCTGCCT	420
GTTCTCTCTG	ACCAAGCTGG	GACCAATCCT	AGTCAGTTGG	CAGCATCGCC	TCTGTTACAA	480
TGTAAAGAAA	GGAATCTTCA	TGATTCAGAT	TTTTAA			516

(2) INFORMATION FOR SEQ ID NO:1262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1262:

```
AAAAATGTTAG AAAACGATAT TAAAAAAGTC CTCGTTTCAC ACGATGAAAT TACAGAAGCA      60
GCTAAAAAAC TAGGTGCTCA ATTAACATAA GATTATGCAG GAAAAAATCC AATCTTAGTT      120
GGGATTTTAA AAGGATCTAT TCCTTTTATG GCTGAATTGG TCAAACATAT TGATACACAT      180
ATTGAAATGG ACTTCATGAT GGTTCCTAGC TACCATGGTG GAACAGCAAG TAGTGGTGTT      240
ATCAATATTA AACAAGATGT GACTCAAGAT ATCAAAGGAA GACATGTTCT ATTTGTAGAA      300
GATATCATTG ATACAGGTCA AACTTTGAAG AATTTGCGAG ATATGTTTAA AGCAAGAGAA      360
GCAGCTTCTG TTAAATATGC TACCTTGTTG GATAAACCAA GAAGGACGTG TTGTAGAAAT      420
TGA                                                                    423
```

(2) INFORMATION FOR SEQ ID NO:1263:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 864 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1263:

```
AAAGGTCTAG AGATGATTTT AATTACAGGG GCAAATGGCC AATTAGGAAC GGAAC TTCGC      60
TATTTATTGG ATGAACGTAA TGAAGAATAC GTGGCAGTAG ATGTGGCTAA GATGGACATT      120
ACCAATGAAG AAATGGTTGA GAAAGTTTTT GAAGAGGTGA AACCGACTTT AGTCTACCAT      180
TGTGCAGCCT ACACCGCTGT TGATGCAGCA GAGGATGAAG GAAAAGAGTT GGACTTCGCC      240
ATCAATGTGA CGGGGACAAA AAATGTCGCA AAAGCATCTG AAAAGCATGG TGCAACTCTA      300
GTTTATATTT CTACCGACTA TGTCTTTGAC GGTAAGAAAC CAGTTGGACA AGAGTGGGAA      360
GTTGATGACC GACCAGATCC ACAGACAGAA TATGGACGCA CTAAGCGTAT GGGGGAAGAG      420
TTAGTTGAGA AGCATGTGTC TAATTTCTAT ATTATCCGTA CTGCCTGGGT ATTTGGAAAT      480
TATGGCAAAA ACTTCGTTTT TACCATGCAA AATCTTGCGA AAAC TCATAA GACTTTAACA      540
GTTGTAAATG ATCAGTACGG TCGTCCGACT TGGACTCGTA CCTTGGCTGA GTTCATGACC      600
TACCTAGCTG AAAATCGTAA GGAATTTGGT TATTATCATT TGTCAAATGA TGCGACAGAA      660
GACACAACAT GGTATGATTT TGCAGTTGAA ATTTTGAAAG ATACAGATGT CGAAGTCAAG      720
```

CCAGTAGATT CCAGTCAATT TCCAGCCAAA GCTAAACGTC CGCTAAACTC AACGATGAGC	780
CTGGCCAAAG CCAAAGCTAC TGGATTTGTT ATTCCAATT GGCAAGATGC ATTGCAAGAA	840
TTTACAAAC AAGAAGTGAG ATAA	864

(2) INFORMATION FOR SEQ ID NO:1264:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...315
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1264:

AAGCTGCTAG AGGAGGGAAA GATGAAAACA AGAAAAATCC CTTTGCGCAA GTCTGTTGTG	60
TCTAACGAAG TGATTGATAA GCGTGATTTG CTCCGCATTG TTAAGAACAA GGAAGGACAA	120
GTCTTTATTG ATCTACGGG CAAGGCCAAT GGCCGCGGCG CTTATATCAA ACTAGACAAT	180
GCAGAAGCCC TAGAGGCGAA AAAGAAGAAG GTCTTTAACC GCAGCTTTAG CATGGAAGTG	240
GAAGAAAGCT TTTATGACGA GTTGATCGCT TATGTGGATC ACAAAGTGAA AAGAAGAGAG	300
TTGGGACTTG AATAA	315

(2) INFORMATION FOR SEQ ID NO:1265:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...492
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1265:

AATCAGCTAG	ATTGTAATCA	TGTAGTTAGT	AGAGATGATC	TAAATTTAGT	ATATGACTAT	60
TTATTCCAGA	AGGAACGATG	GGAGTCCTAT	GAGATAACGC	TGATTGGTAA	TTTATATCAT	120
CTTTTGGAAA	CAGATTATAT	TTACATGGTC	GGAAAAGAAA	TACTAGAACG	TACACATTAT	180
TACGAAAAAA	TCGGCAAGAA	TAGAAATTTA	GTTGTGTCAG	CTTGTTTAAA	TTTTTGGTTC	240
TGTTGCCCTTG	AAAAATTCACA	TCTAATATAT	GCAGACTACT	TTGAAATGAA	ATTACAAAAA	300
TTATTAAAAAG	ATGACACAAA	AGTTTTTTGAA	AAATCTACAT	TCAAATTTGT	AGAAGGATAT	360
AAAATATACC	TGACAGAATC	TAAAGAATCT	GGAATTAAAC	AAATGGACAA	TGTCATAAAA	420
TATTTTGAGT	TTATTGAATC	TAAAAGTATT	GCTTTATATT	TTCAAAAACG	ATTAAATGAG	480
CTGATAGATT	AA					492

(2) INFORMATION FOR SEQ ID NO:1266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1266:

CGAAAGCTAG	AGGTGAAAAG	AATGAACTA	AATCGAGTAG	TGGTAACAGG	TTATGGAGTA	60
ACATCTCCAA	TCGGAAATAC	ACCAGAAGAA	TTTTGGAATA	GTTTAGCAAC	TGGGAAAATC	120
GGCATTTGGTG	GCATTACAAA	ATTTGATCAT	AGTGACTTTG	ATGTGCATAA	TGCGGCAGAA	180
ATCCAAGATT	TTCCGTTCGA	TAAATACTTT	GTAAAAAAG	ATACCAACCG	TTTTGATAAC	240
TATTCCTTAT	ATGCCTTGTA	TGCAGCCCAA	GAGGCTGTAA	ATCATGCCAA	TCTTGATGTA	300
GAGGCTCTTA	ATAGGGATCG	TTTTGGTGTT	ATCGTTGCAT	CTGGTATTGG	TGGAATCAAG	360
GAAATTGAAG	ATCAGGTAAT	TCGCCCTTCAT	GAAAAAGGAC	CCAAACGTGT	CAAACCAATG	420
ACTCTTCCAA	AAGCTTTACC	AAATATGGCT	TCTGGGAATG	TAGCCATGCG	TTTTGGTGCA	480
AACGGTGTTT	GTAAATCTAT	CAATACTGCC	TGCTCTTCAT	CAAATGATGC	GATTGGGGAT	540
GCCTTCCGCT	CCATTAAAGTT	TGGTTTCCAA	GATGTGATGT	TGGTGGGAGG	AACAGAAGCT	600
TCTATCACAC	CTTTTGCCAT	CGCTGGTTTC	CAAGCCTTAA	CAGCTCTCTC	TACTACAGAG	660
GATCCAATC	GTGCTTCGAT	CCCATTTGAT	AAGGATCGCA	ATGGGTTTGT	TATGGGTGAA	720
GGTTCAGGGA	TGTTGGTTCT	AGAAAGTCTT	GAACACGCTG	AAAAACGTGG	AGCTACTATC	780
CTGGCTGAAG	TGGTTGGTTA	CGGAAATACT	TGTGATGCCCT	ACCACATGAC	TTCTCCACAT	840
CCAGAAGGTC	AGGGAGCTAT	CAAGGCCATC	AACTAGCCT	TGGAAGAAGC	TGAGATTTCT	900
CCAGAGCAAG	TAGCCTATGT	CAATGCTCAC	GGAACGTCAA	CTCCTGCCAA	TGAAAAAGGA	960
GAAAGTGGTG	CTATCGTAGC	TGTTCTTGGT	AAGGAAGTAC	CTGTATCATC	AACCAAGTCT	1020
TTTACAGGAC	ATTTGCTGGG	GGCTGCGGCG	TGCAGTAGAA	GCTATCGTCA	CCATCGAAGC	1080
TATGCGTCAT	AA					1092

(2) INFORMATION FOR SEQ ID NO:1267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1267:

GAGGGGCTAG AGATTATCCC CTACTCGATA TTTTTTTTTT TCGTATTTCA TAAACATTTC	60
ATATTTGGGT TTTATAATAG TCTTACAAAT ATGGAGGTGA CAAATGAATC CAATCCAAAG	120
ATCTTGGGCT TATGTCAGCA GAAAGCGACT GAGAAGTTT ATTTTATTC TGATTTTATT	180
GGTCTTATTG GCCGGAATTT CAGCCTGTTT GACTCTGATG AAGTCCAACA AAACAGTAGA	240
AAGCAATCTT TATAA	255

(2) INFORMATION FOR SEQ ID NO:1268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 855 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1268:

CTGTTTATAG ACAACATGGC TTTCGGTTTG AAATTGCGTA AATACAGCAA AGAAGACATT	60
AACAAACGTG TTCAAGAAGC AGCTGAAATA CTTGGATTGA AAGAATTCTT GGAACGTAAA	120
CCGGCTGACC TTTCAGGTGG TCAACGTCAA CGTGTTGCCA TGGGGCGTGC GATTGTCCGT	180
GATGCGAAAAG TATTCTTGAT GGACGAACCT TTGTCAAAC TGGATGCCAA ACTTCGTGTA	240
TCAATGCGTG CTGAAATCGC TAAAATTCAC CGTCGTATCG GAGCTACAAC TATCTATGTA	300
ACTCACGACC AAACAGAAGC GATGACACTT GCAGACCGTA TCGTTATTAT GTCAGCTACT	360
AAGAACCCTG CTGGTACAGG TACAATCGGA AGTGTAGAAC AAATCGGTAC TCCTCAAGAA	420
GTTTACAAAA ATCCAGTTAA CAAATTCTGT GCAGGATTCA TCGGAAGCCC AGCTATGAAC	480
TTCATCAACG TGAAATTGGT TGGTAGCGAA ATTGTTTCTG ACGGTTTCCG TTTGAAAGTG	540

CCAGAAGGAG	CATTGAAAGT	TCTTCGTGAA	AAAGGCTACG	AAGGAAAAGA	ATTGATCTTT	600
GGTATCCGTC	CAGAAAACGT	GAATGCAGAA	CCTGCTTTCC	TTGAAACATT	CCCAGACTGT	660
GTTGTAAAAG	CGACTATCTC	TGTATCAGAA	CTGCTTGGTT	CAGAATCTCA	CCTTTACTGC	720
CAAGTTGGTA	AAGACGAGTT	TGTTGCAAAA	GTTGATGCTC	GTGACTACTT	GCAAACAGGT	780
GCAACAGTTG	AGCTTGGATT	TGACTTGAAC	AAAGCACACT	TCTTCGATGT	AGAAACTGAA	840
AAAACAATCT	ACTAA					855

(2) INFORMATION FOR SEQ ID NO:1269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...921

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1269:

CCCTCTATAG	AAAGGATTTT	TATGACATCA	AAAGTTAGAA	AGGCAGTTAT	CCCTGCTGCT	60
GGACTAGGAA	CTCGATTTTT	ACCAGCAACC	AAGGCCCTTG	CCAAAGAAAT	GTTGCCAATC	120
GTAGACAAAC	CAACTATCCA	GTTTATCGTG	GAAGAAGCTC	TCAAATCAGG	TATTGAAGAT	180
ATTCTAGTTG	TCACTGGTAA	ATCAAAACGT	TCTATTGAGG	ACCACTTCGA	TTCAAAC TTC	240
GAATTGGAAT	ATAACCTCAA	AGAAAAAGGG	AAAACAGATC	TTTTGAAGCT	AGTTGATGAA	300
ACAACTGGCA	TGCGTCTGCA	TTTTATCCGC	CAAACATCATC	CACGCGGTCT	CGGAGATGCT	360
GTTTTGCAAG	CCAAGGCTTT	CGTCGGAAAT	GAACCTTTTG	TCGTTATGCT	TGGTGATGAC	420
TTGATGGATA	TCACAGACGA	AAAGGCTGTT	CCACTTACCA	AACAACATCAT	GGATGACTAC	480
GAGCGTACCC	ACGCGTCTAC	TATCGCTGTC	ATGCCAGTCC	CTCATGACGA	AGTATCTGCT	540
TACGGGGTTA	TTGCTCCGCA	AGGCGAAGGA	AAAGATGGTC	TTTACAGTGT	TGAAACCTTT	600
GTTGAAAAAC	CAGCTCCAGA	GGACGCTCCT	AGCGACCTTG	CTATTATCGG	ACGCTACCTC	660
CTCACGCCTG	AAATTTTTGA	GATTCTCGAA	AAGCAAGCTC	CTGGTGCTGG	AAATGAAATC	720
CAACTTACTG	ATGCAATCGA	TACTCTTAAT	AAAACACAGC	GTGTTTTTGC	CCGTGAATTT	780
ACAGGAGCTC	GTTACGACGT	TGGGGATAAG	TTTGGCTTTA	TGAAAAACATC	TATTGACTAC	840
GCCCTCAAAC	ACCCACAAGT	CAAAGATGAT	TTGAAGAATT	ACCTCATCCA	ACTTGAAAAA	900
GAATTGACTG	AGAAGGAATA	A				921

(2) INFORMATION FOR SEQ ID NO:1270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1270:

AGTAGAATAG	ATATTAAGGA	CCTATCTTTC	TCTTATTCCA	AAGACTCAGC	TCCTGTAATA	60
GAAAAATTTAA	ATTTGACTAT	TGAGCCAGGA	CAGAGAATTG	CACTAGTCGG	TCAATCGGGG	120
TCAGGAAAAA	GTACGTTATC	AAAAATACCA	TCAGGATTAT	ATAAGATTGA	TACAGGAAAA	180
GTTTTATTTG	ATGGTGTA	TATTAATCAA	ATAGATAAAA	AAATATTAAG	TCAAAAATTTA	240
GGAGTAGTTC	CACAGGATTC	GTTTTTATTG	AACAGAAGTA	TTCTTGATAA	TATAACTTTA	300
AAGCACGAAG	TTACTTCACA	AAAGATAGAG	GAAGTTTGTA	AAGCAGTTCA	AATCTATGAT	360
GAAATCATGG	CTATGCCGAT	GAAATTTAAT	ACTATCATCT	CAGAGATGGG	GTCAAATATT	420
TCAGGTGGGC	AAAGGCAACG	GATAGCACTG	GCACGTGCAT	TAATAAATAA	TCCTAGTATT	480
GTAATTTTAG	ATGAAGCAAC	TAGTGCATTA	GACACTATTA	ATGAGAAAAG	AATAACAAAG	540
TATATACAAA	GTCAGGGTTG	TACTCAAATA	ATTATAGCTC	ATAGATTGTC	AACGATTAAG	600
GATGCGGATA	TTATTTTGT	AATGAAAGGT	GGTAAGATTG	TTGAGTCAGG	AAATCATAAG	660
TACTTAATGA	CTCTTGGTGG	AGAGTACTAC	AGCTTATATA	CAAAAAGGAA	ATGA	714

(2) INFORMATION FOR SEQ ID NO:1271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1271:

TTAGCAGTAG	ATTTCAAAAT	GATAAAAACG	TATAATAGTA	GGTGTAGTGT	ACTGCCCCCC	60
AAAAAGTTAG	ACAGAAAAAA	TCTAACTTTT	TGGGGTGTTT	TTATTATGAA	ATTAAGTTAT	120
GATGATAAAG	TTCAGATCTA	TGAACCTAGA	AAACAAGGAT	ATAGCTTAGA	GAAGCTTTCA	180
AATAAATTTG	GGATAAACAA	TTCTAATCTT	AGGTACATGA	TTAAATTTGAT	TGATCGTTAC	240
GGAATAGAGT	TCGGCAAAAA	AGGAAAAAAT	CGTTACTATT	CTCCTGATTT	AAAACAAGAA	300
ATGATTCATA	AAGTCTGA					318

(2) INFORMATION FOR SEQ ID NO:1272:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1080 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1080
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1272:

ATAGGAGTAG	AAATGACAAA	AGAAAAAAT	GTAATTTTGA	CTGCTCGCGA	TATTGTCGTG	60
GAATTTGACG	TTCGTGACAA	AGTATTGACA	GCCATTCGCG	GCGTTTCCCT	TGAACTAGTT	120
GAAGGAGAAG	TATTAGCCTT	GGTAGGTGAG	TCAGGATCAG	GTAAATCTGT	TTTGACAAAG	180
ACCTTCACAG	GTATGCTCGA	AGAAAATGGT	CGCATTGCCC	AAGGTAGTAT	TGACTACCGT	240
GGTCAGGATT	TGACAGCTTT	ATCTTCTCAC	AAGGAGTGGG	AACAAATTCG	TGGTGCTAAG	300
ATTGCGACTA	TCTTCCAGGA	CCCAATGACT	AGTTTGGACC	CCATTAAAAC	AATTGGTAGT	360
CAGATTACAG	AAGTTATTGT	AAAACACCAA	GGAAAAACAG	CTAAAGAAGC	GAAAGAATTG	420
GCCATTGACT	ACATGAATAA	GGTTGGCATT	CCAGACGCAG	ATAGACGTTT	TAATGAATAC	480
CCATTCCAAT	ATTCTGGAGG	AATGCGTCAA	CGTATCGTTA	TTGCGATTGC	CCTTGCCTGC	540
CGACCTGATG	TCTTGATCTG	TGATGAGCCA	ACAACCTGCC	TGGATGTAAC	TATTCAAGCT	600
CAGATTATTG	ATTTGCTAAA	ATCTTTACAA	AACGAGTATC	ATTTCACAAAC	AATCTTTATT	660
ACCCACGACC	TTGGTGTGGT	GGCAAGTATT	GCGGATAAGG	TAGCGGTTAT	GTATGCAGGA	720
GAAATCGTTG	AGTATGGAAC	GGTTGAGGAA	GTCTTCTATG	ACCCTCGCCA	TCCATATACA	780
TGGAGTCTCT	TGTCTAGCTT	GCCTCAGCTT	GCTGATGATA	AAGGGGATCT	TTACTCAATC	840
CCAGGAACAC	CTCCGTCACT	TTATACTGAC	CTGAAAGGGG	ATGCTTTTGC	CTTGCGTTCT	900
GACTACGCAA	TGCAGATTGA	CTTCGAACAA	AAAGCTCCTC	AATTCTCAGT	ATCAGAGACA	960
CATTGGGCTA	AAACTTGGCT	TCTTCATGAG	GATGCTCCAA	AAGTAGAAAA	ACCAGCTGTG	1020
ATTGCAAATC	TCCATGATAA	GATCCGTGAA	AAAATGGGAT	TTGCCCATCT	GGCTGACTAG	1080

(2) INFORMATION FOR SEQ ID NO:1273:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 780 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...780

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1273:

ACAGGAGTAG	AGATGAGTAT	TCGAGTAATT	ATTGCCGGTT	TTAAGGGAAA	GATGGGCCAG	60
GCTGCTTGTC	AGATGGTATT	GA CTGATCCA	GA CTTGGA CT	TGGTGGCAGT	TTTGGATCCT	120
TTTGAGTCTG	AGTCAGAAATG	GCAGGGTATT	CCTGTTTTCA	AGGATAAGGC	TGATTTAGCT	180
GGTTTTGAAG	CGGATGTCTG	GGTAGATTTT	ACTACTCCAG	CTGTTGCCTA	CGAAAATACA	240
CGTTTTTGCTC	TTGAAAATGG	CTTTGCTCCA	GTAGTTGGAA	CGACTGGTTT	CACGAGTGAA	300
GAAATTGCAG	AGCTAAAAGA	ATTTTCTCGT	GCCCAAGACT	TGGGTGGCCT	GATTGCCCCCT	360
AAC TTTGCCT	TGGGTGCTGT	CTTACTCATG	CAATTTGCGA	CGCAGGCTGC	CAAATATTTT	420
CCAAATGTGG	AGATTATTGA	GCTCCATCAT	GACAAGAAAA	AGGATGCTCC	GAGTGGAACA	480
GCCATTAAAA	CAGCTGAGTT	GATGGCAGAG	GTTCGAGAGT	CAATTCAGCA	AGGTGCAGCA	540
GATGAGGAAG	AGCTGATTGC	TGGTGCTCGT	GGTGCTGACT	TTGATGGTAT	GCGCATCCAC	600
TCAGTTCGTT	TGCCAGGCTT	GGTAGCTCAT	CAGGAAGTCA	TCTTTGGCAA	TCAGGGAGAA	660
GGGTTGACCC	TCCGTCATGA	CTCCTATGAT	CGCATCTCCT	TCATGACAGG	AGTCAATTTG	720
GGAATTAAAG	AAGTTGTCAA	GCGTCATGAG	CTTGCTCTATG	GATTAGAACA	CTTATTATGA	780

(2) INFORMATION FOR SEQ ID NO:1274:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1725 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1274:

TTCGGGGTAG	ATGTCTTTTT	CACATTTTCA	GGTTTCCTGA	TTACAGCTCT	ACTCATTGAA	60
GAA TTTTCTA	AAAACCATGA	GATTGATTTG	ATAGGATTTT	TTAGAAGACG	CTTTTATCGG	120
ATTGTGCCAC	CTGTGGTTTT	GATGGTCTTG	GTGACCATGC	CTTTTACTTT	CTTGGTTTCGC	180
CAAGACTATG	TTGCTGGAAT	TGGTGGCCAG	ATTGCGAGCG	TCTTAGGCTT	TATGACCAAC	240
TTCTATGAAC	TCCTAACAGG	TGGGAGTTAT	GAATCTCAGT	TCCATCCTCA	TTTGTTTTGTT	300
CATAATTGGA	GTCTGGCAGT	TGAGGTTTCA	TACTATATTC	TNTGGGGATT	GGCAGTTTGG	360
TTCTTATCCA	CACACGCTAA	ATCAAATGGT	CAGTTGAAGG	GGATGGTCTT	TCTCTTATCT	420
GCTGTTGCCCT	TCTTGATCAG	TTTCTTCTCC	ATGTTTATTG	GTAGTTTTCT	AGTGACCTCT	480
TATTCCTCTG	TTTATTTCTC	CAGTTTAACT	CATGTCTATC	CATTCTTTTT	GGGAAGTATG	540
TTAGCAACTA	TTGTAGGCGT	TCGTCAGACG	ACTTCCCTCG	TCAAGCAGTT	GGATAAAATC	600
TGGGATTTAC	GAAAGACTTT	GGTAGTTTTT	GGAGGAGGCT	TTGGTTTCCT	AGTTCTTTTG	660

ACTTTCTTTG	TCAAATTCAC	TTATCTTTTT	GCCTATCTTA	TCGGCTTCTT	ACTTGCCAGT	720
CTTGACGCTC	TTGCCATGAT	TCTGGCGGCG	CGTGTCTTAC	ATGAAAAGAC	ACATCATATA	780
CAGGAGCCGA	AGATTATCAG	CTTTTTAGCG	GATACTAGCT	ATGCGGTTTA	TCTTTTCCAT	840
TGGCCTTTCT	ATATCATTTT	CTCACAGTTG	ACATCAAATC	TTCTTGCTGT	ATTACTGACT	900
CTGATTTGTT	CTTATGGCTT	TGCCAGTCTG	TCATTTTATG	TATTGGAACC	TTGGATTGCA	960
GGCAAGAACA	CACCTATTGT	CCAAACCCCT	CGTCCCCGTC	CTTATATTCA	CGCAATTCTT	1020
GCAGCAGGTA	CAGGAATCTT	GACCATCATT	GTCTGCACGG	TGAACCTGTT	GGCAACACAA	1080
GTGGGAGCGT	TTGAGACAGA	CTTGACTGTC	AATGGCTTGA	AGCAAGCTGC	AACAAATATT	1140
GGCCAGACCA	AGGTGATGGC	AGAACGGGCA	GATGCAAACA	GTTTGGGAAT	TGCTGATGGC	1200
ACTATGTTAA	TTGGTGACTC	AGTGGCTTTA	AGGGCAAATA	CAGCACTACA	GACAGCTCTT	1260
CCTGGAGCAC	AGATTAACGC	GCAGGTCAGC	GTAACAACCA	AGACCGCAA	TGAAATCATG	1320
CTAAATAATA	GCCAGAATAA	ATTTTTACCT	AAGACGGTGG	TCATTGCGAC	TGGGGTAAAT	1380
AATCCTGAGA	ATTACAAGGA	TGACTGGGAC	AGTATCGTGA	AAAATCTTCC	TAAGGGACAC	1440
CATATGATTT	TGGTGACTCC	TTATGAGGGA	GATAAGACAA	AAGAGACCTA	TGCCATCGTT	1500
GAGAAGGCTG	CTGCCTATAT	GAGAGAATTG	GCAGAGAAGA	CACCTTACAT	TACGATAGCA	1560
GATTGGAATC	AAGTTGCGAA	AGAGCATCCA	GAAATTTGGG	CAGGAACAGA	CCAGGTTTAT	1620
TTCGGGAGTG	AGAGTAGCAC	TATCGAAGCA	GGAGCAAAAT	TGTATGCAGA	TACGATTGCC	1680
ACAGCTTTGC	AGACAGCTCA	AGACAAGCCG	GTAAATCAA	AATAA		1725

(2) INFORMATION FOR SEQ ID NO:1275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1275:

CCAAACTCAG	AAGGCTTAAT	TGGAGCAACT	ATTCCTGCCT	TTGAAGAAAA	ATATGGTATC	60
AAAATAGAAC	TGATTCAAGC	TGGTACTGGA	GAACTTTTCA	AAAAACTAGA	GTCAGAAAAA	120
GAAGTTCTTG	TAGCTGATGT	TATCTTTGGT	GGTTCTTATA	CACAATATGC	TACCCACGGA	180
GAACCTTTTG	AAAACTATAT	TTCAAAAGAA	AATGATAATG	TTATCAAAGA	ATATCAAAAC	240
ACAACTGGCT	TCTCTACTCC	TTATACACTA	GATGGTAGTG	TTTTAATCGT	CCACCCTGAT	300
TTAACTAAAG	GCATGAACAT	CGAAGGATAT	AGCGACCTTC	TCAAACCTGA	ACTAAAAGGA	360
AAAATCGCAA	CTGCTGACCC	AGCAAACCTC	TCTAGCGCCT	TTGCTCAATT	AACAAATATG	420
CTACAAGCTC	AAGGTGGTTA	CAAAGATGAT	AAGGCTTGGT	CTTATGTAAA	AGATCTTTTC	480
ACACTTATTG	ATGGTATAGT	AAAATGA				507

(2) INFORMATION FOR SEQ ID NO:1276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1203 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1276:

GGGAAATCAG	AAGGAGCATT	TTCGTCAGGG	CAAGCCGAAG	TGATTGCCTA	TTATCCTCTC	60
CAAGGGGAGA	AAGTGATTTT	CTCTGTTAGG	GAGTTGATAA	ATCAAGATGT	TAAGGACAAG	120
CTAGAAAGTA	AGGACAATCT	TGTTTTCTAC	TATACAGAGC	AAGAAGAGTC	AGGTTTAAAG	180
GGAGTCGTTA	ATCGTAATGT	GACCAAACAA	ATCTATGATT	TAGTTGCTTT	TAAGGTTGAA	240
GAGACTGAAA	AGACCAGTCT	AGGAAAGGTT	CACTTAACAG	AAGATGGGCA	ACCTTTTACA	300
CTTGACCAAC	TGTTTTCAGA	TGCTAGTAAG	GCTAAGGAAC	AGCTGATAAA	AGAGTTGACC	360
TCCTTCATAG	AGGATAAAAA	AATAGAGCAA	GACCAGAGTG	AGCAGATTGT	AAAAAACTTC	420
TCTGACCAAG	ACTTGTCTGC	ATGGAAATTTT	GATTACAAGG	ATAGTCAGAT	TATCCTTTAT	480
CCAAGTCCTG	TGGTTGAAAA	TTTAGAAGAG	ATAGCCTTGC	CAGTATCTGC	TTTCTTTGAT	540
GTTATCCAAT	CTTCGTACTT	ACTCGAAAAA	GATGCGGCCT	TGTACCAATC	TTACTTTGAT	600
AAGAAATATC	AAAAAGTTGT	CGCTCTAACC	TTTGATGATG	GTCCAAATCC	AGCAACGACC	660
CCGCAGGTAT	TAGAGACCCT	AGCTAAATAT	GATATTAAAG	CGACTTTCTT	TGTGCTTGGG	720
AAAAATGTTT	CTGGGAATGA	GGACTTGGTG	AAGAGGATAA	AATCTGAAGG	TCATGTTGTT	780
GGAAACCATA	GTTGGAGCCA	TCCGATTCTC	TCGCAACTCT	CTCTTGATGA	AGCTAAAAAG	840
CAGATTACTG	ATACTGAGGA	TGTGCTAACT	AAAGTGCTGG	GTTCTAGTTC	TAAACTCATG	900
CGTCCACCTT	ATGGTGCTAT	TACAGATGAT	ATTTCGCAATA	GCTTGGAATT	GAGCTTTATC	960
ATGTGGGATG	TGGATAGTCT	GGACTGGAAG	AGTAAAAATG	AAGCATCTAT	TTTGACAGAA	1020
ATTCAGCATC	AAGTAGCTAA	CGGCTCTATC	GTTTTGATGC	ATGATATTCA	CAGTCCGACA	1080
GTCAATGCCT	TGCCAAGGGT	CATTGAGTAT	TTGAAAAATC	AAGGTTATAC	CTTTGTGACC	1140
ATACCAGAGA	TGCTCAATAC	TCGCCTAAAA	GCTCATGAGC	TGTACTATAG	TCGTGATGAA	1200
TAA						1203

(2) INFORMATION FOR SEQ ID NO:1277:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1047 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1277:

AAAATGTCAG	ATTCACCAAT	CAAATATCGT	TTGATTAAGA	AAGAAAAACA	CACAGGAGCT	60
CGTCTGGGAG	AAATCATCAC	TCCCCACGGT	ACCTTTCCGA	CACCTATGTT	TATGCCAGTT	120
GGGACACAAG	CCACTGTCAA	AACTCAGTCA	CCTGAAGAAT	TGAAGGAGAT	GGGTTCGGGA	180
ATTATCCTAT	CAAACACCTA	TCATCTCTGG	CTTCGCCCTG	GAGATGAAC	CATTGCACGC	240
GCTGGTGGTC	TCCACAAGTT	CATGAATTGG	GACCAGCCTA	TCTTGACAGA	TAGTGGTGGT	300
TTTCAGGTTT	ATTCTTTAGC	AGATAGCCGT	AATATCACAG	AAGAAGGAGT	AACCTTTAAA	360
AATCATCTAA	ATGGTTCCTA	GATGTTCCCTA	TCCCCAGAAA	AAGCCATCTC	TATTCAGAAT	420
AATCTGGGTT	CAGACATCAT	GATGTCCTTT	GATGAATGTC	CTCAGTTTTA	TCAACCTTAT	480
GACTACGTTA	AGAAATCGAT	CGAGCGTACC	AGCCGTTGGG	CTGAGCGTGG	TTTGAAGGCT	540
CACCGTCGTC	CACATGACCA	AGGTTTGTTT	GGAATTGTGC	AAGGTGCAGG	ATTTGAAGAC	600
CTTCGCCGCC	AATCAGCTCA	TGATCTTGTC	AGCATGGATT	TCTCAGGCTA	CTCTATCGGT	660
GGTTTGGCAG	TGGGAGAAAC	CCATGAAGAG	ATGAATGCGG	TCTTGGA	CTT	720
CTGCTGCCTG	AAAATAAACC	TCGTTATCTG	ATGGGTGTGG	GAGCGCCAGA	TAGCTTGATC	780
GATGGGGTCA	TTCGTGGGGT	GGATATGTTT	GACTGTGTCT	TACCGACTCG	AATTGCTCGT	840
AACGGGACTT	GTATGACCA	TCAAGGACGT	TTGGTTGTGA	AAAATGCCCA	GTTTGTCTGAG	900
GACTTTACGC	CACCTGGATCC	TGAGTGTGAT	TGCTACACAT	GTAATAACTA	TACACGCGCT	960
TACCTTCGTC	ACCTGCTCAA	GGGTGATGAA	ACCTTTGGTA	TCCGCTTGAC	TAGCTACCAC	1020
AATCTTTACT	TCTTGCTTAA	CCTGATG				1047

(2) INFORMATION FOR SEQ ID NO:1278:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 447 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1278:

AGATGGTCAG	ATTGGGAAAAG	ATCCAGTCAA	GAGATTGGTG	AGCTGATAGT	GGAGACTATC	60
TTGGGTATTC	TAAGTAGTAG	AGGTATCCAT	TTAGCAGTTC	AAGGTTGTGA	GCATGTCAAT	120
CGGGCTCTCG	TTGTTGAACG	TCAGGTGGCA	GAGCAGTTTG	GTCTGGAAAT	TGTCAGTGTC	180
CATCCTACTC	TTCATGCAGG	AGGTTCGGGG	CAGTTGGCAG	CCTTTAAGTT	TATGCAGGAT	240
CCAGTTGAGG	TTGAATTTAT	CAAGGCTCAT	GCTGGATTGG	ATATCGGAGA	CACTGCAATT	300
GGCATGCATG	TCAAGCATGT	TCAGGTTC	CGG	ATTCGCCCTA	TTTTGAGAGA	360
GCCCATGTAA	CGGCACTGGC	TAGTCGTCCA	AAATTAATCG	GAGGTGCGCG	TGCGCACTAT	420
CCGCAAGACG	CTATTAGAAA	GTCTTGA				447

(2) INFORMATION FOR SEQ ID NO:1279:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 645 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...645
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1279:

GATGATACAG	AGAGCCTGAA	TTGGTCAGGT	GACGTGCTTA	TTTACATTAG	CCTGATAATG	60
AAAATGGAGA	GATTATCGAT	GGTTATATTG	GAATTGTACC	AAAATGATTA	TTCTAAAGAT	120
TTAGTAGCAT	TTGATTCCAT	AGAAGATGGG	AAAGCCTTTG	TAGCTCAAAT	CCCGGGATAC	180
ACTCTGGAAA	CAGAAGATGG	TTTTGAAGTG	GAGTATTTTA	ATCCTAAAAA	CATACCGGAT	240
TATATGGAAA	TTATTTTTTAA	CGGAAATATT	GTTCCTTTTAT	CTAAATTTAT	GTTCGATCCT	300
GAGGAAAATG	TAAACATTAT	TTGGAAAGAG	ATTTCAAATT	TATCCCTCAA	AAATGATAGA	360
GTGATCGAAG	GATATTCAAA	AATTGATGCA	TATGTCGTTA	ACAACCATGA	AGTTAAAGCC	420
TATGTGCAAA	CAAGAGAAAC	GAAGTATCGT	AAAGCAAAAG	ACTTCTTAGA	AAGCCGCGGA	480
TATGAAATCG	ACAGAAGCTT	TTTCGGAAGT	GAAGACGGTG	AAGCGATTCT	TTACAGAAAA	540
AAAGGGATCG	AAGTTTGGCA	TTTCTTGTGT	CACTTAGACC	CAATGTTTGT	AGAGATTGAA	600
GATGTAGAAG	GATATGTTAA	AGAAGAAGTT	GGAGAGATTC	AATAG		645

(2) INFORMATION FOR SEQ ID NO:1280:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1280:

AGAGATACAG	ACATGGATAA	ACAATACCTA	CACGAAAAGC	TGGATGCCAT	GCGCCAGAAT	60
TTTGTGAAT	CAACCCACCA	CGAACGAGCG	GTGGGCGTGC	TAGACCAAGC	GCATATGAGC	120
AAAAAATGC	TTAAAAATCA	GAAAAAATTA	GTTGCTCTTG	AAATGGAACG	GTGCCAGAGA	180
AAAATTGAGC	ACAAAGACTG	TTCCAAGATT	GACCAAAAAA	TCAAAGAGCA	GAAGGAGATA	240
TTTGAATCCT	GTTGTAAAAA	AGATTAA				267

(2) INFORMATION FOR SEQ ID NO:1281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1281:

GAAATCACAG	ATGCAGATAC	TCGAGCTTTG	GTAGCTGGAA	CCATGGTTGA	AAATCCAGAA	60
GGCTTCCACT	TTGATGATTT	ACAACTTCAA	ACTCATGCAG	ATAATGACAT	TGAAGCGCTC	120
GTTAGCCTAG	CCAATATGGA	TGGTGAGAAA	GTCGAATTTA	ATGCGACAGG	GCAAGGTTCC	180
GTTCAAGCAA	TCTTTAACGC	TATCGATAAG	TTCTTTAACC	AATCTGTTCC	TTTGGTGTCC	240
TACACTATCA	ATGCGGTAAC	AGATGGAATC	GATGCCCAGG	ATCGGGTTTT	GGTCACTGTT	300
GAAAACAGAG	ATACAGAAAC	CATCTTTAAT	GCAGCAGGGC	TTGATTTTGA	TGTGTTGAAG	360
GCTTCTGCTA	TTGCCTATAT	AAACGCTAAT	ACCTTTGTTC	AAAAAGAGAA	TGCAGGTGAG	420
ATGGGACGCA	GTGTTTCTTA	CCACGATATG	CCTAGTGTGT	AA		462

(2) INFORMATION FOR SEQ ID NO:1282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1282:

TCTGCGACAG	ATAGCAAGGA	AGAAGTAGAA	AGTCTTTTGA	GCAAGGCAAA	TCAACTCTTG	60
GAACAAATCC	ATGAAGAAGG	AATCAGACAA	TCCTTGGCAG	AAGAAGTAGA	AAATCTAAAA	120
GCTGCCACAA	ACAAGGTTGA	TGCAGACTTG	GATGAAGTAA	ACAGTCAGGT	AAAAGATGTT	180
TTGACTCGTA	TCGCTAGCGC	CCTTCAACAA	GAAAAGGAAA	ATGCTGAGCA	AGATTCTCAG	240
ACACTTGTA	TCTATCAAAA	ACTCTACGAT	ATTCTCATGT	CGCTTAGAAA	GTAA	294

(2) INFORMATION FOR SEQ ID NO:1283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1283:

CTATTTGCAG	ATAACAAGCA	TCTATATAAG	GTTATCAAAG	AAGACTTCCC	CATGACTCTA	60
AATGAATATA	TCTTACAATA	TCGCCTGAAA	CAAGCTATAG	ATAAGATGGC	TGAATCTCCC	120
AACTCCCCTT	TAAGCGCTAT	CTCTGACCAA	GTTGGATTTT	CAGACTATAA	ATATTTTGCC	180
AAAGTATTTA	AAAAGCATCT	CCATATTTCC	CCAAAGGAAT	TGAAATTACT	CGGAAGAATA	240
GTAAAATAG						249

(2) INFORMATION FOR SEQ ID NO:1284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1284:

CTGATTGCAG	AAGCTAAGAA	GCGTGACATT	CGTATCATCA	TGGACTTGGT	GGTTAATCAT	60
ACCTCAGATG	AACATGCTTG	GTTTGTGCGAA	GCCTGTGAAA	ATACTGACAG	CCCTGAGCGA	120
GACTACTATA	TCTGGCGCGA	TGAACCCAAT	GACCTAGATT	CTATCTTTAG	TGGGTCTGCT	180
TGGGAATACG	ATGAAAAGTC	AGGTCAATAC	TATCTCCACT	TTTTCAGCAA	AAAACAGCCG	240
GATCTCAACT	GGGAAAATGA	AAAAC TTCG	CAGAAAATTT	ATGAGATGAT	GAAC TTCGG	300
ATTGATAAAG	GTATTGGTGG	TTTCCGTATG	GATGTTATTG	ACATGATTGG	CAAAATTCCT	360
GACGAGAAGG	TAGTCAATAA	TGGTCCTATG	CTCCATCCCT	ATCTCAAGGA	AATGAATCAG	420
GCGACCTTTG	GAGATAAGGA	TCTCTTGACA	GTAGGGGAGA	CTTGGGGAGC	AACGCCAGAG	480
ATTGCCAAGC	TCTACTCTGA	TCCAAAGGGG	CAAGAA TTGT	CTATGGTCTT	CCAGTTTGAA	540
CATATCGGTC	TTCAGTATCA	GGAAGGTCAG	CCTAAATGGC	ACTATCAAAA	AGAGCTGAAT	600
ATCGCTAAGT	TAAAAGAAAT	CTTCAACAAA	TGGCAGACAG	AGTTAGGAGT	TGAGGACGGC	660
TGGAATTCCC	TCTTCTGGAA	CAACCATGAC	CTCCCTCGTA	TTGTCTCAAT	CTGGGGAAAT	720
GACCAAGAA	ACCGCGAAAA	ATCTGCCAAA	GCCTTTGCAA	TCTTGCTTCA	TCTTATGAGA	780
GGAAC TCCTT	ATATCTACCA	AGGTGAGGAG	ATTGGGATGA	CCAAC TATCC	GTTTGAAACA	840
CTGGATCAAG	TAGAAGATAT	TGAATCTCTC	AACTATGCGC	GTGAGGCTCT	TGAAAAAGGT	900
GTTCCGATTG	AAGAAAATCAT	GGACAGTATC	CGTGT TATTG	GACGTGACAA	TGCCCCGTACC	960
CCTATGCAAT	GGGACGAGAG	CAAAAACGCT	GGTTTCTCAA	CAGGTCAACC	TTGGTTGGCG	1020
GTTAATCCAA	ATTACGAGAT	GATCAATGTC	CAAGAAGCGC	TGGCAAATCC	AGATTCTATT	1080
TTCTATACCT	ATCAGAAACT	GGTCCAAATT	CGCAAGGAGA	ATAGCTGGCT	AGTTCGAGCT	1140
GACTTTGAAT	TGCTTGATAC	GGCTGATAAG	GTCTTTGCTT	ATATACGTAA	GGATGGCGAC	1200
CGTCGCTTCC	TAGTCGTGGC	TAATTTATCC	AATGACAAAC	AAAAC TTTTC	AGTAGATGGA	1260
AAAGTTAGAT	CTGTCTTGAT	TGAAAACACT	GCGGCTAAAG	AAGTACTTGA	AAAACAGGTC	1320
TTGGCTCCAT	GGGATGCTTT	CTGTGTGGAA	ATGACTGATT	AG		1362

(2) INFORMATION FOR SEQ ID NO:1285:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2328 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1285:

GAATATCAAG	ATAGACTAGA	CCAAGAATTG	TCTGTTATTG	ATGATATGGG	CTTTGATGAT	60
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TATTTCTTGG	TTGTTTGGGA	TTTGTTCGCT	TTTGGACGAT	CGAATGGCTA	TTATATGGGA	120
ATGGGAAGGG	GTTCTGCAGT	AGGCAGTTTG	GTTTCTTATG	CCTTAGACAT	CACGGGGACT	180
GACCCAGTAG	AGAAAAATCT	GATTTTTTGAA	CGCTTCTTAA	ATCGTGAACG	CTATACCATG	240
CCTGATATTG	ATATTGATAT	CCCAGATATT	TATCGTCCAG	ATTTTATCAG	ATATGTTGGT	300
AATAAATATG	GTAGTAAACA	TGCGGCACAA	ATCGTTACTT	TTTCAACCTT	TGGAGCCAAG	360
CAAGCTCTTC	GAGATGTCTT	GAAACGCTTT	GGTGTGCCAG	AGTATGAATT	ATCTGCAATT	420
ACTAAGAAAA	TCAGTTTTCG	TGACAACTTT	AAGTCGGCCT	ATGAGGGCAA	TCTCCAGTTT	480
CGTCAGCAAA	TCAATAGTAA	GTTAGAATAC	CAAAAAGCTT	TTGAGATTGC	TTGCAAGATA	540
GAGGGCTATC	CAAGGCAAAC	CTCTGTCCAT	GCGGCTGGTG	TTGTAATTAG	TGACCAAGAT	600
TTAACCAACT	ACATTCCCTCT	AAAGTATGGT	GATGAAATTC	CACTGACTCA	GTATGATGCT	660
CATGGAGTTG	AGGCTAGCGG	ACTTTTGAAG	ATGGACTTTC	TGGGACTACG	AAATTTGACC	720
TTTGTCCAGA	AGATGCAAGA	GTTGCTTGCT	GAAATAGAAG	GTATTCACCT	TAAAATTGAA	780
GAAATAGATT	TGGAAGACAA	AGAAACGTTA	GATTTATTTG	CCTCTGGAAA	TACAAAAGGT	840
ATCTTTC AAT	TTGAGCAACC	TGGTGCTATT	CGCTTGCTCA	AACGTGTTCA	ACCAGTCTGT	900
TTTGAAGATG	TCGTAGCAAC	TACTTCTCTA	AATCGACCGG	GTGCTAGTGA	CTATATCAAT	960
AATTTTGTGG	CAAGAAAGCA	TGGGCAGGAA	GAAGTGACTG	TTCTGGATCC	AGTACTGGAG	1020
GATATGTTGG	CTCCAACCTA	CGGCATAATG	CTCTATCAGG	AGCAGGTTAT	GCAGGTTGCC	1080
CAGCGATTTG	CCGGATTTAG	TCTTGGGAAA	GCCGATATTT	TGCGTCGGGC	TATGGGGAAA	1140
AAGGATGCCCT	CTGCCATGCA	TGAGATGAGG	GCTTCCTTTA	TTCAAGGTTT	ATTAGAGGCT	1200
GGTCATACTG	TGGAAAAAGC	AGAGCAGGTC	TTTGATGTTA	TGGAGAGGTT	TGCAGGCTAT	1260
GGTTTTAACA	GGTCACACGC	CTATGCCCTAC	TCAGCATTGG	CCTTCCAGTT	GGCTTATTTT	1320
AAAACACATT	ATCCAGCCAT	ATTTTATCAG	ATCATGTTGA	ATTCTGCCAA	CAGTGATTAC	1380
TTAATAGATG	CACTTGAAGC	AGGTTTTTGAA	GTGGCGCCTC	TGTCCATCAA	CACGATTCCC	1440
TATCACGATA	AAATTGCCAA	CAAGGCCATC	TATCTAGGTT	TGAAATCCAT	TAAAGGAGTC	1500
AGTAATGATT	TAGCTCTCTG	GATTATTGAA	CATAGACCTT	ATTCTAATAT	TGAAGATTTT	1560
ATAGCTAAAT	TACCTGAGAA	TTATCTGAAA	CTTCTCTGCT	TAGAACCCTT	GGTAAAAGTT	1620
GGTCTTTTCG	ATTCAATTTGA	AAAAAATCGT	CAAAAAGTAT	TTAATAACTT	AGCTAATCTA	1680
TTTGAATTTG	TGAAAGAGTT	GGGAAGTTTG	TTTGGAGATG	CTATTTATAG	TTGGCAGGAA	1740
TCGGAAGATT	GGACGGAACA	AGAAAAATTT	TATATGGAAC	AAGAGCTTTT	AGGGATAGGT	1800
GTCAGCAAAC	ATCCACTACA	AGCTATTGCA	AGTAAGGCTA	TTTACCCGAT	TACCCCAATC	1860
GGAAATTTGT	CAGAAAATAG	CTATGCTATT	ATTTTGGTTG	AAGTTCAGAA	AATAAAAGTG	1920
ATTCGTACCA	AAAAGGGTGA	AAATATGGCC	TTCTTACAGG	CAGATGATAG	TAAGAAAAAA	1980
TTGGATGTCA	CTCTCTTTTC	AGACTTATAT	CGTCAGGTTG	GACAGGAAAT	AAAAGAGGGA	2040
GCTTCTTACT	ATGTAAAAAG	AAAAATACAA	TCACGTGATG	GCCGTCTGCA	AATGATTGCA	2100
CAAGAAATAA	GAGAAGCAGT	TGCTGAACGC	TTTTGGATAC	AGGTGAAAAA	TCATGAATCG	2160
GATCAAGAAA	TTTCACGTAT	TTTAGAACAA	TTTAAAGGCC	CAATCCCAGT	CATCATCCGG	2220
TATGAAGAGG	AACAGAAAAAC	CATCGTTTCT	CCCCATCATT	TTGTAGCTAA	ATCCAATGAA	2280
TTAGAGGAGA	AATTGAATGA	AATCGTTATG	AAAACGATTT	ATCGCTAA		2328

(2) INFORMATION FOR SEQ ID NO:1286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1286:

CCTGGTCAAG	AAGTTACTTT	TAACGAAGTT	GTTCTTGTTG	GTGGTGAAAA	CACTGTTGTC	60
GGAAGTCCAC	TTGTTGCTGG	AGCTACTGTA	GTTGGAAGTG	TTGAAAAACA	AGGAAAAACA	120
AAGAAAGTGG	TTACTTACAA	GTACAAACCT	AAAAAAGGTA	GCCACCGTAA	ACAAGGTCAC	180
CGTCAACCAT	ATACAAAAGT	TGTCATCAAC	GCAATCAACG	CTTAA		225

(2) INFORMATION FOR SEQ ID NO:1287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1287:

AATCTACAAG	ATTTTACGAA	TAAACTAATG	AAACTAAAAA	AGGAGAAGAA	AATGGCAGAA	60
TTTACATTTG	AAATCGAAGA	GCACTTGTTG	ATTCTTTCTG	AAAACGAAAA	AGGTTGGACC	120
AAGGAAATTA	ACCGTGTGAG	CTTTAATGGT	GCCCCGCAA	AGTTTGATAT	TCGTGCTTGG	180
AGTCCAGACC	ATACTAAAAT	GGGCAAAGGG	ATTACTCTCT	CAAATGAAGA	ATTTCAAACG	240
ATGGTGGATG	CCTTTAAAGG	CAACTAA				267

(2) INFORMATION FOR SEQ ID NO:1288:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 876 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1288:

AAAGGACAAG	ATGTGACAAA	ACAAGCCTTC	AAAGAAGCAG	TTTTTAGGGC	AATTTTTTTTC	60
ATGAGTGCAA	CAGTAGCTGT	TGTAGCTATT	TTGCTAATCT	GTTTCTTTAT	TTTTAGTAAT	120
GGCTTACCTT	TCATGGCTAA	CTACGGCTTT	GCCCGTTTTT	TATTAGGCAG	TGATTGGTCG	180
CCAACGAACA	TTCCGGCAAG	CTATGGTATT	TTACCAATGA	TCGTTGGTTC	CTTATTAATT	240
ACCTTAGGAG	CGATTGTGAT	TGGGGTGCCA	ACAGGCATCT	TGACATCGGT	GTTTATGGTT	300
TATTATTGTC	CAAAGCCCGT	CTATGGCTTC	TTAAAATCAG	CTATCAACTT	GATGGCGGCC	360
ATTCCATCTA	TTGTTTATGG	TTTTTTCGGC	CTACAATTAT	TGGTGCCTTG	GATTAGAACC	420
TTTTTAGGAA	ATGGCATGAG	TGTCCTAACC	GCTTCGTTAC	TATTAGGAAT	AATGATTTTG	480
CCAACCATTA	TCAGTTTGTC	AGAATCTGCT	ATCCGAACAG	TTCCCAAAC	GTATTATTCT	540
GGTAGCTTGG	CTCTAGGAGC	TAGTCATGAA	CGGAGTATTT	TTAGTGTCAT	CTTGCCAGCT	600
GCGAGATCTG	GTATTTTATC	AGCAGTTATT	TTAGGAATCG	GTCGCGCAGT	AGGTGAAACC	660
ATGGCAGTTA	TTTTGGTGGC	AGGCAACCAG	CCGATTATTC	CAAGCGGACT	CTTTTCAGGA	720
ACCAGAACCT	TAACAACCAA	TATTGTTCTG	GAAATGGCTT	ACGCATCAGG	TCAGCATAGG	780
GAAGCCCTTA	TTGCAACCTC	AGCAGTTCTC	TTTTTCCTTA	TTCTCTTGAT	TAATGCCTAC	840
TTTGCCTACT	TGAAAGGAAA	ATCATCTTAT	GAGTAA			876

(2) INFORMATION FOR SEQ ID NO:1289:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1289:

ACTGTTAAAG	ACGTTGACTT	GAAAGGTAAA	AAAGTCCTCG	TTCGTGTTGA	CTTCAACGTA	60
CCATTGAAAAG	ATGGCGTAAT	CACTAACGAT	AACCGTATCA	CAGCAGCTCT	TCCAACCTATT	120
AAGTACATCA	TCGAACAAGG	TGGACGTGCA	ATTCTTTTCT	CTCACCTTGG	ACGTGTGAAA	180
GAAGAAGCTG	ATAAAGCTGG	TAAATCACTT	GCTCCTGTAG	CAGCAGACTT	GGCAGCAAAA	240
CTTGGTCAAG	ATGTTGTTTT	CCCAGGTGTC	ACTCGTGGTG	CTGAATTGGA	AGCGGCAATC	300
AACGCTCTTG	AAGATGGACA	AGTTCTCTTG	GTTGAAAACA	CTCGTTACGA	AGATGTTGAC	360
GGCAAGAAAAG	AATCTAAAAA	CGATCCTGAA	CTTGGTAAAT	ACTGGGCATC	ACTTGGAGAT	420
GGTATCTTCG	TAAACGATGC	ATTCGGTACA	GCTCACCGTG	CACACGCATC	TAACGTTGGT	480
ATCTCAGCAA	ACGTTGAAAA	AGCAGTTGCT	GGTTTCCTTC	TTGAAAACGA	AATTGCCTAC	540
ATCCAAGAAG	CAGTTGAAAC	TCCAGAACGT	CCATTTCGTGG	CTATCCTTGG	TGGTTCAAAA	600
GTTTCAGACA	AGATCGGTGT	TATCGAAAAAC	TTGCTTGAAA	AAGCTGATAA	AGTCCTTATC	660
GGTGGTGGGA	TGACTTACAC	ATTCTACAAA	GCACAAGGTA	TCGAAATCGG	TAATCACTTT	720
GTAGAAGAAG	ACAAATTGGA	TGTTGCGAAA	GCTCTTCTTG	AAAAAGCAAA	TGGTAAATTG	780

ATCTTGCCAG	TTGACTCAAA	AGAAGCTAAC	GCATTTGCTG	GTTACACTGA	AGTGCGTGAC	840
ACTGAAGGTG	AAGCAGTTTC	TGAAGGCTTC	CTTGGTCTTG	ACATCGGTCC	AAAACTATC	900
GCCAAATTTG	ACGAAGCTTT	GACTGGTGCC	AAAACAGTTG	TATGGAACGG	ACCTATGGGT	960
GTATTTGAAA	ACCCAGATTT	CCAAGCTGGT	ACAATCGGTG	TGATGGACGC	TATCGTGAAA	1020
CAACCAGGAG	TTAAATCAAT	CATCGGTGGT	GGTGACTCAG	CTGCCGCAGC	GATTAACCTT	1080
GGCCGTGCAG	ACAAGTTCTC	ATGGATTAGT	ACGGGTGGTG	GAGCATCAAT	GGAACCTTCTT	1140
GAAGGTAAGG	TTCTTCCACA	ACTTGCAGCC	TTGACAGAAA	AATAA		1185

(2) INFORMATION FOR SEQ ID NO:1290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2361

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1290:

ACATTCAAAG	ACAAGGAAAT	AAAGATGAAT	AAGAAAATAT	TAGAAACATT	AGAGTTCGAT	60
AAGGTCAAAG	CCTTGTTTGA	GCCTCATTTG	TTGACCGAGC	AGGGCTTGGA	GCAATTGAGA	120
CAGCTGGCTC	CGACTGCCAA	AGCAGATAAA	ATCAAACAGG	CTTTTGCTGA	GATGAAAGAA	180
ATGCAGGCTC	TTTTCGTCTG	GCAACCGCAT	TTTACTATTC	TCTCAACTAA	GGAAATTGCA	240
GGAGTCTGCA	AGAGGTTGGA	GATGGGAGCG	GATCTCAATA	TCGAGGAGTT	CCTACTCTTG	300
AAACGCGTGC	TTCTTACCAG	CCGAGAACTT	CAAAGTTTTT	ACGCCAATCT	GGAAAATGTC	360
AGCTTGGAAG	AATTAGCCCT	TTGGTTTGAG	AAATTACATG	ATTTTCCGCA	ATTACAAGGA	420
AATCTTCAGG	CCTTTAATGA	TGCGGGTTTC	ATTGAAAATT	TTGCCAGTGA	AGAATTGGCG	480
CGAATCCGTC	GAAAAATACA	TGATAGCGAG	AGTCAGGTAC	GCGATGTTTT	ACAAGACTTG	540
CTCAAGCAAA	AAGCGCAGAT	GTTGACGGAA	GGAATTGTTG	CTAGCAGAAA	TGGCCGTCAG	600
GTTTTACCAG	TCAAAAACAC	CTACCGCAAT	AAGATTGCAG	GTGTCTGTTCA	TGATATTTCT	660
GCTAGTGGAA	ACACCGTCTA	TATCGAACCA	CGTGAGGTAG	TCAAACTGAG	CGAAGAAATT	720
GCTAGTCTGC	GAGCAGATGA	GCGCTATGAA	ATGCTTCGCA	TTCTCCAAGA	AATTTCTGAG	780
CGTGTCCGCC	CTCATGCGGC	TGAGATTGCT	AATGACGCTT	GGATTATCGG	TCATCTGGAC	840
TTGATTTCGTG	CCAAGGTTTC	ATTTATCCAA	GAAAGACAAG	CAGTCGTGCC	TCAGCTGTCA	900
GAAAAATCAAG	AGATTCAACT	GCTCCATGTC	TGCCATCCTT	TGGTCAAAAA	TGCCGTCGCA	960
AATGATGTCT	ATTTTGGTCA	AGATTTAACA	GCTATTGTCA	TTACAGGTCC	CAATACAGGT	1020
GGGAAGACCA	TCATGCTCAA	AACTCTGGGC	TTGACACAGG	TCATGGCCCA	GTCAGGATTG	1080
CCGATTTTAG	CAGACAAGGG	AAGTCGTGTT	GGTATTTTTC	AAGAAATTTT	TGCTGATATT	1140
GGAGATGAGC	AGTCTATTGA	GCAGAGCTTG	TCTACCTTCT	CTAGCCATAT	GACCAATATC	1200
GTGGATATTC	TTGGCAAGGT	CAACCAACAT	TCACTCTTAC	TTTTGGATGA	GTTGGGGGCT	1260
GGTACTGATC	CCCAAGAGGG	AGCAGCCCTT	GCCATGGCTA	TTCTGGAGGA	CCTTCGCCCTG	1320
CGTCAAAATCA	AGACCATGGC	GACGACCCAC	TATCCAGAAC	TCAAGGCCTA	CGGTATTGAG	1380
ACAGCCTTTG	TGCAAAATGC	CAGTATGGAG	TTTGATACTG	CAACTCTTCG	CCCGACCTAT	1440
CGCTTTATGC	AGGGTGTTCC	TGGCCGAAGT	AATGCCTTTG	AAATTGCCAA	ACGTCTAGGC	1500
CTATCTGAAG	TTATCGTAGG	AGATGCCAGT	CAGCAGATCG	ATCAGGACAA	TGACGTCAAT	1560

CGTATCATTG	AGCAACTAGA	AGAGCAGACG	CTGGAAAGCC	GCAAACGCTT	GGACAATATC	1620
CGTGAGGTGG	AGCAAGAAAA	TCTCAAGATG	AACCGTGTGC	TAAAAAACT	CTACAACGAG	1680
CTTAATCGTG	AAAAGGAAAC	CGAGCTTAAC	AAGGCGCGTG	AACAGGCTGC	TGAGATTGTG	1740
GATATGGCCC	TAAGTGAAAG	TGACCAGATT	CTCAAAAATC	TCCACAGTAA	ATCCCAACTC	1800
AAGCCCCACG	AAATCATTGA	AGCCAAAGCC	AAGTTGAAAA	AATTGGCTCC	TGAAAAAGTG	1860
GACTTGTCTA	AAAACAAGGT	CCTTCAAAAG	GCCAAGAAAA	AACGAGCTCC	AAAGGTGGGA	1920
GATGATATCG	TGGTTCTCAG	TTATGGTCAG	CGTGGTACCT	TGACCAGTCA	ACTCAAGGAC	1980
GGTCGCTGGG	AAGCCCAAGT	TGGCTTGATT	AAGATGACCT	TGGAAGAGAA	AGAGTTTGAT	2040
CTTGTTCAAG	CCCAGCAAGA	AAAACCAGTC	AAGAAGAAAC	AGGTCAATGT	TGTGAAACGA	2100
ACTTCTGGGC	GAGGACCTCA	AGCTAGACTG	GATCTTCGAG	GCAAGCGCTA	TGAAGAAGCC	2160
ATGAATGAGC	TAGATGCCCT	CATCGACCAA	GCCTTGCTTA	ACAATATGGC	TCAAGTTGAT	2220
ATCATCCATG	GTATCGGAAC	AGGAGTCATC	CGTGAAGGAG	TTACCAAATA	CTTGCAAAGA	2280
AACAAACATG	TCAAGAGTTT	CGGCTATGCC	CCACAAAATG	CTGGAGGCAG	TGGTGCGACT	2340
ATTGTCACCT	TTAAAGGATA	G				2361

(2) INFORMATION FOR SEQ ID NO:1291:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 186 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...186
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1291:

TCCATCAAAG	AAATGCATAC	GATTGATGTC	ATCGGTAAGG	CTCCAGACGT	GACTCCAAGT	60
CAAGTGTCAA	AAGAGTTGAT	GGTAACTCTT	GGAACGTGTA	CGACAAGTTT	GAACAATTTA	120
GAGCGTAAGG	GCTACATTGA	GCGAGTTCGG	TCAGAACAGG	ATCGTCGTGT	GGTGCACTCTG	180
CATTTG						186

(2) INFORMATION FOR SEQ ID NO:1292:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1566 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1292:

AGAATCAAAG	AAAGAGAACT	TATGAATATT	CAAGAAGAAA	TTAAGAAACG	TCGTACCTTT	60
GCCATTATCT	CCCACCCGGA	CGCGGGGAAA	ACAACCATCA	CTGAGCAGTT	ACTCTACTTT	120
GGGGGTGAGA	TTCGTGAGGC	TGGTACGGTA	AAAGGGAAGA	AAACAGGGAC	TTTTGCTAAA	180
TCTGACTGGA	TGGATATCGA	GAAGCAACGT	GGGATTTCTG	TTACTTCATC	TGTTATGCAA	240
TTTGACTACG	ACGGCAAGCG	CGTGAATATC	TTAGACACGC	CAGGGCACGA	GGACTTCTCA	300
GAAGATACCT	ATCGTACCTT	GATGGCGGTG	GATGCTGCGG	TCATGGTCGT	GGACTCTGCC	360
AAGGGGATCG	AGGCTCAAAC	CAAGAAATTG	TTTGAGGTTG	TGAAACATCG	TGGCATTCCT	420
GTCTTTACCT	TTATGAACAA	GCTGGACCGT	GACGGTCGTG	AGCCTTTTGA	ACTCTTGCAA	480
GAATTGGAAG	AAATCTTGGG	CATTGCTAGC	TACCCATATG	ACTGGCCTAT	CGGGATGGGG	540
AAAGCCTTTG	AGGGCTTGTA	TGACCTCTAT	AACCAACGTT	TAGAACTTTA	TAAAGGGGAT	600
GAGCGTTTTG	CTAGCCTAGA	AGATGGAGAC	AACTTTTTTG	GTAGCAATCC	TTTCTACGAG	660
CAAGTCAAGG	ATGACATTGA	GCTTTTAAAT	GAAGCTGGGA	ATGAGTTTTC	AGAGGAAGCT	720
ATTCTGGCTG	GAGAATTGAC	GCCTGTCTTT	TTCGGTTCAG	CCCTGACAAA	CTTTGGTGTG	780
CAGACCTTCC	TTGAAATCTT	CCTCAAGTTT	GCTCCAGAAC	CACATGGTCA	CAAGAAAACA	840
GATGGTGACA	TTGTGGATCC	TTATGACAAG	GATTTCTCAG	GCTTTGTCTT	TAAAATCCAA	900
GCCAACATGG	ATCCTCGTCA	CCGTGACCGT	ATTGCCTTTG	TCCGTATCGT	ATCAGGCGAA	960
TTTGAGCGCG	GCATGAGTGT	CAATCTCCCT	CGTACTGGTA	AGGGGGCTAA	ACTATCTAAT	1020
GTTACCCAGT	TTATGGCGGA	GAGTCGTGAG	AATGTGACCA	ATGCCGTGGC	AGGTGATATT	1080
ATCGGGGTTT	ACGATACCGG	TACTTATCAG	GTTGGGGATA	CCTTGACGGT	TGGAAAAAAC	1140
AAGTTTGAAT	TTGAACCATT	GCCAACCTTT	ACTCCTGAAA	TTTTTCATGAA	AGTTTCTGCT	1200
AAGAAATGTTA	TGAAGCAAAA	ATCCTTCCAC	AAGGGGATTG	AGCAATTGGT	GCAAGAAGGA	1260
GCCGTTTCAGC	TTTATAAGAA	TTACCAAACA	GGTGAGTACA	TGCTGGGAGC	TGTTGGTCAA	1320
CTCCAGTTTG	AAGTCTTTAA	ACACCGTATG	GAAGGCGAAT	ACAATGCGGA	AGTGGTCATG	1380
AGCCCAATGG	GTAAAAAGAC	CGTTCGTTGG	ATCAAGCCTG	AGGACTTGGA	TGAACGGATG	1440
TCGTCAAGTC	GCAATATCTT	AGCCAAAGAC	CGTTTTGACC	AACCAGTCTT	TCTCTTTGAA	1500
AATGACTTTG	CCCTCCGCTG	GTTTGCGGAC	AAGTATCCAG	ACGTAGAGTT	AGAGGAGAAG	1560
ATGTGA						1566

(2) INFORMATION FOR SEQ ID NO:1293:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 744 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1293:

TTATCCAAAG	AAGATTTAAG	TGCTCACAAT	AACTGTATTA	TTTCTAGATG	GGAGGTTCTA	60
TTTTTGGATT	GGTCCATTGT	TGAACAATAT	CTACCACTAT	ATCAAAAGGC	ATTCTTTCTG	120
ACCTTGATA	TTGCAGTTTG	GGGAATTTTG	GGATCCTTTC	TGCTCGGTTT	AATCGTTAGT	180
ATCATCCGAC	ATTATCGAAT	CCCTGTTTTG	GCGCAAGTAG	CGACAGCCTA	CATTGAATTG	240
TCACGTAATA	CGCCCCTTTT	GATTCAACTC	TTCTTTCTCT	ACTTCGGTCT	TCCCCGAATC	300
GGGATTGTCC	TATCTTCAGA	AGTCTGTGCA	ACGCTTGGCC	TTGTCTTTTT	AGGAGGCTCC	360
TATATGGCAG	AATCTTTCCG	AAGTGGGCTG	GAAGCCATCA	GTCAAACCCA	GCAGGAGATT	420
GGCCTCGCTA	TTGGTCTGAC	ACCTCTACAG	GTCTTTCGCT	ATGTGGTTCT	TCCGCAAGCA	480
ACAGCGGTGG	CACTCCCCTC	CTTTAGTGCC	AATGTCATTT	TCCTTATCAA	GGAAACCTCT	540
GTTTTCTCAG	CAGTGGCTTT	GGCCGACCTC	ATGTACGTCG	CCAAGGATTT	GATTGGTCTC	600
TACTATGAGA	CAGACATTGC	GCTAGCTATG	TTGGTAGTTG	CTTATCTGAT	CATGCTGCTA	660
CCCATCTCAC	TGGTCTTTAG	CTGGATAGAA	AGGAGGACCC	GCCATGCAGG	ATTCGGGAAT	720
CCAAGTACTC	TTTCAAGGAA	ATAA				744

(2) INFORMATION FOR SEQ ID NO:1294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1294:

AACATAAAAG	AAAAGAAGAA	AAATCCACTT	TTTGTGGGTA	TCTTGTCGAT	TATTCTTGGT	60
TTGTTATTTT	CAATTGTAGG	CCTGATTTTG	GGTATCATAG	GATTGGTCTT	GGCTATTTCA	120
TACCAAAAAG	AGTCACAATT	AGACTATAAA	ATAGAAAAGA	TTCTTAATAT	CATAGGAATT	180
GTGATTTCTG	TAGTTAACTG	GATTGTAGCA	ATCGCCTTAA	TTTTTCGGTA	A	231

(2) INFORMATION FOR SEQ ID NO:1295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1295:

ATGTCAAAAG	ATAAGAAAAA	TGAGGACAAA	GAAATCCTCG	AAGAATTGAA	AGAGTTATCA	60
GAATGGCAGA	AACGAAACCA	AGAATATCTA	AAAAAGAAGG	CTGAAGAAGA	AGCGGCTCTA	120
GCTGAGGAGA	AGGAAAAGGA	AAGACAAGCT	CGGATGGGAG	AAGAATCTGA	GAAGTCAGAG	180
GACAAACAGG	ACCAGGAGAG	TGAAACAGAC	CAGGAAGATT	CAGAATCAGC	TAAGGAAGAG	240
TCTGAAGAAA	AAGTAGCATC	CTCAGAGGCT	GACAAAGAGA	AAGAAGAGAA	AGAAGAATCA	300
GAGTCTAAAG	AGAAGGAGGA	ACAGGATAAA	AAGCTTGCTA	AAAAGGCTAC	AAAGGAAAAA	360
CCAGCCAAAAG	CAAAGATTCC	TGGTATCCAT	ATCTTGCGAG	CCTTCACGAT	TTTATTTCCA	420
AGTCTGCTTT	TATTGATTGT	CTCTGCCTAC	TTGCTCAGTC	CTTATGCGAC	CATGAAAGAT	480
ATTCGTGTTG	AGGGAACGGT	GCAAACTACA	GCTGATGATA	TTCGACAGGC	TTCAGGCATT	540
CAGGATTCGG	ATTATACGAT	TAACCTTCTG	CTAGACAAGG	CAAAATATGA	AAAGCAGATT	600
AAGTCTAACT	ATTGGGTTGA	ATCAGCTCAA	CTTGTCTATC	AATTTCCAAC	TAAGATCACT	660
ATTAAAGGTCA	AGGAATATGA	TATTGTGGCC	TACTATATTT	CTGGTGAAAA	TCATTATCCT	720
ATTCTTTCCA	GTGGTCAGCT	TGAGACTAGT	TCTGTGAGTC	TGAACAGTTT	ACCAGAAACT	780
TATTTATCAG	TTCTCTTTAA	TGATAGTGAA	CAAAATCAAGG	TTTTTGTCTC	AGAACTTGCT	840
CAAATTAGCC	CAGAACTCAA	GGCGACTATC	CAAAAGGTGG	AATTAGCTCC	AAGCAAGGTG	900
ACATCCGATT	TAATTCGATT	GACCATGAAT	GATTCGGACG	AAGTCTTGGT	TCCCTCTATCT	960
GAAATGAGTA	AGAAACTGCC	ATATTACAGT	AAGATTAAGC	CTCAATTGTC	AGAACCGAGT	1020
GTGGTCGACA	TGGAAGCTGG	AATCTACAGC	TACACTGTGG	CGGATAAATT	AATTATGGAA	1080
GCTGAGGAAA	AAGCCAAACA	AGAGGCTAAG	GAAGCTGAGA	AAAAACAAGA	AGAAGAACAG	1140
AAAAACAAG	AGGAAGAGAG	CAATCGAAAC	CAAACGACCC	AGCGCTCATC	GCGTCGCTAG	1200

(2) INFORMATION FOR SEQ ID NO:1296:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 609 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1296:

CTTGCAAAAAG	AAACTAACTT	TGCAAAATTT	GATGCAACTG	TAGAAGTTGC	TTACAACTTG	60
AACATCGATG	TTAAAAAAGC	TGACCAACAA	ATCCTGTGTG	GAGCAATGGT	ATTGCCAAAC	120
GGTACTGGTA	AAACTTCACG	CGTTCTTGTT	TTCGCACGTG	GTGCAAAAGC	TGAAGAAGCA	180
AAAGCTGCTG	GTGCAGACTT	TGTTGGTGAA	GATGACCTTG	TTGCTAAAAT	CAACGACGGT	240
TGGTTGGACT	TCGACGTAGT	TATCGCTACA	CCTGATATGA	TGGCTCTTGT	TGGACGTCTT	300
GGACGTGTCC	TTGGACCACG	TAACTTGATG	CCAAACCCTA	AAACTGGTAC	TGTAACAATG	360
GATGTTGCTA	AAGCAGTTGA	AGAGTCTAAA	GGTGGTAAAA	TCACTTACCG	TGCTGACCGT	420
GCAGGTAAACG	TTCAAGCAAT	CATCGGTAAA	GTATCATTTG	AAGCTGAAAA	ATTGGTTGAA	480
AACTTCAAAAG	CTTTCAACGA	AACAATCCAA	AAAGCAAAAC	CAGCTACAGC	TAAAGGAACT	540
TACGTAACAA	ACTTGACTAT	CACAACTACT	CAAGGTGTTG	GTATCAAAGT	TGACGTAAAC	600
TCACCTTTAA						609

(2) INFORMATION FOR SEQ ID NO:1297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 873 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1297:

GTAGAAAAAG	AAATGGAGTT	ATTTATGAAA	ATCACAAACT	ATGAAATCTA	TAAGTTAAAA	60
AAATCAGGTT	TGACCAATCA	ACAGATTTTG	AAAGTGCTAG	AATACGGTGA	AAATGTTGAT	120
CAGGAGCTTT	TGTTGGGTGA	TATTGCAGAT	ATATCAGGTT	GTCGTAATCC	AGCCGTTTTT	180
ATGGAACGTT	ATTTTCAGAT	AGACGATGCG	CATTTGTCGA	AAGAGTTTCA	AAAATTTCCA	240
TCTTTCTCTA	TTTATAGATG	CTGTTATCCT	TGGGATTTGA	GTGAAATATA	TGATGCGCCT	300
GTACTTTTAT	TTTACAAGGG	AAATCTTGAC	CTCCTGAAAT	TCCCGAAGGT	AGCGGTCTGT	360
GGCAGTCGTG	CTTGTAAGCA	ACAGGGAGCT	AAATCAGTTG	AAAAAGTCAT	TCAAGGCTTG	420
GAAAAATGAAC	TGGTTATTGT	CAGTGGTCTG	GCCAAGGGCA	TTGACACAGC	AGCTCATATG	480
GCAGCTCTTC	AGAATGGCGG	AAAAACCATT	GCAGTGATTG	GAACAGGACT	GGATGTGTTT	540
TATCCTAAAAG	CCAATAAACG	CTTGCAAGAC	TACATCGGCA	ATGACCATCT	GGTTTTAAGT	600
GAATATGGAC	CTGGCGAACA	ACCTCTGAAA	TTTCATTTTC	CTGCCCCGTA	TCGCATCATT	660
GCTGGACTTT	GTCGTGGTGT	GATTGTAGCA	GAGGCTAAGA	TGCGTTCAGG	TAGTCTCATT	720
ACGTGTGAGC	GAGCAATGGA	AGAAGGACGC	GATGTCTTTG	CTATTCTCTG	TAGCATTTTA	780
GATGGACTAT	CAGACGGTTG	CCATCATTTG	ATTCAAGAAG	GAGCAAAATT	GGTCACCACT	840
GGGCAAGATG	TTCTTGCGGA	ATTTGAATTT	TAA			873

(2) INFORMATION FOR SEQ ID NO:1298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1298:

AAAGAAAAAG	AGGTTTTACA	GATGGCTATT	ATCTTACCAG	AACTTCCATA	TGCATACGAC	60
GCTTTGGAAC	CATACATCGA	TGCGGAAACA	ATGCATTTGC	ACCATGACAA	ACACCATCAA	120
ACTTATGTCA	ACAATGCCAA	TGCAGCTTTA	GAAAAACACC	CTGAAATCGG	TGAAGACCTT	180
GAAGCCTTGC	TTGCTGATGT	AGAATCTATC	CCAGCTGATA	TCCGTCAAGC	ACTTATCAAC	240
AATGGTGGCG	GACACTTGAA	CCACGCTCTT	TTCTGGGAAT	TGATGACTCC	CGAGAAAACA	300
GCTCCTTCAG	CAGAACTGGC	AGCAGCAATC	GATGCAACAT	TTGGTTCATT	TGAAGAATTG	360
CAAGCAGCCT	TCACTGCAGC	AGCAACAAC	CGTTTTGGTT	CAGGTTGGGC	ATGGTTGGTT	420
GTCAACAAAG	AAGGGAAACT	TGAAGTGACT	TCAACAGCAA	ACCAAGACAC	ACCAATCTCA	480
GAAGGTAAAA	AACCAATCTT	GGGCTTGGAC	GTTTGGGAAC	ATGCTTACTA	CGTGAAATAC	540
CGCAACGTGC	GTCCTGACTA	CATCAAAGCT	TTCTTTTCAG	TAATCAACTG	GAATAAAGTA	600
GATGAATTGT	ACGCAGCTGC	TAAATAA				627

(2) INFORMATION FOR SEQ ID NO:1299:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 909 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1299:

AATAGAAAAG	ATAAAAATAC	ACAAATCCTA	GTTTCATATAT	GTAAGGTAAA	TATAACTAGG	60
ATTTATAAAG	TTTACAGAGG	ACGGTCTATA	ATGTCAGATA	GAAAAAACAT	GAACTTTTTC	120
GCACTCAACT	CTAACCAAGA	GATTGCACAA	AAAAATGCCC	AAGCTGTTGG	TGTCCCACTT	180
GGAAAACTAT	CATCACGTCA	ATTTTCAGAC	GGAGAAATCC	AAGTAAATAT	CGAAGAAAGT	240
GTCCGTGGTT	ATGATGTTTA	CATCATCCAA	TCAACAAGTT	TCCCTGTCAA	CAACCACCTA	300

ATGGAATTGT	TAATCATGGT	CGATGCTTGT	GTGCGTGCAA	GTGCCCACAG	TATCAACGTT	360
GTCCTTCCAT	ATTTTGGCTA	TGCACGTCAA	GACCGCATTG	CTTGTCTCTG	TGAGCCACTT	420
ACAGCAAAAC	TAGTTGCCAA	TATGCTGGTT	AAGGCTGGAG	TTGATCGTAT	CCTGACTCTT	480
GATTTGCATG	CCGTTCAGGT	TCAAGGTTTC	TTTGATATTTC	CAGTGGATAA	TCTTTTCACT	540
GTTCCCCCTAT	TCGCAAAACA	TTACTGCGAT	AAAGGATTGC	TTGGTTCAGA	TGTTGTTGTC	600
GTTAGCCCTA	AAAATTTCAGG	TGTCAAACGT	GCGCGTAGCC	TGGCTGAATA	TCTTGATGCT	660
CCTATCGCCA	TTATCGACTA	CCCTCAAGAC	GATGCAACTC	GTAACGAAGG	TTATATTATT	720
GGTGATGTTG	AAGGTAAGAC	AGCTATCTTG	ATTGATGATA	TTTTAAATAC	AGGACGTACC	780
TTCTCTGAAG	CTTCTAAAT	CGTTGAACGT	GAAGGAGCTA	CAGAAATTTA	TGCTGTTTCT	840
AGCCACGGTC	TCTTCGTCGA	GGGAGCTGCT	GAGCTTCTTG	ACAATACTAA	TATTAAAGAA	900
ATCTTGTGA						909

(2) INFORMATION FOR SEQ ID NO:1300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1029 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1300:

AAAAGAAAAG	AGGAAATCAA	AATGAAGAAA	ACATGGAAAG	TGTTTTTAAC	GCTTGTAACA	60
GCTCTTGTAG	CTGTTGTGCT	TGTGGCCTGT	GGTCAAGGAA	CTGCTTCTAA	AGACAACAAA	120
GAGGCAGAAC	TTAAGAAGGT	TGACTTTATC	CTAGACTGGA	CACCAAATAC	CAACCACACA	180
GGGCTTTTATG	TTGCCAAGGA	AAAAGGTTAT	TTCAAAGAAG	CTGGAGTGGA	TGTTGATTTG	240
AAATTGCCAC	CAGAAGAAAG	TTCTTCTGAT	TTGGTTATCA	ACGGAAAGGC	ACCATTTGCA	300
GTGTATTTCC	AAGACTACAT	GGCTAAGAAA	TTGGAAAAAG	GAGCAGGAAT	CACTGCCGTT	360
GCAGCTATTG	TTGAACACAA	TACATCAGGA	ATCATCTCTC	GTAAATCTGA	TAATGTAAGC	420
AGTCCAAAAG	ACTTGTTTGG	TAAGAAATAT	GGGACATGGA	ATGACCCAAC	TGAAC'TTGCT	480
ATGTTGAAAA	CCTTGGTAGA	ATCTCAAGGT	GGAGACTTTG	AGAAGGTTGA	AAAAGTACCA	540
AATAACGACT	CAAAC'TCAAT	CACACCGATT	GCCAATGGCG	TCTTTGATAC	TGCTTGGATT	600
TACTACGGTT	GGGATGGTAT	CCTTGCTAAA	TCTCAAGGTG	TAGATGCTAA	CTTCATGTAC	660
TTGAAAGACT	ATGTCAAGGA	GTTTGACTAC	TATTCACCAG	TTATCATCGC	AAACAACGAC	720
TATCTGAAAG	ATAACAAAGA	AGAAGCTCGC	AAAGTCATCC	AAGCCATCAA	AAAAGGCTAC	780
CAATATGCCA	TGGAACATCC	AGAAGAAGCT	GCAGATATTTC	TCATCAAGAA	TGCACCTGAA	840
CTCAAGGAAA	AACGTGACTT	TGTCATCGAA	TCTCAAAAAAT	ACTTGTCAAA	AGAATACGCA	900
AGCGACAAGG	AAAAATGGGG	TCAATTTGAC	GCAGCTCGCT	GGAATGCTTT	CTACAAATGG	960
GATAAAGAAA	ATGGTATCCT	TAAAGAAGAC	TTGACAGACA	AAGGCTTCAC	CAACGAATTT	1020
GTGAAATAA						1029

(2) INFORMATION FOR SEQ ID NO:1301:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1179 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1301:

TTTATGAAAG	ATGTTAGTCT	ATTTTTATTG	AAAAAAGTTT	TCAAAAGTCG	TTTAAACTGG	60
ATTATCTTAC	TTTATTTTGC	ATCTGTACTC	GGTGTTTACCT	TTTATTTTAAA	TAGTCAGACT	120
GCAAACCTCAC	ACAGCTTGGG	GAGCAGGTTG	GAAAGTCGCA	TTGCAGCCAA	CGAGAGAGCC	180
ATCAATGAAA	ATGAAGCGAA	ACTTTCCCAA	ATGTCTGACA	CCAGCTCGGA	GGAATACCAG	240
TTTGCTAAAA	GTAATTTAGA	ATTGCAAAAA	AATCTTTTGA	AGCGAAAGAC	AGAAATTCTG	300
ACTTTATTAA	AAGAAGGGCG	CTGGAAAGAG	GCCTACTATC	TGCAGTGGCA	AGATGAAGAG	360
AAGAATTATG	AATTTGTATC	AAATGACCCG	ACTGCTAGCT	CTGGCTTAAA	AATGGGGGTT	420
GACCGCGAAC	GGAAGATTTA	CCAAGCCCTG	TATCCCTTGA	ACATAAAAGC	ACATACTTTG	480
GAGTTTCCGA	CCCACGGGAT	TGATCAGATT	ATCTGGATTT	TAGAGGCTAT	CATCCCAAGC	540
TTGTTTGTGG	TTGCTATTAT	TTTTATGCTA	ACACAACTAT	TTGCAGAAAG	ATATCAAAAT	600
CATCTGGACA	CAGCTCACTT	ATATCCTGTT	TCAAAAGTGA	CATTTGCAAT	GTCTTCTCTT	660
GGAGTTGGAG	TGGGCTATGT	AACTGTGCTG	TTTATCGGAA	TCTGTGGCTT	TTCTTTTCTA	720
GTGGGAAGTC	TGATAAGTGG	TTTTGGACAG	TTAGATTATC	CCTACCCGAT	TTATAGCTTA	780
GTGAAACAAG	AGGTAACAT	TGGAAAGATG	CAGGATGTAT	TATTTCCCTAG	CTTGCTCTTA	840
GCTTTCTTAG	CCTTTATCGT	CATTGTGGAA	GTTGTGTATT	TGATTGCTTA	CTTTTTCAAG	900
CAAAAAATGC	CTGTCCCTCT	TCTTTCCTC	ATTGGGATTG	TTGGCTTATT	GTTTGGCATC	960
CAAACCATTC	AGCCTCTTCA	AAAGATTGCA	CATCTGATTC	CCTTTACTTA	CTTGCGTTCA	1020
GTGGAGATTT	TATCTGGAAG	ATTACCTAAG	CAGATTGATA	ATGTCGATCT	AAATTGGAGC	1080
ATGGGAATGG	TCTTACTTCC	TTGCCTGATT	ATCTTTTTGC	TATTGGGAAT	TCTATTTATT	1140
GAAAGATGGG	GAAGTTCACA	GAAAAAAGA	ATTTTTTTAA			1179

(2) INFORMATION FOR SEQ ID NO:1302:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1905 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1302:

ATAATGAAAG	AAGAAAGAAG	ACAATTTTTT	GAAAGAATCG	ATGGAAACCA	ATGTCGTGAT	60
TATATCTTGT	CGCACTGTTC	AAAAGACTAT	GAGAAAGTCA	AGAGTTCCT	TGAACGCTTG	120
ATGGACAATC	GTTTTATGTT	TGATAGTCCT	TGGGATATGG	AGCCTTGTTT	AAAAATCCAT	180
CAAAACCAGC	CGATGGTATG	GGATCAAGTA	TTTGAAGATG	ATCCAGAATG	GGCTTATATG	240
CTCAATCGAC	AAGAATATCT	CTTGCAGTTT	ATGATAGGGT	ATGTGGTAGA	AGGAGATAAG	300
GACTATATTC	AAAAGTGCAA	GTTCTTTCTA	TTTGATTGGA	TTGAGCAGGT	GAGAGAATTT	360
TCTCCTCAAT	CCTTGATGAC	TAGAACCCTG	GATACGGGTA	TTCGTTCCCT	TACTTGGTTG	420
AAACTACTCT	TGCTTCTCTT	GAAATTTGAC	TTGCTAGAGG	AGAAAGAACT	AGAGAAAATT	480
TTGGTCAGTC	TAGAAAAGCA	GATTGACTTT	ATGAAAAGCT	ACTATCGCGC	CAAGTACACC	540
CTTAGTAACT	GGGGGATTTT	ACAAACAATT	CCGATGCTTG	CTATCTATCA	TTTCTTTTCA	600
GATAAGATGG	ACCTAGAAGA	AGCTTACCAT	TTTGCTTCAG	AGGAGTTGAA	ACAGCAAATT	660
GAGACACAGA	TTTTAGGAGA	TGGAAGCCAG	TTTGAACAGT	CGATTCTCTA	TCATGTAGAG	720
GTTTATAAAG	CCTTGCTGGA	TTTGTGTCTC	TTGCTTCCAG	ACTTGCAAGA	TAGTTACCAA	780
GAGTTGCTGG	AAAAGATGGC	GACCTATATT	CAAATGATGA	CAGGCTTAGA	TGGACGGACT	840
TTGGCTTTTG	GTGATAGCGA	TTCTACAGAA	ACGACAGAAA	TGTTGAGCCT	GTCTGTCTGT	900
GTTTTGAACA	AGGAAGACCT	TCTTAACGGT	CTGGATGTTA	AAGTTGATTT	GCTTAGCCTC	960
TTGTTCCCTG	GGCGAGAAAA	GGTCAAGCGA	CTGCAGGAAT	TTGAAAGGAG	AGCTTGGCAG	1020
CCTAAGTCCA	TGATCTTTGA	AGACTCTGGA	CATGTCTGCA	TTAAGGATGA	ACATCGTTAT	1080
CTATTTTTCA	AAAATGGTCC	GCTAGGAAGT	GCCCATAGCC	ATAGTGACGA	GAATAGTTTT	1140
TGCTTACAGT	ATCAAGGCCA	ACCTATTTTC	ATAGATGCTG	GGCGTTATTC	TTATCGGGAG	1200
ATATATGAAC	GTTATCTCTT	AAAGAGTGCT	TGGAGTCATT	CGACCTGCAT	TGTAGATGGG	1260
AAAGCTCCGG	AAAGAATCAC	GGGATCCTGG	GAATATGAAT	ACTATCCTCA	CTCCCTGTTT	1320
TGTCACCATA	AAGAAAGGGA	GGGAGTGCAT	TATATTGAGG	GGGCTTATTG	GTCAGCAGAA	1380
CCTGATTTGC	CTTATCTTCA	CAAGAGAAAA	ATCCTCATGT	TGGTAGAGGA	TGTCTGGCTC	1440
TTGGTAGATG	ACATCAGGTG	TCAAGGTCAG	CATGAGGCGT	TGACTCAGTT	TATCCTTGAC	1500
AAGGATGTGA	CCTATCAAGA	TGGGAAAATC	AATCAGTTGA	GACTATGGAG	TGAAGTTGAT	1560
TTTGATTTGG	AAGATACCAT	CATTTCTCCT	AAATACAATG	AGCTTGAAAAG	AAGTAGCAAA	1620
CTCACCAAGC	GCCAATTCTT	TGAGAATCAG	ATGCTGGATT	ATACCATCAT	TGCGCATGAG	1680
AGTTTTGAAA	TCATCCGTCA	TTCTGTCTAC	CAGACAGATG	ATCGTGAAGT	GGAAAATGCT	1740
CTGGCTTTTG	AAGTGAAAAA	TGACGAAACA	GACAAGCTGA	TTCTGTTATT	AAGCGAGGAT	1800
ATTTGTGTAG	GTGAAAAATT	GTGCCTCGTT	GACGGAACAA	AAATGCGTGG	AAAAATGTCTA	1860
GTATATGATA	AAATAAATGA	GAGAATGATT	CGCTTGCAGT	GCTAG		1905

(2) INFORMATION FOR SEQ ID NO:1303:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2181 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1303:

ATGATGAAAG	ATACATTCAA	AAATGTCTTG	TCTTTCGAAT	TTTGGCAAAA	ATTCGGTAAG	60
GCTTTGATGG	TAGTTATCGC	GGTTATGCCG	GCTGCTGGTT	TGATGATTTT	AATCGGTAAG	120
TCTATCGTGA	TGATTAAACC	AACCTTTACA	CCACTTGTCA	TCACAGGTGG	AATTCTTGAG	180
CAAATCGGTT	GGGGGGTTAT	CGGTAACCTT	CACATTTTGT	TTGCCCTAGC	CATTGGAGGA	240
AGCTGGGCTA	AAGAACGTGC	TGGTGGTGCT	TTCGCCGCTG	GTCTTGCCCT	CATCTTGATT	300
AACCGTATCA	CTGGTACAAT	CTTTGGTGTA	TCAGGCGATA	TGTTGAAAAA	TCCAGATGCT	360
ATGGTAACTA	CTTTCTTTGG	TGGTTCAATC	AAAGTTGCTG	ATTACTTTAT	CAGTGTTCCT	420
GAAGCTCCAG	CCTTGAACAT	GGGGGTATTG	GTAGGGATTA	TCTCAGGTTT	TGTAGGGGCA	480
ACTGCTTACA	ACAAATACTA	CAACTTCCGT	AAACTTCCTG	ATGCACTTTC	ATTCCTCAAC	540
GGGAAACGTT	TCGTACCATT	TGTAGTTATT	CTTCGTTTCAG	CAATCGCTGC	AATTCCTACT	600
GCTGCTTTCT	GGCCAGTAGT	TCAAACAGGT	ATCAATAATT	TCGGTATCTG	GATTGCCAAC	660
TCACAAGAAA	CTGCTCCAAT	TCTTGCACCA	TTCTTGTATG	GTACTTTGGA	ACGTTTGCTC	720
TTGCCATTTG	GTCTTCACCA	CATGTTGACT	ATCCCAATGA	ACTACACAGC	TCTTGGTGGT	780
ACTTATGACA	TTTTAACTGG	TGCAGCTAAA	GGTACTCAAG	TATTCGGTCA	AGACCCACTA	840
TGGCTTGCAT	GGGTAACAGA	CCTTGTA AAC	CTTAAAGGTA	CTGATGCTAG	TCAATACCAA	900
CACTTGTTAG	ATACAGTACA	TCCAGCTCGT	TTCAAAGTTG	GACAAATGAT	CGGTTTCATT	960
GGTATCTTGA	TGGGTGTGAT	TGTTGCTATC	TACCGTAAAT	TTGATGCTGA	CAAGAAACAT	1020
AAATACAAAG	GTATGATGAT	TGCAACAGCT	CTTGCAACAT	TCTTGACAGG	GGTTACTGAA	1080
CCAATCGAAT	ACATGTTTCAT	GTTTCATCGCA	ACACCTATGT	ATCTTGTTTA	CTCACTTGTT	1140
CAAGGTGCTG	CCTTCGCTAT	GGCTGACGTC	GTAAACCTAC	GTATGCACTC	ATTCGGTTCA	1200
ATCGAGTTCT	TGACTCGTAC	ACCTATTGCA	ATCAGTGCTG	GTATTGGTAT	GGATATCGTT	1260
AACTTCGTTT	GGGTAACGTG	TCTCTTTGCT	GTAATCATGT	ACTTTATCGC	AACTTCATG	1320
ATTCAAAAAT	TCAACTACGC	AACTCCAGGG	CGCAACGGAA	ACTACGAAAC	TGCTGAAGGT	1380
TCAGAAGAAA	CCAGCAGCGA	AGTGAAAGTT	GCAGCAGGTT	CTCAAGCTGT	AAACATTATC	1440
AACCTTCTTG	GTGGACGTGT	AAACATCGTT	GATGTTGATG	CATGTATGAC	TCGTCTTCGT	1500
GTAAGTGTTA	AAGATGCAGA	TAAAGTAGGA	AATGCAGAGC	AATGGAAAGC	AGAAGGAGCT	1560
ATGGGTCTTG	TGATGAAAGG	ACAAGGGGTT	CAAGCTATCT	ACGGTCCAAA	AGCTGACATA	1620
TTGAAATCTG	ATATCCAAGA	TATCCTTGAT	TCAGGTGAAA	TCATTCCCTGA	AACTCTTCCA	1680
AGCCAAATGA	CTGAAGCACA	ACAAAACACT	GTTCACTTCA	AAGATCTTAC	TGAGGAAGTT	1740
TATTCAGTAG	CAGACGGTCA	AGTTGTTGGT	TTGGAACAAG	TAAAGGATCC	AGTATTTGCT	1800
CAAAAAATGA	TGGGTGATGG	ATTTGCAGTA	GAACCTGCAA	ATGGAAACAT	TGTATCTCCA	1860
GTTTCAGGTA	CTGTGTCAAG	CATCTTCCCA	ACAAAACATG	CTTTTGGTAT	TGTGACGGAA	1920
GCAGGTCTTG	AAGTATTGGT	TCACATTGGT	TTGGACACAG	TAAGTCTTGA	AGGTAAACCA	1980
TTTACAGTTC	ATGTTGCTGA	AGGACAAAAA	GTTGCAGCAG	GAGATCTCCT	TGTCACAGCT	2040
GACTTGGATG	CTATCCGTGC	AGCAGGACGT	GAAACATCAA	CAGTAGTTGT	CTTCACAAAT	2100
GGTGATGCAA	TTAAATCAGT	TAAGTTAGAA	AAAACAGGTT	CTCTTGACAG	TAAAACAGCA	2160
GTTGCTAAAAG	TAGAATTGTA	A				2181

(2) INFORMATION FOR SEQ ID NO:1304:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 201 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1304:

AAAGTGAAAG AAGAGAAAAA AGCGATTGTC TTAGGTGCAG ATAATGCTTA TATGGATAAA	60
GTTGAAACAA CAATAAAATC TCTTTGTGTT CATCATTATA ATCTTAAGTT TTATGTTTTT	120
AATGATGACC TTCCGCGAGA ATGGTTCCAA TTGATGGAAA AAAGACTAGA GACTTTGAAT	180
AGTGAGATTG TGAATGTTTA G	201

(2) INFORMATION FOR SEQ ID NO:1305:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 750 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1305:

ACTCGGAAAG ATTTTGTGGT CTGCGGTAAT CGGGCTAACT TTATTTTGTAG GAGGAATCTG	60
AATACAAGTT TTGTTTCATGC TGCTGATGGG ATTCAATATG TCAGAGATGA TACTAGAGAT	120
AAAGAAGAGG GAATAGAGTA TGATGACGCT GACAATGGGG ATATTATTGT AAAAGTAGCG	180
ACTAAACCTA AGGTAGTAAC CAAGAAAATT TCAAGTACGC GAATTCGTTA TGAAAAAGAT	240
GAAACAAAAG ACCGTAGTGA AAATCCTGTT ACAATTGATG GAGAGGATGG CTATGTAACT	300
ACGACAAGGA CCTACGATGT TAATCCAGAG ACTGGTTCATG TTACCGAACA GGTTACTGTT	360
GATAGAAAAG AAGCCACGGA TACAGTTATC AAAGTTCCAG CTAAAAGCAA GGTTGAAGAA	420
GTTTTGTGTT CATTTGCTAC TAAATATGAA GCAGACAATG ACCTTCTGCT AGGACAGGAG	480
CAAGAGATTA CTCTAGGAAA GAATGGGAAA ACAGTTACAA CGATAACTTA TGATGTAGAT	540
GGAAAGAGTG GACAAGTAAC TGAGAGTACT TTAAGTCAAA AAGAAGACTC TCAAACAAGA	600
GTGTTTAAAA AAGGAACCAA GCCCAAGTT CTTGTCCAAG AAATTCCAAT CGAAACAGAA	660
TATCTCGATG GCCCAACTCT TGATAAAAGT CAAGAAGTAG AAGAAGTAGG AGAAATTGGT	720
AAATTACTCT TACTACAATC TATACTGTAG	750

(2) INFORMATION FOR SEQ ID NO:1306:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 528 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1306:

CCTAGGAAAG	AAGTGTTAGA	GGGCACTTGC	AGTTTTTGGT	ATAATGGAAG	ATATTTGAAA	60
GAAAAGAGAA	GTGATATGAC	ACAGATTATT	GATGGGAAAG	CTTTAGCGGC	CAAATTGCAG	120
GGGCAGTTGG	CTGAAAAGAC	TGCAAAATTA	AAGGAAGAAA	CAGGTCTAGT	GCCTGGTTTG	180
GTAGTGATTT	TGGTTGGGGA	TAATCCAGCC	AGCCAAGTCT	ACGTTCGCAA	CAAGGAGAGG	240
TCAGCTCTTG	CGGCTGGTTC	CCGTAGCGAA	GTAGTGCGAG	TTCCAGAGAC	TATTACTCAA	300
GAGGAATTGT	TAGACCTGAT	TGCTAAATAT	AATCAGGATC	CAGCTTGGCA	TGGGATTTTG	360
GTCCAGTTGC	CATTACCAAA	ACATATCGAT	GAAGAGGCGG	TTTTATTAGC	CATTGACCCA	420
GAAAAGGATG	TGGATGGTTT	CCATCCCCTA	AACATAGACG	TCTTTTGGGT	CTGGACATCC	480
AGTCATGATT	CCCTCGACAC	CTGCAGGAAT	TATGGAAATG	TTTCATGA		528

(2) INFORMATION FOR SEQ ID NO:1307:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1307:

TGGGTTGAAG	AAAAGCTAAG	CTCGAGAAAG	GACAAATTTT	GTCCTTICTT	TTTTGATGTT	60
CAGAGCGATG	AAAATCCGTT	TTTTGAAGTT	TTCAAAGTTC	CGAAAACCAA	AGGCATTGCG	120
CTTGATGTCT	TTGATGAGTT	TGTTAGTGGC	CTCAAGTTTA	GCGTTAGAAT	AAGGCAATTC	180
AATGGCGTTA	GTGATGTAGT	TTTTATAGCA	AATAAATGTG	CTCAAAGTGG	TTTTAAAGGT	240
GCGGTTGAGA	TGAGGTAA					258

(2) INFORMATION FOR SEQ ID NO:1308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1308:

GCTGGTGAAG	ACCACATCAT	GTCTAAAAAA	GTATTATTTA	TCGTCGGATC	ACTACGCCAA	60
GGTTCTTTCA	ACCACCAAAT	GGCCCTCGAA	GCTGAGAAAG	CACCTGCTGG	TAAAGCAGAA	120
GTTAGCTACC	TTGATTATTC	AGCCCTTCCT	CTCTTCAGCC	AAGATTTGGA	AGTTCCAAC	180
CATCCAGCTG	TAGCGGCAGC	TCGTGAAGCT	GTCCTTGCTG	CGGATGCCAT	CTGGATCTTC	240
TCTCCAGTCT	ACAACTTCTC	TATCCCTGGA	ACAGTGAAAA	ACTTGCTTGA	CTGGCTATCT	300
CGTGCCCTTG	ACTTGTCTGA	TACACGCGGC	GCTTCTGCCC	TTCAAGACAA	GTTCGTCACA	360
GTATCATCTG	TAGCCAATGC	AGGTCACGAT	CAACTCTTCG	CTATCTACAA	AGACCTCTTG	420
CCATTTATCC	GTACACAAGG	CGTTGGTGAT	TTCACTGCTG	CACGTGTTAA	TGACTCTGCC	480
TGGGCAGACG	GAAAAATTGGT	TCTTGAAGAA	ACAGTCCTAA	ACTCACTTGA	AAAACAAGCT	540
CAAGACTTGA	TCGAAGCTAT	CAAGTAA				567

(2) INFORMATION FOR SEQ ID NO:1309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1309:

AGAATAGAAG ATAGGATGGG GAAACTCTTG ACCAGAGGGT TTCATATCCT TTTTGTGAAA	60
AGAAGTTTAT ACTCAATGAA AATCAAAGAG CAAACTAGGA AGCTAGCGCA GGCTGCTCAA	120
AACAGTGTTT TGAGGTTGTG GATAGAAGT AAGAAGTCAG CTCAAGACAG TGTTTTGAGG	180
TTGCAGATAG AACTGACGAA GTCAGTAACA TATATACGGT AA	222

(2) INFORMATION FOR SEQ ID NO:1310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1310:

CAACCAGAAG AGGCAGAAGC TCATCCGCAA AAAAATATTA TCACCCAGTC TATTGGGCAA	60
AAAGATGAAA TTCAGCCTGA TTTTGGGACA GTTATCCTTG AGTCAGGTGA CTATCTCTTG	120
CTCAATAGTG ACGGCTTGAC CAACATGATT TCAGGCAGTG AGATTCGTGA TATTGTAACC	180
AGTGATATTC CTTTAGCAGA TAAAACGGAG ACACTTGTTT GTTTTGCTAA CAATGCAGGA	240
GGTTTAGACA ACATTACGGT TGCCCTTGTT TCTATGAACG AGGAGGATGA AGAATGA	297

(2) INFORMATION FOR SEQ ID NO:1311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 948 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1311:

GAAGGAGAAG	ATATGACAAA	ACTAATCTTT	ATGGGGACCC	CCGACTTTTC	AGCAACAGTC	60
TAAAAAGGAC	TTTTGACAGA	TGACCGTTAC	GAAATTCTAG	CCGTTGTGAC	CCAGCCAGAC	120
CGTGCTGTTG	GTCTGTAATA	AGTTATCCAA	GAAACCCAG	TCAAGCAGGC	TGCCAAGGAA	180
GCAGGACTAT	CTATCTACCA	ACCTGAAAAA	TTATCTGGAA	GTCCAGAGAT	GGAAGAAC'TT	240
ATGAAGCTAG	GAGCAGATGG	AATTGTGACT	GCTGCTTTTG	GGCAGTTTCT	CCCAAGCAAA	300
CTCCTTGATA	GCGTGGACTT	TGCTGTCAAC	GTTTCATGCCT	CCCTCCTTCC	TAGACACCGT	360
GGTGGTGCGC	CTATCCATTA	TGCCCTTGATT	CAAGGGGATG	AGGAAGCTGG	TGTGACCATC	420
ATGGAAAATGG	TTAAGGAAAT	GGATGCAGGA	GATATGATTT	TTCGTCGCAG	CATTCCGATC	480
ACAGATGAGG	ACAATGTTGG	CACCTTGTTT	GAAAAATTGG	CGCTAGTTGG	TCGTGATTTG	540
CTTTTGACACA	CTCTGCCTGC	CTATATTGCT	GGTGATATCA	AACCTGAACC	GCAGGATACG	600
AGTCAGGTTA	CCTTCTCTCC	AAATATAAAG	CCAGAGGAAG	AAAAACTGGA	CTGGAACAAA	660
ACCAATCGTC	AACCTCTTAA	CCAAATTCGT	GGAATGAACC	CCTGGCCTGT	TGCCCATACT	720
TTCCTTAAGG	GCGACCGCTT	TAAGATTTAT	GAAAGCCCTAC	CAGTAGAAGA	TCAGGGAAAT	780
CCAGGTGAGA	TTCTCTCTAT	CGGCAAGAAA	GAATTGATTG	TCGCAACGGC	TGAAGGGGCT	840
CTATCCCTCA	AACAAGTGCA	GCCAGCTGGT	AAGCCTAAGA	TGGACATTGC	TTCTTTCCTC	900
AACGGAGTTG	GACGTACATT	GACTGTAGGA	GAACGATTTG	GTGACTAA		948

(2) INFORMATION FOR SEQ ID NO:1312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1312:

AATATGGAAG	AAAATTATAA	TTTATCTATA	ACTCAAATAA	AGAATTCTAT	TAAAGAAAAT	60
TCCTTAGTTT	TGTTTGTGG	TGCAGGAATA	TCAGCTAATT	CTAATCTACC	AACTTGGGGA	120
GAATTGATTC	AATCATTA	AAAAGAATTG	AACATACCAG	AAGAAAGAAC	AGATAGTCCA	180
CTGAGAATTG	CTCAGTATTA	TTATGATACT	TTTGGGAAAA	ATCAGTACAC	AAAGAAGATA	240
GAAGAAATTT	TCTTTAAGAA	GGGATTGAGT	AAACCAAATG	AGTTACATAA	ATTAATAGAA	300
AAAATTGCAC	CAAAACATAT	TATTACGACA	AACATATGATT	CACTTCTGGA	GAGTCAATTT	360
GAAAGTGGCT	TGTTAAAGTA	CAATGTAGTC	GCTGAGGATA	AAGACATCCC	TTATACGAGT	420
TCGGAAAGAT	ACTTGATTAA	AATGCATGGT	GACTTCAGTA	AGAAAAATAT	TGTTTTGAAA	480
GAAGATGATT	ATTTAGACTA	TCATTTGAAC	TTCCCAATGA	TTTCTACTTT	AATCCAGTCA	540
TTGATAATGA	ATCATACTCT	ATTGTTTGTG	GGGTATTCTC	TAAGTGATTG	GACTTTTAAAT	600
TCAATTTTTA	GAATGATTCA	AAATACATTT	GACCTGGATG	CTAAAAATGC	TTATTTTAT	660
ACTCCCGAGG	AACCGTCTAT	GATCATTCGA	GAGTATTATA	AGAAGCAAGG	AATTTTCATT	720
ATCTCTAATG	AAGAGAATCT	AGGTCAGGAG	ACATCAGAAA	AACAGAACAA	ATTGTATTGC	780
AGGACAAAAG	ATTTTTTAGA	GGTTCTATCA	GAAAACCGAA	GTCAAGATGT	AAATAATGCT	840

GATGATTTAT	GGAATCAACT	GGCTTTTTTA	GATAGACTTA	GTTTTATTGA	TGCGAAAGAT	900
TTTTCTAGAT	ATTCTGATTT	AAAGAAAAGG	GCTTTAAACT	GGGATGATGA	GTATTGCTGG	960
TTTGGAATG	ATCAATTAAG	ATTTGAAATT	GATGGTCATG	AAGAATTACG	AATTATGGTA	1020
TCTAAAAAT	CTTTATTAAA	TCGCTTTCTA	GATATGGAGA	TTGGTGAGCC	TAGGGATTTA	1080
AAGGGGAATC	GATTCTTAAG	TAAGGCTTTT	AAGTTGTATG	AAGAAAAACA	ATATTCTTTA	1140
GCAAAAGCAA	AATTTAGAGA	ACTAGCTAAT	ATAGCTTTTG	TTCAGAAGAA	CTATTTTAAT	1200
TTTCTTAGTT	GGGAATTAA	ATTTTCAGCA	AATTCAAATA	ATTGA		1245

(2) INFORMATION FOR SEQ ID NO:1313:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 627 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...627
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1313:

AAAATGGAAG	AGTTAGTGAC	CTTAGATTGT	TTGTTTATTG	ACGGAACTAA	GATTGAAGCC	60
AATGCCAACA	AGTATAGTTT	TGTGTGGAAG	AAAACGACAG	AGAAATTCTC	CGCCAACTT	120
CAAGAACAGA	TACAAGTCTA	TTTTCAAGAA	GAAATCACTC	CCCTTCTGAT	TAAATATGCC	180
ATGTTTGATA	AGGAACAAAA	GAGAGGCTAT	AAACAGTCAG	CTAGAAACTT	AGCGAATTGG	240
CACTATAATG	ACAAGGAGGA	TAGCTACACA	CATCCTGATG	GCTGGTGCTA	TCGTTTTCAC	300
CATACCAAAT	ATCAGAAAAAC	ACAGACAGAC	TTTCAACAAG	AAATCAAGGT	TTACTACGCC	360
GACGAACCTG	AATCAGCCCC	TCAAAAGGGA	CTGTATATGA	ACGAACGCTA	TCAAACTTG	420
AAAGCTAAAG	AATGTCAGGC	GCTTTTATCT	CCCCAAGGTA	GACAGATTTT	CGCTCAACGC	480
AAGATTGATG	TGGAACCTGT	CTTTGGGCAG	ATAAAGGCTT	CTTTGGGTTA	CAAGAGATGT	540
AATCTGAGAG	GGAAGTGTCA	AGTGAGAAAT	GACATGGGAT	TGGTACTTAT	GGCCAATAAC	600
CTCCTAAAAT	ATAGTGAAAT	GAAATAA				627

(2) INFORMATION FOR SEQ ID NO:1314:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1716 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1314:

AGGAAGGAAG	ACATGGCCTT	AGAAGTAATT	ATGCCAAAAG	CCGGCGTGGA	TATGACAGAA	60
GGACAAATCG	TCCAATGGAA	TAAAAAAGTC	GGAGAAATTTG	TAAAAGAAGG	AGAAATCCTT	120
TTGGAATCA	TGACTGATAA	AGTCAGCATG	GAATTGGAAG	CCGAAGAAGA	TGGGTACTTG	180
ATTGCCATTC	TCAAAGGAGA	TGGTGAAACT	GTCCCTGTAA	CGGAAGTTAT	CGGTTACCTT	240
GGTGAAGAAA	GGGAAAACAT	CCCAACAGCT	GGAGCAGCAT	CGCCAGAAGC	TAGCCCTGTA	300
CCTGTAGCAA	GTACCTCAAA	CGATGATGGT	AATAGCGATG	ATGCTTTTGA	TATCGTTGTG	360
ATTGGTGGAG	GTCTTGCTGG	TTATGTTGCA	GCCATTAAAG	CTGCCCAACT	CGGCGGTAAG	420
GTTGCCCTTG	TTGAGAAATC	TGAACTTGGT	GGAACCTGCT	TAAACCGTGG	ATGTATTCCA	480
ACCAAGACCT	ACCTTCATAA	CGCTGAAATT	ATTGAAAATA	TCGGTCATGC	TGCAAATCGT	540
GGTATCGTGA	TTGAAAATCC	TAACCTTCACT	GTTGATATGG	AAAAACTTTT	AGAAACTAAA	600
TCTAAAGTTG	TTAATACTCT	TGTTGGTGGT	GTTGCAGGAC	TTCTTCGTAG	CTACGGAGTT	660
ACTGTTTATA	AAGGAATTGG	TACAATCACT	AAAGACAAGA	ACGTCTTGGT	AAATGGTTCT	720
GAAATGCTTG	AAACCAAGAA	AATCATTTCTT	GCTGGTGGTT	CAAAAGTCAG	CAAGATCAAC	780
GTCCCTGGTA	TGGAATCTCC	ACTTGTCATG	ACTAGTGATG	ACATTCTTGA	AATGAACGAA	840
GTCCAGAAA	GCCTTGTATT	CATCGGTGGT	GGAGTTGTCT	GTATCGAACT	CGGTCAGGCC	900
TTCATGACAT	TTGGTTCAAA	AGTGACTGTT	ATCGAAATGA	TGGACCGTAT	AGTTCCAGCT	960
ATGGATGCGG	AAGTTTCTAA	GAACCTTCGC	TTGATCCTTG	AGCGTAAAGG	AATGACCATC	1020
TTGACTGGTA	CTAAACTGCA	AGAAATCATT	GAGGAAAATG	GTCAACTTCG	TATCAAGGTT	1080
GAAGGAAAAG	ACGATATCAT	CGCAAGCAAA	GCTCTTCTTT	CAATTGGTCG	TATGCCAGAC	1140
CTTGAAGGTA	TTGGAGAGGT	TGAGTTTGAA	TTGGATCGTG	GTTGTATCAA	GGTCAACGAA	1200
TACATGGAAA	CTTCAGTTCC	AGGCATTTAT	GCACCAGGTG	ACATCAACGG	TACTAAGATG	1260
TTGGCTCACG	CAGCTTTCCG	CATGGGTGAA	GTTGCCGCTG	AAAATGCCCT	TAAAGGAAAT	1320
CATGCAGTTG	CCAAATTGAA	TTTGACTCCT	GCAGCCATCT	ACACTCTCCC	TGAAGTAGCA	1380
GCAGTAGGTT	TGACAGAAGA	ACAAGCCCCT	GAGAAATACG	ATGTTGCCAT	CGGTAAGTTT	1440
AACTTTGCTG	CTAACGGTCG	TGCTATTGCA	TCTGACGCAG	CTCAAGGTTT	CGTAAAAGTT	1500
ATCGCTGATA	AGAAATGCGG	AGAAATCCTT	GGTGACACA	TTATTGGTCC	TGCAGCCGCA	1560
GAATTAATAA	ACGAAGCATC	AAGCATCATC	GAAATGGAAA	TCACTGTTGA	GGAAATGCTG	1620
AAGACCATCC	ACGGGCACCC	AACTTACTCT	GAAGTGATGT	ACGAAGCGTT	TGCAGATGTT	1680
CTAGGAATGG	CCATCCATTC	ACCTAAGAAA	AAATAA			1716

(2) INFORMATION FOR SEQ ID NO:1315:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 717 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1315:

TTTTGTCGAG	AAGACACCTT	GGCAAATGGC	AGCTCTGCCT	TCATCGTCTC	CCTCCTAGGA	60
TGGATGCCGG	CTCCTATTGA	AATTTTCAGC	ATCAATTCAC	TTTGGTCAGC	TGAAAAGAGA	120
AAGACCGTCA	ACTTTAACAC	AGAAGACGCT	CTGTTTGACT	TTAACACTGG	TTATATTGGA	180
ACAGCTATCC	TAGCCGTCTT	CTTTGTGGCA	CTGGGAGCAC	TGATTCAGTA	TCCTACAGGG	240
CAGGCGGTTG	AAGCTGCTTC	AGCCAAATAC	ATCTCTCAAT	TCGTGGGCAT	GTATGCCTCT	300
GTTCTTGGCG	AATGGTCCCG	TACTTGATT	ACCTTTATTG	CCTTCCTCTG	TATCTTTGGA	360
ACAGTTATAA	CTGTTATCGA	TGGCTATTCT	CGCGTTAATC	AGGAATCTCT	CCGACTGCTA	420
ATCAGTCAAA	AAGAGGACAA	TCGTAAATCT	TTGAACATCT	GGATGACCAT	CACTGCTATC	480
ATCGGTATCG	TCATTATCAA	GTTCTTCGCT	GGTCAGGTTT	CAACCATGCT	CCGCTTTGCC	540
ATGATTGGCT	CTTTCCTGAC	AACACCTTTC	TTTGCTCTTT	TGAATTACGC	CTTGGTAACG	600
CGTGAAAAACA	AAAAATCTTC	TTCTTGCTC	AAACACCTTG	CCATTGCGGG	ATTGATTTTC	660
CTCTTTGGCT	TCGCCATCTT	CTTTATCTAC	GCACTCGCAA	TCGGAAAAGC	AGGGTAA	717

(2) INFORMATION FOR SEQ ID NO:1316:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1263 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1316:

ATGACTAGAG	AAAAATATTAA	ACTTTTTTCA	GAAATGCACG	CTGAACCAAG	CTGGTTGGCT	60
GATCTCCGTC	AAAAAGCTTT	TGACAAAGATT	GAGACTTTGG	AATTACCAGT	TATTGAGCGT	120
GTCAAATTCC	ACCGTTGGAA	TCTGGGTGAT	GGAACGATTA	CAGAAAATGA	GCCATCAGCA	180
AATGTTCCAG	ATTTACAGC	TTTAGATCAT	CACTTGAAGT	TGGTGCAAGT	AGGAACTCAA	240
ACTGTTTTCG	AACAAACTCC	AGTTGAGTTA	GCTGAACAGG	GTGTTGTCTT	CACAGACTTT	300
CACTCAGCTT	TAGAAGAAAT	TCCAGAGCTG	ATCGAAGAAT	TCTTCATGTC	ATCTGTTAAG	360
TATGATGATG	ACAAGTTGGC	GGCTTACCAC	ACAGCTTACT	TTAACAGTGG	TGCTGTACTC	420
TATATTCCAG	ATAACGTAGA	AATCACAGAG	CCAATTGAAG	GAATTTTCTA	CCAAGATAGC	480
GATAGCAATG	TGCCGTTTAA	CAAGCATATT	ATGATTATCG	CTGGTAAAAA	TTCTAAGATT	540
AGTTATCTGG	AGCGTTTAGA	GTCACGCGGT	GAAGGAAGTG	ACAAAAGTAAC	TGCCAATATC	600
ACAGTGGAAG	TGATTGCACG	TTCTGGTGCG	CAAGTCAAGT	TTGCTGCTAT	CGACCGTCTA	660
GGTGAAAACG	TCACTGCCTA	CATTAGCCGT	CGTGGTAAAT	TAGGCAACGA	TGCAAGTATT	720
GA CTGGGCTA	TCGGTGTCAT	GAACGAAGGA	AATGTCGTTG	CTGATTTTGA	TAGTGACTTG	780
ATTGGTAATG	GTAGCCATGC	TGACCTCAAG	GTTGTAGCTC	TTTCAAGTGG	TCGTCAGGTA	840
CAAGGGATTG	ATACTCGTGT	AACTAACTAT	GGCTGCAACT	CTATCGGAAA	TATCCTACAA	900

CATGGGGTTA	TCCTTGAAAA	AGCAACTTTG	ACTTTCAATG	GTATCGGCCA	CATCATCAAG	960
GGTGCTAAGG	GAGCAGATGC	GCAACAAGAG	AGCCGTGTTT	TCATGCTTTC	AGACCAAGCG	1020
CGTTCAGATG	CTAACCCAAT	TCTTTTGATT	GATGAAAATG	ATGTCACGTC	AGGACACGCA	1080
CGGTCTATCG	GACAAGTTGA	TCCAGAAGAC	ATGTATTACC	TCATGAGTCG	TGGATTGGAT	1140
AAGGCAACTG	CAGAGCGTTT	GGTTGTTTCG	GGTTTCCTTG	GATCTGTTAT	CGTGGAGATT	1200
CCAGTCAAGG	AAGTTCGTGA	TGAAATGATT	GCAACTATCG	AAGAGAAATT	GTCAAAACGC	1260
TAA						1263

(2) INFORMATION FOR SEQ ID NO:1317:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 708 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1317:

TATAATAGAG	ATAAGAATTT	TTATAAGGGG	AAACTGATGA	AATCACTTCG	TTTTCAATCT	60
GTCTTTGATA	TCATCGGACC	AGTTATGATT	GGCCCATCTA	GTAGCCATAC	CGCTGGTGCT	120
GTTCGTATTG	GGAAGATTGT	CTCTTCCATT	TTTGATGATA	CTCCGACAGA	AGTTGAATTC	180
CAACTTTTFA	ACTCATTTGC	CAAGACCTAT	CGTGGTCACG	GAACAGACCT	AGCCCTTGTT	240
GCAGGTATTT	TAGGAATGGA	TACAGATGAT	CCTGAAATTC	CAAATAGTCT	GGAAATTGCC	300
CACAAGCGTG	GTATCAAGAT	TGTCTGGACC	ATTCAAGAAAG	ACAGCAATGC	CCCTCACCCCT	360
AACACCACTA	AAATTACTGT	TAAAAATGCC	CACAAGACCA	TCAGCGTGAC	TGGTATTTCT	420
ATCGGTGGAG	GAAATATTCA	GGTAACCGAA	CTCAATGGTT	TTGCCGTCTC	TCTCAATATG	480
AATACACCGA	CTATCATCAT	CGTTCATCAA	GATATTCCAG	GTATGATTGC	CCTTGTTACA	540
GAGGCGCTTT	CCCGCTATGG	TATCAATATC	GCCCAGATGA	ATGTCACGTC	TGAAAAAGCT	600
GGTGAAAAAG	CCATTATGAT	TATCGAAGTT	GACAGTCGCA	ACTGTGATGA	GGCTATCGAA	660
GAAATTCGAA	AAATCCCTCA	TCTCCACAAT	GTCAATTTCT	TTAAATAG		708

(2) INFORMATION FOR SEQ ID NO:1318:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1017 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1318:

GAGTGTAGAG	ATGCTGGTTT	ATTGAATCAT	GTATCTCTCA	CTCTTGTTTT	TTCAGGAGAA	60
ATTAAAAATGA	AAAAATATAT	TCTAAAAAAA	GTATTATTCA	TGATTCCCTAT	GTTGTTGATT	120
ATTAGCTTTT	TAGTATTCAT	TGCACTAGAT	TTAACACCAG	CAGATCCATT	GACATATATG	180
GTATCTCCAG	ATATGGCTAG	TAGTGCAGAA	CAAATCGAAA	AGCTAAGACA	GCAATTAGGT	240
TTAAATGATC	CAGTATTAGT	TCGCTATGGA	AGATGGCTTT	GGCAATTACT	CCATGGTGAT	300
TTTGGATACA	GTATTGTAAG	TGGTAACCCA	ATTTCCAAAA	TTGTAGGACA	AGCATTGCCT	360
GCAACTTTTG	AATTAGCTTT	TGTGTCATTA	ATTATTTCAA	CAATTGTTGG	TATTGTAATT	420
GGGGTTATAT	CAGCCGTTAA	ACAAAATGGT	ATTATCGATA	ATGTTGCTCG	TTTTCTAGCT	480
GTTATCGGAA	CTGCGATTCC	ACAATTTTTC	TTTGGTATTT	TAATTTTAAA	CTTCTTTGCA	540
ATTCAGTTAA	GAATTTTACC	TATTGGTGGT	AGATTTGCCA	GTGGAGATTT	TACATTTATT	600
AATAGAGTTG	AACACTTAAT	TCTACCACTA	ATGGCTATGT	CAATTGCATT	GGTAGCTGCT	660
TTAATGAGAT	ACACACGTAA	TTCTATGTTG	GATGTTTTTA	ATGCAGATTA	TGTTAAAACA	720
GCTCGTGCAA	AAGGTGTTCC	TGAATGGAAA	GTTTATTTTA	AACACATATT	TAGAAATGCT	780
ATGCGACCAA	TTTTAGTGTT	ATTGATTTTC	CGTCTACCAA	TGTTAATTGG	TGGATCAGTA	840
ATTATCGAGA	GTGTCTTTTC	TTGGCCTGGA	ATTGGTTCTA	TCATCCTATC	TAGTGTAACA	900
GCAGGTGACT	ATCCTGTAAAT	TATGATTACC	ACATTAATGA	TTTCTGTCGT	AGTGTATTAT	960
GCTAGTCTAC	TTGTAGATAT	TATGGCTGCA	ATATTAGACC	CACGTATTCT	TTATTAG	1017

(2) INFORMATION FOR SEQ ID NO:1319:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 990 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1319:

ACCAAAAAGAG	ATTACAGAAC	GTTTTGTAGC	GGGATTAAAA	TAGCATGCCA	GAGTAAGAGG	60
TGTAATATGA	AAATTGATGT	TATAAATCAT	TTAGACTCAC	CAGGATTAGC	TGGGATGATT	120
TGTAGACGGA	TTAATAATAG	AATTTTAGTT	TATGGAGGTA	GTTATTTCCC	AAATAACGAT	180
CCTTTAAAAA	GTTCAAAAGT	TCAATCAAAAT	AAAATTAGAG	TTTATGATGA	GAAATTTAAT	240
CTTCTATATG	AACAAGATGG	AAAAATTTCT	CCAGATAAAG	GAATAACGAT	TGAAGTTGAA	300

AATGAAATCT	ATTACATTCT	AGGCTCGAGC	ATTTATCGTA	TTACGATTGG	TGAAAGTGTA	360
GAAGAAACCT	GTATCGGGAA	TTTTGATTTT	CAACTAGAGA	GTGGTTATGG	TTGTTATTTT	420
GATGGCCACT	TATTCTTTGG	ATTTCAGGAA	AGTTATTTGT	TCAATATTGA	GACTCAAGAG	480
CTTTTTAAAA	AATCTGACTT	CCCAGTTTCT	GGTAGAGGCC	AAGGTTTGTG	AGTCAAATAT	540
CAAAATGAAAT	TGTATTATTT	AGGTGGAGCG	AACAATGAAG	CTTATTTAGA	TGGATACAAA	600
TATAGTTTAA	AAAAAGATAA	GTGGGAAAAA	CTTGAGTTTC	AATTACCAAG	CTCAGTTCTA	660
GGAGCATCAA	GTATACAAAT	AAATGAAAGT	GGTTTATTAA	TACTTGGTGG	CTTTAATGAA	720
ATTGTTTATA	ATAAAGCAGT	TATTGATTTA	GCAACCCCTG	GCTATAGGGA	AGAATATTTT	780
TCTAAAGGGA	GAGATTTCCT	TAATTGGAAT	CGTAGCATGC	GAATACTAGA	TTTAGAGACA	840
GGTAAGGTCA	AGATTATTGC	AAACGATGAG	CGTTTTGCTC	TTTGTGGGGC	AGGATTTTTA	900
AAAACGATA	ATGGATATTA	CGTTGTTAGT	GGGGAATGTA	GCCCAGGAAG	ACGTACTTCT	960
GACATACTTT	TGTTAGAGGA	GGAAATGTAA				990

(2) INFORMATION FOR SEQ ID NO:1320:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1008 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1008
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1320:

GGAGAAAGAG	ATAAAATGGA	AACAAAAACA	ATGTCCTTCC	GTGACACCAT	TATCCTTGCT	60
ATGTCTGAGG	AAATGCGTCG	CGATGAAAAT	GTGTTCTTGA	TGGGAGAAGA	CGTCGGTGTC	120
TTCGGAGGAG	ACTTCGGTAC	TTCTGTTGGA	ATGCTTGAAG	AATTTGGTCC	AGAACGTGTC	180
CGTGACTGTC	CGATTTCTGA	AGCTGCCATC	TCTGGAGCAG	CAGCAGGAGC	AGCCATGACA	240
GGACTTCGTC	CAATCGTCGA	TATGACCTTC	ATGGACTTCT	CTGTTATTGC	CATGGACAAT	300
ATCGTCAACC	AAGCTGCTAA	AACACGTTAC	ATGTTTGGTG	GTAAAGGTCA	GGTTCCAATG	360
ACTGTTCTGTT	GTGCAGCTGG	TAACGGAGTT	GGCTCTGCCG	CCCAGCACTC	ACAATCTCTA	420
GAGTCTTGGT	TTACTCACAT	TCCAGGACTT	AAGGTTGTGG	CACCTGGAAC	ACCTGCGGAC	480
ATGAAAGGCC	TGCTTAAGTC	TTCTATCCGT	GATAACAACC	CAGTTATTAT	ACTTGAGTAC	540
AAGTCAGAAAT	TTAACCAGAA	AGGGGAAGTG	CCAGTTGATC	CAGACTACAC	AATTCCACTT	600
GGGGTTGGTG	AAATCAAACG	CCAAGGAACG	GATGTAACAG	TTGTTACTTA	TGGAAAAATG	660
CTTCGCCGTG	TGGTTCAAGC	TGCTGAAGAA	TTAGCAGAAG	AAGGAATTTT	AGTTGAAATT	720
GTTGACCCAC	GTACCTTGT	TCCGCTTGAT	AAGGATATCA	TCATAAACTC	AGTGAAGAAG	780
ACTGGTAAGG	TTGTTCTGGT	CAACGATGCC	CACAAAACAA	GTGGCTATAT	CGGTGAAATT	840
TCAGCTATTA	TTTCAGAATC	AGAAGCATTT	GACTATCTAG	ATGCACCAAT	TCGCCGTTGT	900
GCAGGAGAAG	ATGTGCCGAT	GCCTTATGCA	CAAAACCTAG	AAAATGCAAT	GATTCCAACA	960
GTTGAAAAGTA	TCAAAGATGC	AATCCGAAAA	ACTTATAACA	AAGAATAG		1008

(2) INFORMATION FOR SEQ ID NO:1321:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2043 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1321:

AAAGGAAGAG	AAATGTTTGA	TTATAGAGCA	CTAGTTATTT	TGATGACTTT	GATGGATCAT	60
TGTGAGCTAT	CATTATATGA	ATTATCTGTT	AAGGTGAGCT	TACCTATAAA	GGAAGTCAAA	120
GAAGGAATAG	ATTATTTAGT	GCCTTATCTA	GCTAATAAAG	GGATAGTGCT	GGATAAAAAA	180
CAAGGTCGCT	ATAGTTTATC	AAATCGTACG	AAGCAGTCTT	TGACAGATAT	TATTAAGTCG	240
GATGAATTGG	TTTTACCAAA	GTCGACTCGC	TTAGCTTTAA	TCTATCTTTA	CACTTTTTGC	300
CGATTAGATT	TTATATCGAA	TAATCATTAC	CAAGACTTTT	TGAAAAGTAAG	TAAGAATACA	360
ACCTTATCTG	ATATTCAATC	ATTAAGAAAG	ATTATGTTAG	ATAATGATTT	GGAGCTAGGG	420
TACAGTAGAG	CAAAAGGTTA	TACTTTACAC	GGTTCAGAGT	GGAATAAGCA	CCGTTTAGCT	480
TTTCAAATGG	TTAGTGAGTT	GCTGGAATCC	TCCATAGGGA	TTTGGGGTTT	GGATTATGTT	540
TTATCCAGTT	GGGGGTATTC	ATTAACTTAT	GATTTGATTG	ATCAGGTAGT	TAAAGATTAT	600
TATGAGAAGC	TACAGCTAGT	ACCTATTGTT	AATCAATTAA	AAGTTTACCT	TTTCGGTTTA	660
GTATTCATTG	TGTGTAGGTA	TCAAAGGGAT	GTTGAAAGAG	TATGTCCTTC	AGAGACATTA	720
GTATCTCCTG	TTATTCAAGA	TATAACGACT	ATTTTATTGG	ATACAGTGGT	TGATTTGGGA	780
ATTATAGATA	CGGTGTTTTT	TGAGGATGAT	TATCGCTATA	TCACAGTTTT	ATTATCAAGT	840
TGCTTTGAAG	GTGAAGTAGA	TGTTGCTCCG	GTTTACTTTA	ATCAATTAAC	AGAGGCTATT	900
ATAAGTAGAA	TGGAAGATAT	TTCTTTGTTA	CATTTTAAAC	AAAGGGAAGG	ATTGAGAGAA	960
AATCTTCGTC	GCCACCTTAT	ACCGGCTTAC	TATAGATTAA	AGTTCGGCCT	ACCTAGTTCA	1020
AATGAATATG	TATTGCATGT	TAAAGAACAT	TATCCTGATT	TATTTGAATT	AGTCAAAGAT	1080
TCTTTGATGC	CCTTGATGGA	CGCTATTGAC	AATCCCATAC	CTGATAGTGA	AACAGCATAT	1140
TTTGTTATCC	ATTTTCGGAGG	TTATTTAAAG	AAAGCAGATA	CTTTGCCTCA	AAAATGGTAT	1200
AAAGCAGCAA	TCATTTGTCC	TAATGGTGTT	AGTTCCTTCAT	TGATGTTAAA	AGAGAATCTA	1260
TTAGCATTAT	TTCTCAGAA	TGAGTTTATA	GGAACCTCAA	AGATTGATGA	TTTACAGGTG	1320
AAAGCTAGTA	GTGACTATGA	TATGGTTTTT	TCTACCATAA	AGGTGGAGAC	AGAAAAGCCA	1380
AATTATCTAG	TTTCGGTTAT	GATGACTGAA	GAGCAAGCAA	TACAACCTAGT	AGAACTAGTG	1440
TTAAAAGATT	TTCCGAATTT	AGAGTATGGA	GATTTTGAGA	TTGAACAAAT	CCTGAATATT	1500
GTCAAAAGAT	ATGGAATTAT	TACACAAGAA	TTGGAATTAA	GATTGGCGTT	AAAGAATTAT	1560
CTTTATCAAA	AAAATGATAG	AAAGGAAATT	GTACCACTGC	TAGAACAAC	TATTACCAAA	1620
GAAACCTATC	AGGTTAGTTC	GCAAAAATTA	GGATGGAAGG	AGGCGATTCT	TTTAGCAGCT	1680
AAACCGCTTT	TGGATCAAGA	TAAGATAACG	GAGAACTACC	CTGAGGCAAT	GATTCAAAAA	1740
GTAGAAGAGT	TTGGACCTTT	TATTAATTTA	GGGAAGGGAG	TAGCAATTCC	TCACGCTCCG	1800
CCAGATGAAG	GTGTGAATGA	AATAGGAATG	TCAATGTTAG	TTTTGGGAAGA	ACCGATTTAT	1860
TTATTGGATA	ATCCAGAACA	AGAGGTAAGA	TTGTTGATTT	GTATTGCAGC	CATTGATAAT	1920
GAGAGTCATT	TAAAGGCTTT	GTCACATTTA	ACAACAATTT	TAAGAGATAA	AAATCATGTT	1980
CAAACCTTAA	TATCATCAAA	AAACTATGAT	GATATTAAAA	TGATAATTAA	ACAGGAGGAT	2040
TAG						2043

(2) INFORMATION FOR SEQ ID NO:1322:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 666 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...666
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1322:

AAAGGGAGAG	AGATGAACAT	TTTAGTTGCA	GATGACGAGG	AAATGATTAG	AGAAGGAATT	60
GCAGCATTTT	TGACAGAAGA	GGGTTATCAT	GTCATTATGG	CTAAGGATGG	ACAAGAGGTC	120
TTGGAAAAAT	TTCAAGATCT	CCCTATCCAT	CTCATGGTAC	TGGATTTAAT	GATGCCTAGG	180
AAGAGTGGTT	TTGAAGTGTT	AAAAGAAATC	AATCAAAAAGC	ACGATATTCC	TGTCATCGTC	240
TTGAGTGCTC	TGGGAGATGA	AACTACTCAG	TCACAGGTAT	TTGATCTCTA	TGCTGATGAT	300
CATGTGACAA	AACCTTTTTT	TTTGGTACTG	CTTGTCAAGC	GTATTAAGGC	GCTTATCAGA	360
CGTTACTACG	TCATAGAGGA	TCTTTGGCGA	TATCAGGATG	TAACAGTGGG	TTTTACCTCT	420
TACAAAGCAC	ATTATAAAAA	TGAAGAAATT	GATCTCAAAC	CAAAGGAATT	ACTGGTACTA	480
AAGTGTTTGA	TTCAGCATAA	AAATCAAGTT	TTAAGTAGAG	AGCAGATATT	GGAAGAAATT	540
TCAAAAAGATG	TAGCTGATTT	ACCTTGTGAT	AGGGTCGTTG	ATGTCTATAT	TCGTACTCTT	600
CGCAAAAAAT	TAGCTTTAGA	TTGTATCGTG	ACTGTGAAAA	ATGTTGGGTA	TAAGATTAGC	660
TTATGA						666

(2) INFORMATION FOR SEQ ID NO:1323:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 675 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1323:

AATGATGGAG	AAGAAGCCTA	TCGTGCAGTG	TTAGAAGCCT	TGAAGGCTGG	TTATCGTCAT	60
ATTGATACGG	CGGCGATTTA	TCAGAATGAA	GAAAGTGTG	GTCAAGCAAT	CAAAGATAGC	120
GGAGTTCCAC	GTGAAGAAAT	GTTCGTAAC	ACCAAGCTTT	GGAATAGTCA	GCAAACCTAT	180
GAGCAAAC	GTCAAGCTTT	GGAAAAATCT	ATAGAAAAAC	TGGGCTTGA	TTATTTGGAT	240
TTGTATTTGA	TTCATTGGCC	GAACCCAAAA	CCGCTCAGAG	AAAATGACGC	ATGGAAAACT	300
CGCAATGCGG	AAGTTTGGAG	AGCGATGGAA	GACCTCTATC	AAGAAGGGAA	AATCCGTGCT	360
ATCGGCGTTA	GCAATTTTCT	TCCCCATCAT	TTGGATGCCT	TGCTTGAAAC	TGCAACTATC	420
GTTCCCTGCGG	TCAATCAAGT	TCGCTTGGCG	CCAGGTGTGT	ATCAAGATCA	ATTCGTAGCT	480
TACTGTCGTG	AAAAGGGAAT	TTTATTGGAA	GCTTGGGGGC	CTTTTGGTCA	GGGAGAACTA	540
TTTGATAGCA	AGCAAGTGCA	AGAAATCGCA	GCAAATCACG	GAAAATCGAT	TGCTCAGATA	600
GCCTTGGCCT	GGAGCTTGGC	AGAAGGGATT	TTTACCACCT	CCAAAATCTG	TCACAACCTC	660
TCGTATTCAA	GCTAA					675

(2) INFORMATION FOR SEQ ID NO:1324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1324:

ACTAAAGGAG	ACAATCATAT	GTCACTTGAA	AACAAATTGG	AACAAGCAAC	AGGCGCTGTC	60
AAAGAAGGTT	TTGGTAAAGT	TACTGGAGAC	AGCAAGACAG	AACTTGAAGG	AGCTGTTGAA	120
AAAACAGTTG	CTAAGGCAAA	AGACGTTGTA	GAAGACGCAA	AAGGTGCTGT	AGAAGGTGCC	180
GTTGAAGGTT	TGAAAAACGT	TTTTACTAAA	TAA			213

(2) INFORMATION FOR SEQ ID NO:1325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1325:

CTAAAAGGAG	ACACAATGGC	AGACCGAGGC	TTACTAATCG	TTTTTTCTGG	TCCTTCAGGG	60
GTTGGAAAAG	GAACGGTTAG	AAGAGAGATT	TTTGAGAGTT	CTGAAAACCA	ATTTCAATAT	120
TCTGTATCGA	TGACGACACG	CGCACAACTG	CCTGGAGAAG	TGGACGGTGT	TGACTATTTT	180
TTCCGTACTC	GTGAAGAATT	TGAAGAGCTG	ATTCGTCAAG	GACAGATGTT	GGAATACGCA	240
GAATATGTCG	GCAACTACTA	TGGAACCTCT	CTGACCTATG	TCAATGAAAC	CTTGGACAAG	300
GGAATCGATG	TTTTCCTTGA	AATTGAAGTT	CAGGGTGCTC	TTCAGGTCAA	GAAAAAGGTT	360
CCAGATGCTG	TCTTTATCTT	CCTGACACCA	CCAGATTGCG	ATGAATTGCA	AGATCGCTTG	420
GTAGGTCGTG	GAACAGATAG	TGCAGAAGTG	ATTGTCCAAC	GAATCGAAAA	GGCCAAGGAA	480
GAAATTGCCC	TCATGCGTGA	GTATGATTAT	GCGATTGTCA	ACGATCAGGT	GGCCCTAGCT	540
GCTGAACGTG	TCAAATGTGT	GATTGAAGCA	GAACACTTCT	GTGTGGATCG	TGTCATTGGT	600
CACTATCAGG	AGATGTTACC	AAAATCTCCA	ACTACCCGAT	AA		642

(2) INFORMATION FOR SEQ ID NO:1326:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1326:

AGAAAAGGAG	AAAGAAAAAC	GATGGAATAT	ATTTACCTGG	TAACAATCGT	AGGAATTGGA	60
CTATGGTCGC	TAGTAAATAA	ACTAGATGAC	CACGCTGAAA	TGAAACAAAA	AGAGCGCCAG	120
CTGATGGCAA	ACAATGTCGC	ACGGATGAAT	CTGAGAAATT	CAGATAAGCA	ATTTACTTAT	180
GATGTAGAAC	CGCCTGAAGG	GTTGAAATAA				210

(2) INFORMATION FOR SEQ ID NO:1327:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...252
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:

AAGAAAGGAG	AATCAAGATA	TATTATGGCG	ATATTAGATG	ATTTACAAGC	GTTATATGAT	60
AATGGATGGG	ACGCTTCTTT	TAATTATAAT	GGTCAAGTAT	GTGGCATTTC	CCCTAATTCT	120
ATTTATGATG	TTGTTGTTAT	TATTGCGGAC	GACGAATATA	GAGCATCTTC	TTTTGACGAT	180
TTGATTTCTT	TACAGATTGA	AGGGAAAACT	TTACCGGAAA	TCATGAACGA	AGTTGAAGTA	240
CAATATGGCT	AA					252

(2) INFORMATION FOR SEQ ID NO:1328:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 573 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...573
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1328:

AAAGAAGGAG	AATTTTCGAA	TATGAAATCA	ATAACTAAAA	AGATTAAAGC	AACTCTTGCA	60
GGAGTTGCTG	CCTTGTTTGC	AGTATTTGCT	CCATCATTTG	TATCTGCTCA	AGAATCATCA	120
ACTTACACTG	TTAAAGAAGG	TGATACACTT	TCAGAAATCG	CTGAAACTCA	CAACACAACA	180
GTTGAAAAAT	TGGCAGAAAA	CAACCACATT	GATAACATTC	ATTTGATTTA	TGTTGATCAA	240
GAGTTGGTTA	TCGATGGCCC	TGTAGCGCCT	GTTGCAACAC	CAGCGCCAGC	TACTTATGCG	300
GCACCAGCCG	CTCAAGATGA	AACTGTTTCA	GCTCCAGTGG	CAGAAACTCC	AGTAGTAAGT	360
GAAACAGTTG	TTTCAACTGT	AAGCGGATCT	GAAGCAGAAG	CCAAAGAATG	GATCGCTCAA	420
AAAGAATCAG	GTGGTAGCTA	TACAGCTACA	AATGGACGTT	ATATCGGACG	TTACCAATTA	480
ACAGATTCAT	ACCTGAACGG	TGACTACTCA	GCTGAAAACC	AAGAACGTGT	AGCAGAGCCA	540
AACGGCCACC	AGCTCGAAAA	GTATCATGGG	GGG			573

(2) INFORMATION FOR SEQ ID NO:1329:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...267
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1329:

ATGATGGGAG	ATGGGATGAA	AGAATTTCAA	TTTGAGAGAA	AGCAGCGTTT	TTCTTTGAGG	60
CCATATGCAA	TAGGAGCTTG	TTCGGTCTTG	CTAGGAACGA	GTTTATTTT	TGCTGGTATG	120
GGTGCTCAGC	CTGTACAGGA	TACAGAAACG	AGTTCAGCAC	TAATTTCAAG	TCATTATTTG	180
GATGAGCAGG	ATTTATCTGA	AAAGCTGAAA	TCTGAGTTGC	AATGGCTTGA	ATTAGAAAAC	240
AAGCTTTTGA	ACTTATGGGA	GCATTAG				267

(2) INFORMATION FOR SEQ ID NO:1330:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1086 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1086
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1330:

AGAAAGGGAG	ACTCTCCTAT	GAAAATCAGA	ATCGATATTC	CTCATCATCC	TTATGATATT	60
CAGATTGAAA	AAGGTTGTAT	GGCCCAGGCT	GGTCAGTGGT	TGCGAGAACT	CTGGCAACCG	120
CAAAAGGTAG	TCATTGTGAC	AGATAACCAT	GTAGCCTCTC	TCTATGCAGA	GAAGGTCAAG	180
CTCAGCCTAG	AAGATGCTGG	TTTTCAGGTA	GCTGTTTTTG	ATTTCTTAGA	AGGTGAAGAA	240
AGAAAGAATT	TAACTACTGT	TCAGAAAGTC	TATGAATTTT	TAGTCAAGCA	AGGTCTGACT	300
CGTAGCGATG	GAATCGTTGC	TCTTGGTGGT	GGCGTTGTTG	GGGACCTGGC	TGGCTTTGTA	360
GCCTCTACCT	ATATGCGGGG	TATTCACTTT	GTTTCAGATTC	CGACTAGTTT	GACAGCTCAG	420

GTTGATTCTT	CTATCGGTGG	AAAGACAGGC	GTTAACACAC	CATTTGCTAA	AAATATGGTG	480
GGGACCTTTG	CCCAACCAGA	TGGGGTTCTG	ATTGATCCAC	TTGTTCTTGA	AACCCCTCGGA	540
AAAAGAGAGT	TGATTGAAGG	GATGGGTGAA	GTTATCAAGT	ATGGCTTGAT	TGAGGATCCA	600
GAACTGTGGG	CTCTCTTGAC	GGGACTGAAT	GGTTCTGTTG	AGAGTATTTT	GGAACATGCA	660
GAGACCTTGA	TTGAACATTG	TTGTCAGGTG	AAGCGCAAGA	TGGTGGTTGA	AGATGAGTTG	720
GACAATGGTA	TTCGTCTTTA	CCTCAATTTT	GGCCACACTA	TTGGCCATGC	CATCGAAGCG	780
ACTGCCGTTT	ATGGCAAGGT	CATGCATGGA	GAGGCTGTTG	CCATGGGAAT	GGTACAGATT	840
TCCAAGGTTG	CTGAGGAAAA	AGGCCTCATG	CCAGCTGGCA	TTACCCAATC	TATCACAGAG	900
ATGTGTCAGA	AATTCGGCTT	GCCTGTTGAC	TATGAAAATT	GGGAAGTTGA	CAAGCTTTAT	960
CAGGCTCTTA	CTCATGACAA	GAAAACGCGT	GGTAACACCT	TGAAATTGGT	CTTGGTGTCA	1020
GAGCTTGGTT	CAGCGATCAT	TCACCCAGTT	TCTCTGGAAG	AGATGAAAGA	CTACTTGGTA	1080
AAATAA						1086

(2) INFORMATION FOR SEQ ID NO:1331:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...276
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1331:

AGAGAGGGAG	AGATAGATAA	AAAGTCCACC	CCCATTTTTT	ATGGAGAATT	CAAAAATGTA	60
AGGTAAAGCA	AAGAAGAATA	TAAAAATCTA	AAAGAAAAAT	TAAACTCACA	CACAGATATA	120
ATGATAAATA	AACTATCCAG	ATACATGGAA	AGCAGTGGTA	AGACCTATCA	AAACCACTAT	180
GTGACAATCT	TAAAATGGTA	TGAAGAAGAT	AAAGACAAAC	TAAGACAGAA	AGGTTTAAAT	240
AAAAAATGA	ATTATGATGT	AGGAGAATCT	TTATAG			276

(2) INFORMATION FOR SEQ ID NO:1332:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1332:

ATCTACTTGG AATTTGCATC CTCTTCTCCT TTTTACGAGG CTACCCTGCC TCTACTCTTC	60
TTTTTCTATT ATTATACCCT TTTTAGTTGT AATGTCAATC GTTACCACTT TTCAACCAGT	120
CGTCTAACTC CCGGTCGCAG CCCTCTTTCT GAGCCAATTC TCTCAAAAAT TCCTGATGAT	180
GAGTATGGTG GATCCCATG A	201

(2) INFORMATION FOR SEQ ID NO:1333:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1386 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1333:

ATGGGTCTGG AACTACGAGC GATTCAGTCC CCAATCTTCT CTGAGCCGTT TGATTTTACT	60
TTTCATGCGC AAGCCTTTAC CTTGTTAGTT GGGAGCAGTG GTTCAGGAAA ATCCAGCCTT	120
TTTCAAGTCA TTGCCCAAGT CAGTTCTCTT CCCTATAGTG GTCAAGTCCT GATAGATGGG	180
AGCGAGGTCA GTCAGCTTTC TATCATCGCA CGTGTCCAGA AGGTTGGCAT TCTCTTTCAA	240
AATCCCAATC ATCAATTTAC CATGGAGAAC TTGTTTGAGG AGCTGATTTT CACCTTGGAG	300
AATATCGGCT ATCACCTTCA GGAAATTGAT TCTAAAAATAG CAGAGGTTGT CCAGCAATGT	360
CGTTGCGAGG CAATCTTACA CCGTCCCATT CATCACCTAT CAGGTGGGGA AAAGCAAAAA	420
GCAGCGCTGG CTGTCCTCTT TGCCATGAAT CCTAGGGTCT ATCTCTTGGA TGAGCCCTTC	480
GCTTCTATTG ACCGCAAGAG CAGAAATCGAG ATATTGGAGA TTCTAAAAGA GTTGGCTCTT	540
GATGGGAAGA CAGTTATTTT GTGCGACCAT GATTATCTG ACTATAAAGC CTATATCGAC	600
CATATGGTTG AGCTAAGAGA CGGAAACTA AGGGAAGTGT TTCAAATCCC TTCCTATGAG	660
ATGACACAGG TTGCTTCAAA GGAAGTTGCT TCTAGCCCGG AACTATTCCA TATGAACCGT	720
GTGACTGGTG AGCTTGGTAA TCGCCCCCTC TTTTCAATTG CTGATTTTAC ATTCTATCAA	780
GGGATTTCCCT GTATCCTGGG TGACAATGGT GTCGGGAAAT CAACCCCTCTT TCGCTCTATT	840
CTTCAATTTT AAAAGTATAA GGGGCGCATT GCATGGAAGG GGACAGTCCT GAAAAAGAAA	900
AAGAGTTTGT ACCGTGATCT GACGGGTGTT GTTCAGGAAG CTGAGAAGCA GTTTATCCGA	960
GTCAGTCTGC GAGAGGAGCT TCGATTAGAT GGACCTGATT CTGAAAGAAA TCAGCGGATT	1020
TTTCAAGCTT TACGATATTT TGATTTGGAG CAGGCAGTCG ATAAGAGTCC CTATCAATTA	1080
AGTGGTGGTC AGCAAAAAAT TCTTCAGCTC CTGACCATCT TGACCAGTAA GGCTTCCGTG	1140
ATCTTGCTAG ATGAACCTTT TGCAGGTTTG GATGATAGAG CCTGCCATTA TTTTTCGAAG	1200

TGGATTGTGG AGGAGAGGAA TCAAGGAAGA AGTTTTCTGC TCATTAGTCA TCGTTTAGAC	1260
CCTTTGATTT CTGTGGTTGA TTATTGGATT GAGATGACTA GTCAGGGGCT CAGTCATGTG	1320
AAAGAAGTGA CCATTACCAA ACCACTTACA TCTCAGAGTA GCAATACCCA AGGGGAGGTG	1380
AGATAG	1386

(2) INFORMATION FOR SEQ ID NO:1334:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...213
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1334:

TCGTTGCTGG ACGAGATGGA GTTCAGATTT CAACTTCAAA AAAAGGAAAA TAGAAGGGGG	60
CATAAGATGT CTAAATTTAA TCGTATTCAT TTGGTGGTAC TGGATTCTGT AGGAATCGGT	120
GCAGCACCAG ATGCTAATAA CTTTGTC AAT GCAGGGGTTC CAGATGGAGC TTCTGACACA	180
CTGGGACACA TTTCAAAAAC AGTTGGTTTT TGA	213

(2) INFORMATION FOR SEQ ID NO:1335:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...201
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1335:

ACCATTATGG ATACAGTTAG CAAAAAAGA CTAAAGAAAA CAGATGTAAT AGCTATGGCA	60
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GGACTTACAA CAAATGTTAT GGCACAAATG GGAAAGGATA AACCAATTAC ATTTAAGAAT	120
TTAGAAAGAA TATGTAAGGC TTTATCTTGC ACTCCTAATG ATATTATTAG TTTTGAAGAT	180
AATTTTAGTG ACGAGGAATA G	201

(2) INFORMATION FOR SEQ ID NO:1336:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 972 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1336:

GAAATTATGG AATCAAAAAGT TACAATTATC ATGCAAGAAA TGTTACCTCT TTTAAATAAT	60
GAACAATTAC TAGCGTTGAG AGAGAGTTTA GAACATCATC TAGTAGACGG AAAAAAGCAG	120
CAGAAGTATT CGAATAATAA CCTGTTGCAA CTATTTATTA CCGCCAAGCA GGTAGAGGGC	180
TGTAGCTCAA AAACAATTCG TTATTACCAG AGGACGATTG AAAACTTGTT TAATGCTATT	240
AAAGAGTCTG TGACACAACT CACAACAGAT GATTTAAGGA GTTATTTAGC AAATTACCAG	300
TCTGAAAAGG ATTGTAGTAA GGCAAATTTA GACAATATTA GGCGTATATT GTCTTCTTTT	360
TTTGCTTGGC TTGAGCAAGA GGAATATATC ATTAATAATC CCATTCGACG GATAAAGAAA	420
ATTAAGACTG AGCAAAATGT GAAGGAAACT TATACTGATG AACATTTGGA AATTATGCGT	480
GATAACTGTG AAAATTTGAG AGATTTGGCA ATAATAGACC TACTAGCATC GACAGGTATG	540
CGTGTAGGGG AGCTTGTAACA GTTGAATCGT TCAGATATTG ATTTTGAAAA CAGAGAGTGT	600
GTTGTCTTTG GTAAAGGAAA GAAGGAGAGA CCAGTATATT TTGATGCTCG GACGAAAATT	660
CATTTAAGAA ATTATCTTAA CGACAGAAAA GATAGTCACC CTGCTCTTTT TGTAACGCTA	720
GTTGGAAAAG CCCAGAGACT TGGAATTGCT GGTGTAGAGA TTCGCTTAAG AAAGTTAGGA	780
GACAAACTCG GCATACAAAA GGTTCAACCA CATAAGTTCA GAAGAACTTT AGCGACTAAG	840
GCAATTGATA AAGGTATGCC TATCGAACAA GTCCAAAAAC TGCTAGGTCA TAGCAAGATT	900
GACACAACCC TGGCCTATGC CATGGTCAAT CAAAATAATG TCAAGCATTC ACACCAAAAA	960
TTCATCTCTT AA	972

(2) INFORMATION FOR SEQ ID NO:1337:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 402 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1337:

CAGCCTATGG	ACTCACAAGA	CAATAAACGA	AAATGGAAAA	ATCGTGACCT	GATATCCAGT	60
TTAGAATTTG	CCATCACAGG	AATTTTTTACT	GCTATCAAGG	AAGAACGCAA	TATGCGAAAA	120
CATGCAGTGA	CGGCTCTAGT	GGTCATCCTT	GCAGGTTTTG	GTTTTTCAGGT	GTCACGAATC	180
GAATGGCTCT	TTCTCCTGTT	GAGCATTTTC	TTGGTGGTAG	CCTTTGAAAT	TATCAATTCT	240
GCTATCGAAA	ATGTGGTGGA	TTTGGCCAGT	CACTATCACT	TTTCCATGCT	GGCTAAAAAT	300
GCCAAGGATA	TGGCGGCTGG	CGCGGTATTT	GTGGTTTCTC	TTTTTGCAGC	CTTAACAGGC	360
GCATTGATTT	TTCTCCCACG	AATCTGGGAT	TTATTATTTT	AA		402

(2) INFORMATION FOR SEQ ID NO:1338:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 999 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1338:

GTTGTCATGG	ACTTCCTTCT	CATGGGAGCA	CTCTTCATCG	TTCTTCCCCG	AACTATGGTC	60
TCTGCTAAGC	GGATTAATCA	AGTTTTTAGAT	TTGCATTCTT	CTATCCAAAA	CCCTGCTCAA	120
GTGCAGCTGA	CTGATGAAAA	CTTCAAAGGT	CAGGTCGAGT	TTAAGGATGT	GACCTTCCGC	180
TATGCGGCAA	ATTCGGAGGC	AGTTATTGAA	CATGTTAGCT	TTAAAGCAGA	AACTGGTCAA	240
ACAGTGGCCT	TTATTGGGTC	AATAGGTTCT	GGTAAATCAA	CTCTGGTCAA	TCTGATTCCA	300
CGTTTCTACG	ACGTGTCAGC	AGGAGAAATT	CTGGTGGACG	GTGTCAATGT	TCAAGACTAT	360
GACTTCTCTG	CGACAGCTCA	TGCTGGTCAA	AGGGTTGCCA	TTGTTGGGCC	GACTGGGGCT	420
GGTAAGACAA	CCATTGTCAA	TCTTTTGTATG	AAATTCATATG	AGATTGATAA	GGGAAGTATT	480
CGCATTGATG	GTGTGGATAC	CAAGGCTATG	ACGCGTTCAG	AAGTGCATGA	TGCCTTTTCA	540
ATGGTCTTGC	AGGATACCTG	GCTCTTTGAA	GGAACATATC	GAGACAATCT	CATCTATAAT	600
CAAATAGGGA	TTAGTGATGA	ACGAATGATG	GAAGCTAGTA	AGGCTGTGGG	AATTCACCAC	660
TTTATTATGA	CCTTGCCAGA	TGGCTATGAT	ACCATCTTGG	ATGACACCGT	GACCTTGTCT	720
GTAGGACAAA	AACAACTATT	GACTATTGCT	TGTGCCCTTC	TTAAGGATGC	ATCGCTTTTG	780
ATTTTGGATG	AGGCGACTTC	TTCTGTTGAC	ACACGGACAG	AGGAATTGAT	CCAAAAAGCC	840
ATGGACCGTT	TGATGGAAGG	ACGCACATCC	TTTGTTCATTG	CCCACCGCTT	GTCAATCATC	900

CGAAATGCAG	ACTTGATCTT	GGTCATGAAA	GATGGAAATA	TCATCGAGCA	AGGCAACTAT	960
GAGGAACTGA	TGGCGTCTTC	ACCACGAGGT	TCCGGCCAA			999

(2) INFORMATION FOR SEQ ID NO:1339:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3732 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...3732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1339:

GAATTGATGG	ATAAACGTAT	TTTTGTTGAA	AAAAAGGCTG	ATTTTCAGGT	CAAGTCAGAG	60
AGTTTGTTTA	GAGAGCTCCA	GCACAACTTG	GGACTGTCAA	GCTTGAAAAG	TATTCGTATT	120
GTGCAAGTAT	ATGATGTATT	TGACTTGGCT	GAGGACTTGT	TTGCACCTGC	AGAGAAGCAC	180
ATTTTCTCTG	AGCAGGGAAC	CGACCATGTT	TTAGATGAAG	TATCTGTGCA	GGCGGATCTT	240
GCTAACTATG	CTTTCTTTGC	CATTGAAAGT	CTGCCAGGGC	AGTTTGACCA	GCGTGCAGCT	300
TCGTCACAGG	AAGCCTTGCT	TTGTTGGGA	AGTTCGAGTG	ACGTGACAGT	CAACACAGCC	360
CAACTTTACT	TGGTGAATAA	AGATATTGAT	GCGACTGAGT	TGGAAGCTGT	CAAAAACCTAC	420
CTGCTCAATC	CAGTTGATTC	TCGTTTCAAG	GATATCACGA	CAGGGATTGC	CAAGCAGGAG	480
TTTTCAGAGT	CAGACAAGAC	CATTCCAAAA	TTGACTTTCT	TTGAAAGCTA	TACAGCAGAA	540
GACTTTGCTC	GCTACAAGGC	CGAGCAAGGG	ATGGCCATGG	AAGTGGATGA	TTTGCTCTTT	600
ATCCAAGACT	ACTTTAAGTC	AATCGGGCGC	GTGCCAACTG	AGACTGAACT	CAAGGTTTTG	660
GACACTTACT	GGTCTGACCA	CTGCCGTCAT	ACGACTTTTG	AGACAGAGTT	GAAACACATC	720
GACTTTTCAG	CTTCTAAATT	TCAAAAGCAA	TTGCAGTCAA	CCTATGACAA	GTATATTGCC	780
ATGCGCGAGG	AGTTAGGTCG	GTCTGAAAAA	CCACAAACCT	TGATGGATAT	GGCGACTATT	840
TTCGGTCGTT	ATGAGCGTGC	TAACGGACGA	TTGGATGATA	TGGAAGTCTC	TGACGAAATC	900
AATGCCTGCT	CAGTTGAAAT	TGAAGTGGAT	GTTGATGGTG	TCAAGGAACC	TTGGCTCCTC	960
ATGTTTAAAA	ATGAAAACCA	CAACCATCCA	ACAGAAATTG	AGCCATTGGG	TGGAGCGGCT	1020
ACCTGTATCG	GTGGAGCTAT	TCGTGATCCG	TTGTCAGGCC	GTTCCATATG	TTACCAAGCC	1080
ATGCGTATTT	CAGGTGCTGG	TGATATTACA	GCACCGATTT	CGGAAACTCG	TGCTGGGAAA	1140
TTGCCACAAC	AAGTCATTTT	TAAAACAGCA	GCTCATGGTT	ATTCTTCATA	TGGTAACCAG	1200
ATTGGGCTTG	CCACAACCTA	CGTTCGTGAA	TACTTCCACC	CAGGCTTTGT	AGCTAAACGT	1260
ATGGAACCTG	GTGCCGTTGT	TGGTGCGGCT	CCCAAGGGCA	ATGTTGTCCG	TGAAAAACCT	1320
GAAGCAGGTG	ATGTGATCAT	CCTTCTCGGA	GGCAAAACAG	GTCGTGATGG	TGTCGGTGGT	1380
GCGACGGGCT	CTTCTAAGGT	TCAAACAGTT	GAGTCTGTAG	AGACTGCTGG	TGCTGAGGTT	1440
CAAAAAGGAA	ATGCCATCGA	AGAACGCAAG	ATTGAGCGCC	TCTTCCGTAA	TGGCAATGTC	1500
ACTCGTCTGA	TCAAGAAGTC	CAATGACTTT	GGGGCAGGCG	GCGTCTGTGT	GGCTATCGGT	1560
GAATTGGCAG	ACGGTCTTGA	AATCGACCTC	AACAAGGTGC	CTCTTAAATA	CCAGGGCTTG	1620
AATGGTACAG	AAATTGCCAT	CTCTGAATCA	CAAGAACGGA	TGGCGGTCGT	GGTTCGTCCCT	1680
GAAGATGTGG	ATGCCTTCGT	TGCCGAATGT	AACAAAGAAA	ATATTGATGC	TGTTGTGGTG	1740
GCGACAGTAA	CTGAAAAACC	AAATCTTGTC	ATGCACTGGA	ATGGTGAGAC	AATCGTTGAC	1800
TTGAGCGGTC	GTTTCCTTGA	CACCAATGGT	GTGCGCGTGG	TTGTGATGTC	CAAAGTTGTG	1860

GACAAGGATG	TCAAACCTCCC	AGAAGAGCGT	CAAACATCTG	CTGAAACACT	GGAATCAGAT	1920
ACCCTTACGG	TTCTATCTGA	CCTCAACCAT	GCAAGTCAAA	AAGGATTACA	GACTGTCTTT	1980
GACTGCTCTG	TTGGACGCTC	AACGGTTAAT	CACCCACTTG	GTGGTCGTTA	CCAACTCACA	2040
CCAAC TGAGG	CATCTGTGCA	GAAATTGCCA	GTTCAACACG	GTGTGACTCA	TACTGCGTCG	2100
GTCAATTGCTC	AAGGTTTCAA	CCCATATGTA	GCTGAAATGGT	CTCCATACCA	CGGTGCTGCT	2160
TACGCGGTTA	TCGAAGCAAC	TGCTCGTTTTG	GTGGCTGCTG	GTGCCAACTG	GTCTAAGGCT	2220
CGTTTTCTCTT	ACCAAGAAATA	TTTCGAGCGG	ATGGACAAGC	AAGCAGAGCG	TTTTGGTCAG	2280
CCAGTAGCCG	CCCTTCTAGG	CTCTATTGAA	GCTCAGATTTC	AACTTGGCTT	GCCATCTATC	2340
GGTGGTAAGG	ACTCCATGTC	TGGTACCTTT	GAAGAATTGA	CTGTTCCGCC	AACCTTG GTT	2400
GCCTTTGGGG	TGACGACGGC	AGATAGCCGT	AAGGTGCTCT	CTCCAGAATT	TAAAGCTGTT	2460
GGGGAAAATA	TCTACTACAT	CCCAGGTCAA	GCCCTCTCTG	CAGAGATTGA	TTTTGACTTG	2520
ATTAAGAAAA	ATTTTGCTCA	GTTTGAAGCA	AGCCAAGCTG	ACCATAAAGT	GACATCTGCA	2580
TCAGCTGTCA	AATACGGTGG	TGTAGTTGAA	AGTTTGGCTC	TTGCTACCTT	TGGAAACTAT	2640
ATTGGTGCAG	AGGTGACCTT	GCCTGAACTT	AAAACAGCTT	TGACAGCTCA	ATTAGGCGGC	2700
TTTGTCTTCA	CATCTCCTGA	AGAAAATTGCT	GGAGTAGAGA	AGATTGGACA	AACGAAAGCA	2760
GACTTTACAC	TGACTGTCAA	CGGTGTGAAG	CTAGATGGAC	ACAAGCTTGA	CAGTGCATTT	2820
CAAGGGACAT	TGGAAGAAGT	TTACCCAACA	GAATTTACCC	AAGCGAAAGA	ACTAGAAGAA	2880
GTACCAGCTG	TGGCATCAGA	TGTTGTGATT	AAAGCCAAAG	AAAAGGTTGA	AAAACCTGTG	2940
GTTTACATCC	CAGTCTTTCC	AGGAACCAAC	TCAGAAATATG	ATTCAGCTAA	GGCCTTCGAA	3000
AAAGAAGGTG	CAGAGGTCAA	TTTGGTGCCA	TTCGTGACCT	TGAATGAAGA	AGCTATTGTC	3060
AAGTCAGTTG	AAACTATGGT	TGACAATATC	GACAAGACTA	ATATTCTCTT	CTTTGCCGGT	3120
GGATTCTCGG	CTGCGGATGA	ACCAGATGGT	TCAGCTAAGT	TTATCGTCAA	TATCCTGCTT	3180
AATGAAAAAG	TGCGTGTGGC	TATTGATAGC	TTTATCGCCC	GTGGTGGCTT	GATTATCGGT	3240
ATTTGTAAATG	GATTCCAAGC	CTTAGTCAAA	TCGGGTCTCC	TACCATACGG	AAACTTTGAA	3300
GATGCTAACA	GTACTAGTCC	AACCCTCTTC	TACAATGATG	CCAACCAACA	CGTGGCCAAG	3360
ATGGTGGAAA	CTCGCATTGC	CAATACCAAC	TCACCATGGT	TGGCTGGTGT	GCAAGTGGGC	3420
GATATCCACG	CTATTCCCTGT	TTCGCACGGT	GAAGGGAAGT	TTGTCTGTGAC	GGCTGAGGAA	3480
TTTGCAGAGC	TCCGTGACAA	TGGACAAATT	TTCAGCCAAT	ACGTTGACTT	TAACGGTAAA	3540
CCAAGTATGG	ATTCTAAGTA	CAATCCGAAT	GGTTCTGTCC	ATGCCATCGA	AGGAATTACC	3600
AGCAAGAATG	GTCAAATCAT	CGGTAAGATG	GGCCACTCAG	AACGTTATGA	GGATGGTCTT	3660
TTCCAAAATA	TCCCAGGCAA	TAAAGACCAA	CACCTGTTTCG	CATCAGCGGT	TAAACATTTT	3720
ACTGGAAAAT	AA					3732

(2) INFORMATION FOR SEQ ID NO:1340:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1248 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1248
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1340:

GAGATGATGG	AGTTTTTTTCA	ACAGCTTCCT	CATTTAGAGC	CATATGGCAA	TCCTCAGTAT	60
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TTTGTTTATG	TGATTGCTGC	AACCTTGCCC	ATCTTTATAG	GCCTCTTTTT	CAAGAAACGC	120
TTTGCCTGGT	ATGAAGTGTT	GGTAAGTCTC	TTCTTTATTG	TCACCATGTT	GGTGGGTGGA	180
AAGACCAATC	AACTAGCTGC	CTTGGGTATT	TACCTTTGCT	GGGAAATATT	GCTCCTGCTT	240
TTCTACAAGC	ATTATCGAAA	AAGCAAGGAT	GGCAAGTGGG	TCTTCTACTT	AGTTAGTTTT	300
CTGTCCCTAC	TTCCGATTAT	CTTTGTCAAG	GTGCAACCAG	CTATCAATGG	AACGCAGTCT	360
TTGCTTGGGT	TCTTGGGAAT	TTCTTACCTG	ACCTTTTCGTT	CTGTTGGGAT	TATCATCGAG	420
CTGAGAGATG	GAGTGATTAA	GGATTTTACC	CTCTGGGAAT	TCCTCCGTTT	CCTTCTCTTC	480
ATGCCAACTT	TCTCGAGTGG	TCCAATCGAT	CGCTTTAAGC	GATTTAATGA	AAATTATCAG	540
GCCATTCCCTG	AGCGAGATGA	GTTGATGGAT	ATGCTGGATG	AATCTGTCCG	CTATATCATG	600
CGGGGCTTTT	TGTATAAGTT	TATCCTAGCT	CATGTTTTAG	GAGAGACCTT	ACTCCCTCCT	660
CTGAAGAATT	TAGCCTTGCA	GTCAGGTGGC	TTCTTTAATC	TCTATGCCTT	GGCAGTTATG	720
TATACTTTTG	GTCTGGAGCT	CTTCTTTGAC	TTTGCAGGTT	ATTCTATGTT	TGCTTTGGCC	780
ATCTCAAAC	TGATGGGAAT	CCGTAGCCCT	ATCAACTTTA	ACAAGCCCTT	TTTATCAAGG	840
GATTTAAAGG	AGTTTGGAA	TCGCTGGCAT	ATGAGTCTGT	CTTTCTGGTT	CCGTGACTTT	900
GTCTTTATGC	GAATGGTGAT	GGTGTTAACC	AGAAAGAAAG	TCTTTAAAAA	TCGTAATGTA	960
ACCTCAAGCA	TGGCCTACAT	TGTAAATATG	CTGATTATGG	GATTTTGGCA	TGGCGTGACC	1020
TGGTACTATA	TCGCCTATGG	ACTCTTTCAT	GGACTAGGCT	TGGTCATCAA	TGATGCCTGG	1080
GTTGCAAGA	AAAAAACGCT	CAATAAGAAA	CGGAAAAAAG	CAGGGAAGGC	TGCCCTACCT	1140
GAGAATCGCT	GGATTCAAGT	TCTTGGCATG	GTTGTCACTT	TCCATGTTGT	CATGTTGTCA	1200
TTCTTAATCT	TTTCTGGATT	CTTGAATAAT	CTATGGTTTA	AAAAATAA		1248

(2) INFORMATION FOR SEQ ID NO:1341:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...579
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1341:

TTGCAGATGG	AGATGCGGCT	GATGGCGTTC	GAACTGGTGG	ATTTGGATCG	ACAGGGCACT	60
AGAATGAAGA	TTATCTTTGT	ACGTCATGGG	GAGCCAGATT	ACCGTGAGTT	AGAGGAGCGT	120
TCTTATATAG	GATTTGGGAT	AGATTTGGCA	CCCTTGCTCG	AGATGGGACG	GCAGCAAGTC	180
CAGAAATTGA	GCAAAAATCC	TTTACTCTCG	TCAGCTGAAA	TAATCGTATC	TTCTGCAGTC	240
ACAAGAGCTT	TAGAAACGGC	TTCGTATGTG	GTCTGTGCTA	CGGGTTTTCC	TTTAAGAGTA	300
GAGCCTTTAT	TACATGAATG	GCAGGTCTAT	AAAACAGGAA	TAGAAAACCT	TGAAACAGCT	360
AGAAGACTGT	TTTTAGAAAA	CAAGGGGGAG	TTGCTTCCCTA	ATAGTCCCTAT	TCAATATGAG	420
ACAGCTACGG	AAATGAAGTC	TCGGTTTCTA	GAATGTATGT	CTAAGTATCG	AGAACATCAG	480
ACTGTGGTAG	TTGTTGCTCA	TCGAATGCTC	ATGCGCCAGT	TTGTGCCAAA	TGAGAAGATT	540
GATTTTTGCC	AAGTGATTGA	GTGTGAGTTA	GAGATATAG			579

(2) INFORMATION FOR SEQ ID NO:1342:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1347 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1347
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1342:

GTGGAGATGG	AAAAGTATTT	ATCGGTAACA	ACTTTGACCA	AGTATCTGAA	AATGAAATTC	60
GATAAAGACC	CATACTTGGG	ACGGGTCTAT	TTAACTGGTC	AAGTTTCCAA	CTTTCGTAAA	120
CGACCTACTC	ACCAATATTT	CTCCCTAAAG	GATGACCATG	CAGTTATTCA	AGCGACCATC	180
TGGTCTGGGA	TTTATCAGAA	ATTAGGGTTT	GACCTGGAAG	AAGGAATGAA	GATCAATGTG	240
ATTGGGCGTG	TACAGGTCTA	TGAACCAAGT	GGTAGCTACT	CCATCATCAT	TGAAAAAGCT	300
GAGCCTGATG	GGGTTGGGGC	GCTTGCGATT	CAGTTTGAAC	AACTTAAGAA	AAAATTGACA	360
GAAGAAGGCC	TGTTTCAAGA	ACGCTTCAAG	CAAGCTCTAC	CCCAATTTTC	TAAGAGAATT	420
GGGGTAGTAA	CCAGCCGTAG	TGGAGCCGTT	ATTGAGATA	TTATCACGAC	CGTCAGCAGG	480
CGATTCCCAG	GTGTTGACAT	CCTTCTTTAT	CCGACCAAGG	TTCAAGGTGA	AGGGGCTGCG	540
GAGGAAATTG	CTAGAAATAT	TGCGCGTGCT	AATCAATGGG	ACGATTTGGA	TTTGCTCATT	600
ATTGGTCGTG	GAGGTGGTTC	TATTGAGGAT	CTCTGGGCCT	TTAACGAAGA	AATTGTGGTA	660
CGAGCTATTT	TTGAATCTCG	TTTGCCAGTT	ATCTCTAGTG	TGGGGCATGA	GACGGATGTG	720
ACCTTGGCAG	ATTTTGTGGC	AGATCGACGC	GCTGCAACGC	CAACAGCGGC	GGCTGAACTG	780
GCAACACCTG	TGACCAAGTT	GGATGTATTA	GCTCATTTGC	AAAATCAGGA	AAAACGGATG	840
GTAACGGCAG	TCCGAAATGT	TCTATCTAAG	AAACAAGAGG	CTTTGAAAAA	ATGCAGTCAG	900
TCTGTTATCT	TTAGACAACC	TGAGCGCTTG	TATGACGGTT	ATTTGCAACG	CTTGGACCAA	960
CTGCAACTGC	GTTTGAAACA	AAGTTTGCGA	ACTCGGATTT	CTGATAACAA	ACAATTAGTT	1020
CAAGCAAGAA	CTCATCAATT	AGTACAATTA	TCACCTGTTA	CCAAAATCCA	ACGCTATCAA	1080
GACCGTTTAG	GACAGTTGGA	CAAGCTCTTA	GGTAGCCAAG	TGGCGTTAGT	TTATGACGCC	1140
AAGGTTGCTG	AGGTCAAGCG	ACTTTCGGAA	GCTTTGCTCA	TGTTGGATAC	TAGCCGAATC	1200
GTGGCGCGTG	GTTATGCTAT	TGTCAAAAAA	GAAGAGTCCG	TTGTAGATTG	GGTTGAGAGT	1260
TTGAAGAGAA	AAGACCAAGT	AACGCTTTTG	ATGCGAGATG	GTCAAGTAGA	ATTAGAGGTT	1320
AAAGATGTCA	AAACAAAAGA	AATTTGA				1347

(2) INFORMATION FOR SEQ ID NO:1343:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1092 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1343:

TGGCTGGTGG	AAACTTGGGA	AAGGAGAAGA	GTGATGTCTA	AAAAATTACA	ACAAATTTTCG	60
GTTCCCTTGA	TTTCTGTATT	CCTAGGAATT	TTACTCGGAG	CCATTGTCAT	GTGGATCTTC	120
GGTTATGATG	CTATTTGGGG	CTACGAAGAA	TTGTTCTATA	CAGCCTTTGG	CAGTCTGCGT	180
GGGATTGGAG	AAATCTTCCG	TGCTATGGGT	CCTCTGGTCT	TGATTGGTCT	TGGTTTTGCG	240
GTTGCCAGTC	GAGCTGGTTT	CTTTAACGTC	GGACTTCCTG	GTCAGGCTTT	GGCAGGTTGG	300
ATTCTCAGTG	GTTGGTTTGC	CCTGTCGCAT	CCAGATATGC	CCCGTCCCTT	GATGATTCTA	360
GCAACCATCG	TGATTGCCTT	GATTGCTGGT	GGGATTGTCTG	GAGCGATTCC	AGGTATTCTT	420
AGGGCCATATC	TAGGGACGTC	AGAGGTTATT	GTAACCATCA	TGATGAACTA	CATTGTCTTG	480
TATGTAGGGA	ATGCCCTTTAT	CCATGCTTTC	CCTAAAGACT	TCATGCAAAG	TACAGATTCTG	540
ACCATTCGTG	TTGGGGCTAA	TGCAACCTAT	CAGACACCTT	GGTTGGCTGA	GTTGACTGGT	600
AACTCACGGA	TGAATATTGG	TATTTTCTTT	GCCATCATTG	CCGTTGCAGT	TATTTGGTTC	660
ATGCTCAAGA	AAACAACCTC	TGGTTTTGAA	ATCCGTGCAG	TTGGTCTTAA	TCCACATGCT	720
TCAGAATATG	CTGGTATTTT	TGCCAAGCGG	ACTATTATCC	TATCTATGAT	TATTTTCAGGT	780
GCCTTGGCAG	GTCTTGGTGG	ATCTGTTGAA	GGTTTGGGAA	CCTTCCAGAA	CGTCTATGTT	840
CAAGGTTTCGT	CATTAGCTAT	CGGATTTAAC	GGAATGGCGG	TTAGTTTGCT	TGCGGCCAAC	900
TCACCAATTG	GTATACTCTT	TGCAGCCTTC	CTATTTGGCG	TTCTCCAAGT	TGGGGCTCCT	960
GGTATGAATG	CGGCGCAGGT	ACCATCTGAG	CTTGTCAGCA	TTGTAACAGC	GTCTATTATC	1020
TTCTTTGTCA	GTGTTCAATTA	CCTTATCGAA	CGCTTTGTCA	AACCGAAAAA	ACAAGTTAAA	1080
GGAGGTAAGT	AA					1092

(2) INFORMATION FOR SEQ ID NO:1344:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 390 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1344:

ATGAAGGTGG	AACCACGTTG	CGACGTCCTT	TCGAGGATGT	CGCATTTTTT	TATTAGGATA	60
CTAATTATGG	AGTTGCAAGA	ATTAGTGGAG	CGCAGTTGGG	CAATCCGACA	AGCTTATCAC	120
GAACTGGAAG	TTAAGCATCA	TGATTCCAAG	TGGACGGTAG	AAGAAGACCT	CTTGGCTTTA	180

TCTAATGATA TTGGAAATTT CCAACGACTG GTGATGACAA AGCAAGGACG CTACTATGAT	240
GAAACACCCCT ACACACTGGA ACAAAAACTT TCAGAAAATA TCTGGTGGCT ATTAGAACTT	300
TCTCAACGTT TGGATATAGA CATCTGACG GAAATGGAAA ACTTCCTCTC TGATAAAGAA	360
AAGCAATTGA ACGTTAGGAC TTGGAAGTAG	390

(2) INFORMATION FOR SEQ ID NO:1345:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...249
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1345:

CTTCTAGTT TGTCTTTGA TTTTCATTGT GTATTTAAAC AAAAAACAC CCTAAAACAT	60
CAGGGTGCCA TTCTTACATC AAATATAAAA TTGCTAGGGT CAGGAGACTT GCTAGAAGCC	120
CAACTCCCCA AAAGAAGAAG TCAACCTTCC ACTCGCTCCA AGGATTCCT TTACCAGACA	180
ATCCCCCAAG CTCAAAATGG TGATGTACAG GCGTCATACG GAAAATACGT TTACCACCTG	240
TCAGTTTGA	249

(2) INFORMATION FOR SEQ ID NO:1346:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...324
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1346:

GATTCTAGTT	TTGCAGGAAG	TCTACTATTT	TCCTTATTGT	CTGTAAGTCT	ACTGACCTTG	60
TTGTTTATCC	CAGTCATGGT	TTCTAGTTCG	GGCTCAGAGT	TTCAAAGTGG	ATGGCAAGAG	120
CATCAATTGA	TTGCTGAGAA	GGTTAGTAAA	ACACTTGACA	AGACATTTGA	TAAGGATGTC	180
AGAGAAATTC	CGACCACTCA	GTTTTATCAA	AAATTTGTAG	ATCAGATGGG	AAGGACTTAC	240
TCAGGAAATT	TGATCCTCCA	GGAGCTGATA	ACTGTGAATG	GAGCTTATAA	AGCTACTTAT	300
ATCGGTGAAC	TCTCTAGCAA	CTAA				324

(2) INFORMATION FOR SEQ ID NO:1347:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 519 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...519
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1347:

GCATCAACGG	AGTTGAGATT	CAGGTATTTT	CTAGTGAAAA	AGGATTGGAG	GTCTACCATG	60
GTTCAGAACA	GTTGTTGGCA	ATCAAAGAGC	CATAAGGTCA	AGGCTTTTAC	CTTGTTAGAA	120
TCCCTGCTTG	CCCTCATTGT	CATCAGTGGG	GGATTACTCC	TTTTTCAAGC	TATGAGTCAG	180
CTCCTCATTT	CAGAAGTTCG	CTACCAGCAA	CAAAGCGAGC	AAAAGGAGTG	GCTCTTGTTT	240
GTGGACCAAC	TTGAGGCAGA	ATTAGACCGT	TCGCAGTTCG	AAAAAGTAGA	AGGCAATCGC	300
CTATACATGA	AGCAAGATGG	CAAGGACATC	GCCATCGGTA	AGTCAAAGTC	AGACGATTTT	360
CGTAAACCG	ATGCTAGTGG	ACGGGGGTAT	CAGCCTATGG	TTTATGGCCT	CAAATCAGCT	420
CAGATTACAG	AGGACAATCA	ACTGGTTCAT	TTTCGTTTCC	AGTTTCAAAA	AGGCTTAGAA	480
AGGGAGTTCA	TCTATCGTGT	GGAAAAAGAA	GAAAGTTAA			519

(2) INFORMATION FOR SEQ ID NO:1348:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 744 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1348:

AAAGTGACGG	AGGAATTTAT	GAATGTAAAT	CAGATTGTAC	GGATTATTCC	TACTTTAAAA	60
GCTAATAATA	GAAAATTAAA	TGAAACATTT	TATATTGAAA	CCCTTGGAAT	GAAGGCCTTG	120
TTAGAAGAAT	CGGCCTTTCT	GTCAC TAGGT	GACCAAACGG	GTCTTGAAAA	GCTGGTTTTA	180
GAAGAAGCTC	CCAGTATGCG	TACTCGTAAG	GTAGAGGGAA	GAAAAAAACT	AGCTAGATTG	240
ATTGTCAAGG	TGAAAAATCC	CTTAGAAATT	GAAGGAATCT	TATCTAAAAC	AGATTGCGATT	300
CATCGATTAT	ATAAAGGTCA	AAATGGCTAC	GCTTTTGAAA	TTTCTCACC	AGAAGATGAT	360
TTGATTTTGA	TTCATGCGGA	AGATGACATA	GCAAGTCTAG	TAGAAGTAGG	AGAAAAGCCT	420
GAATTTCAAA	CAGATTTGGC	ATCAATTTCT	TTAAGTAAAT	TTGAGATTTT	TATGGAATTA	480
CATCTCCCAA	CTGATATCGA	AAGTTTCTTG	GAATCATCTG	AAATTGGGGC	ATCCCTTGAT	540
TTTATTTCCAG	CTCAGGGGCA	GGATTTGACT	GTGGACAATA	CGGTTACCTG	GGACTTATCT	600
ATGCTCAAGT	TCTTGGTCAA	TGAATTAGAC	ATAGCAAGTC	TTCGCCAGAA	GTTTGAGTCT	660
ACTGAATATT	TTATTCCTAA	GTCTGAAAAA	TTCTTCCTTT	GTAAAGATAG	AAATAATGTT	720
GAATTGTGGT	TTGAAGAAAT	ATGA				744

(2) INFORMATION FOR SEQ ID NO:1349:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1349:

AGTGGTCAGG	AACTTACTCC	TGACCTTTTT	CTTTTGCAAA	ATGACAAAAA	TCATAAACTT	60
TTTGACAAC	TACTTGTC	AAAAGAAAAA	GATGTGTTAC	AATGTAAGCA	AGTTAAGAGA	120
AAAGAAGAAA	GGAGCTATGA	TGTGGGTACT	AGGGTTTATA	CTATTTCTGA	TTTCTTTTA	180
TTCTAA						186

(2) INFORMATION FOR SEQ ID NO:1350:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 879 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...879
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1350:

ACTTACCAGG	AATTAATTTG	GAGTTCTAAT	ATGAAATTAG	CTGTTTTTCAC	AGATTCCTCT	60
GCTTATCTCA	GTGAAGAGAC	CTTGCAAAGA	GAAGACTTGT	TTGTCTTGGA	TATTCCTGTC	120
AATATTGATG	GTGAGGAATA	TGTCGAAGGC	ATCAATCTGT	CTGCTGAGGA	ATTTTACCAA	180
AAAATGGCTC	AGGCTTCTGA	ATTGCCTAAG	ACCAGTCAAC	CAAGTATTGC	CAAGTTAGAT	240
GAGATCTTAA	CTTCGCTCAA	AGAACAAGGC	TATACACATG	CCTTGGGGCT	TTTCCTATCT	300
TCTGGAATTT	CAGGTTTTTA	CCAAAATATC	CAGTATATGG	TCGATGACTA	TGAGGGCTTA	360
ACCATTGCTT	TCCCAGACAC	TTTGATTACA	AGTGCTCCCC	TAGGCATCAT	GGTTGAAAGC	420
GTCTTTAATT	GGCGTGATCA	GGGCGATGAT	TTTGCCAGCA	TTCAGGATAA	GCTAGCCATT	480
CAAATCAGCC	GTACGTCAGC	CTTTATCATG	GTAGATGACT	TGGATCATT	GGTAAAAGGT	540
GGACGCCTTT	CAAATGGGGC	TGCCATTTTG	GGCAATTTGC	TTAGCATTAA	GCCAATCCTT	600
TATTTTAAACG	ATCAAGGTGT	GATTGAAGTT	TACGAAAAAG	TTCGTACTGA	AAAGAAGGCC	660
ACCAAGCGCT	TAATTGAAAT	TATCAAGGAA	ACAACGGCTT	CAGGTCAATA	CCGGGTCATT	720
GTCATTTCATG	GGAATGCTCC	TGAAAAGGCT	GAAGAATTGC	GTCAGCACTT	GCTTGATTTT	780
GGCTTGGGTT	CGGATGTTTC	ACTTGCTACA	TTTGGTAGTG	TCATTGGAAC	GCACCTAGGA	840
GCAGGAAGTA	TTGCTCTGGG	TTATATTCCA	GTGATTAG			879

(2) INFORMATION FOR SEQ ID NO:1351:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 498 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...498
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1351:

CTAATACAGG	AGGTTTTTTTT	TATGGGACAG	ACAATCATAT	CTGCTATTGG	TGTTTATATT	60
TCCACCAGTA	TCGATTATTT	AATTATTTTA	ATTATTTTAT	TTGCACAGCT	ATCACAGAAT	120
AAACAGAAAT	GGCATATTTA	TGCGGGGCAA	TATCTAGGCA	CAGGCTTACT	TGTAGGGGCG	180

AGTTTAGTTG	CTGCTTATGT	CGTTAATTTT	GTGCCTGAAG	AATGGATGGT	TGGATTGCTT	240
GGTTTAAATCC	CTATCTATTT	AGGGATTTCG	TTTGCAATTG	TTGGAGAAGA	TGCGGAAGAA	300
GAAGAGGAAG	AAATTATTTGA	AAGATTAGAA	CAAAGCAAGG	CAAATCAACT	GTTTTGGACA	360
GTTACATTGC	TGACAAATGC	GTCTGGCGGA	GATAATTTAG	GTATCTATAT	ACCTTATTTT	420
GCTTCGTTAG	ATTGGTCACA	GACCTCGTG	GCCTTGCTTG	TGTTTGTAAT	CGGCATAATT	480
ATCTTTTGC	AGAATTAG					498

(2) INFORMATION FOR SEQ ID NO:1352:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...327
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1352:

AGCAAGCAGG	ATCTGCTTTA	CCCTAGAAAA	GGAAAAGCGC	TTAAGAAACA	GGCCAGCACC	60
AACTTTAAAC	CTGCTGGTCA	ATCCATCGAA	CAGCGGCCTG	AAGCTATCAA	TTTTCGCTTG	120
GAGAATGGGC	ATTATGAGAT	TGATACGGTT	CTACTTACGA	GAGCGAAAAA	CTACTGCTTG	180
CTTGTCCTGA	CGGATCGAAA	AAGTAGACAT	CAGATCATCC	GATTGATTCC	AAATAAAAAGT	240
GCTGACGTGG	TCAATCAGGC	TCTAAAACTC	ATCTTAAAAAC	AGCCCAAGTT	CTTTCCNTCN	300
CATNNGCAGA	AGCTATCATG	CCACTAA				327

(2) INFORMATION FOR SEQ ID NO:1353:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 252 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1353:

TTTTATAAGG	AAATTGACTT	TATTCACCGT	AAGTGGCCAG	ATG TTCAGAA	GTATCTGGTT	60
TATTTTCAAA	ATTTTACCAA	CACCCGTGAA	AAGGTGGAAG	TTATTCGAGA	GCGTTATGAA	120
CAGGCTATCA	ATGAGCCAGG	TGTGGTAGGA	ATCAATATTG	GAACGCGCCC	AGACTGTTTA	180
CCAGACGAAA	CCATCGAATA	TTTGGCTGAG	TTATCGGAGT	GCATGCATGT	GACGGTTGAA	240
TTGGGCTTGT	AG					252

(2) INFORMATION FOR SEQ ID NO:1354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1354:

GAAAATAAGG	AGCATTGTGT	GAGTCTCTTC	TTGAAAAAAA	CACGAAATTT	TGGTAAAATG	60
AGTCTTATGA	AAACATTCTA	TGATGTGCAG	CAATTCCACA	AGAGATTGTTG	TATTAATGTT	120
TACATGGGAA	AACGCTTATA	TGATATTGAA	CTGATGAAGT	TGGAACTATC	TCGGATTTAC	180
AATGCGAGGT	GGATGGATAA	ATAA				204

(2) INFORMATION FOR SEQ ID NO:1355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1355:

AAATTAAAGG	AGAAAAATTT	GATGAGATAC	ATAACTCTTG	GTCAAGATGA	CAAAGAATTA	60
TCAGAAATTG	TTCTCGGAAT	GATGAGAATA	AAAGATAAGT	CTGTAAAAGA	AGTTGAAGAG	120
CTTGTAGAAA	CAGCACTTTC	TGTTGGAATC	AATGCCCTTC	ACTTGGCTGA	TATTTATGGT	180
CGTGGTCGTT	GTGAAGAACT	GTTAGGTCTT	GTCCTAAAAA	ATCGTCCAGA	TTTAAGAGAA	240
AAGATGTGGA	TTCAGTCCAA	ATGTGGCATT	CGTATTGAAG	AATTTACCTA	TTTTGATTTT	300
CCTAAGGACT	ATATTATAAA	ATCAGTAGAC	GGTATTTTGC	AAAGATTGAA	GATTGATCAT	360
CTAGATAGCT	TGCTCCTTCA	TCGACCAGAT	GCTTTGATGG	AATCTGACCA	AGTAGCAGAA	420
GCCTTTGATC	TCCTTTATAA	ACAAGGTAAA	GTTTCGAGATT	TTGGAGTTTC	TAATCAAAAT	480
CCTATGATGA	TGGAGTTACT	TAAAAAAGA	TGTCAAGCAG	CCGTTAGCTG	TTAA	534

(2) INFORMATION FOR SEQ ID NO:1356:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 708 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1356:

AGAATAAAGG	AGATTCGTGT	GAAAGCCATT	ATCTTAGCAG	CGGGATTGGG	AACTCGCTTG	60
CGTCCTATGA	CTGAAAATAC	CCCTAAAGCC	TTGGTTCAGG	TTAATCAAAA	ACCTTTGATT	120
GAATACCAAA	TTGAGTTTCT	CAAAGAAAAA	GGAATCAATG	ACATCATCAT	CATTGTTGGT	180
TATCTTAAAG	AACAATTTCG	TTACTTAAAA	GAAAAATACG	GTGTTCGCCT	CGTTTTCAAT	240
GATAAATACG	CTGACTACAA	TAACTTTTAC	TCTCTCTATC	TTGTAAAAGA	AGAATTGGCC	300
AACAGCTATG	TTATTGATGC	AGATAACTAT	CTCTTTAAAA	ATATGTTCCG	CAATGATTTG	360
ACTCGTTCGA	CTTATTTTAT	TGTTTATCGT	GAAGATTGTA	CCAACGAATG	GTTCTTGGTC	420
TATGGAGATG	ACTACAAGGT	TCAAGACATT	ATTGTTGATA	GCAAGGCAGG	TCGCATCCTT	480
AGTGGTGTAT	CCTTCTGGGA	TGCTCCAAC	TGCAGAAAAGA	TTGTCAGCTT	TATCGACAAG	540
GCTTATGCAA	GTGGCGAATT	TGTTGATCTC	TACTGGGACA	ATATGGTTAA	GGATAATATC	600
AAAGAGCTAG	ATGTCTATGT	TGAAGAAATTA	GAAGGCAATA	GCATTTATGA	GATCGATAGT	660
GTCCAAGACT	ATCGTAAATT	AGAAGAAATT	CTTAAAAACG	AAAATTAA		708

(2) INFORMATION FOR SEQ ID NO:1357:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1056 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1357:

TGTGTAAAGG	AGAAGGCTAT	GGCAAAGAAA	ATAGTAGCTC	TAGTAGGAGA	CGGAATTGGC	60
CCAGAAATCA	TGGAGGCTGG	TTTAGAAGTT	CTGGAGGCTC	TAGCTGAAAA	AACAGGTTTT	120
GACTATGAGA	TTGACAGACG	ACCGTTCGGA	GGTGACAGATA	TTGATGCAGC	AGGACCTCCC	180
TTACCTGATG	AAACCCTTAA	GGCAAGTAGG	GAAGCAGATG	CTATCCTACT	AGCAGCTATC	240
GGTAGTCCTC	AGTATGATGG	AGCAGCGGTT	CGCCCTGAAC	AAGGCCTGAT	GGCTCTCCGT	300
AAGGAATCA	ATCTTTACGC	TAATATTTCG	CCTGTAAAAA	TCTTTGACAG	TCTCAAGTAT	360
TTGTCACCCAC	TCAAACCGGA	ACGAATTTCT	GGGTAGACT	TTGTCGTGGT	GCGTGAATTG	420
ACAGGCGAGA	TTTACTTTGG	AGATCATATT	CTTGAAGAGC	GCAAAGCGCG	TGATATCAAC	480
GACTATAGCT	ATGAGGAAGT	GGAGCGGATT	ATTTCGCAAAG	CCTTTGAAAT	TGCAAGAAAT	540
CGCAGAAAAA	TCGTTACTAG	TATCGATAAG	CAAAATGTTC	TAGCGACCTC	AAAACTCTGG	600
CGGAAAGTAG	CTGAGGAAGT	CGCACAGGAT	TTCCCAGATG	TAACCTTGGA	ACACCAGCTG	660
GTAGACTCAG	CTGCTATGCT	TATGATTACC	AATCCTGCTA	AGTTTGATGT	TATTGTAACG	720
GAGAATCTTT	TTGGAGATAT	TTTATCTGAT	GAATCAAGCG	TCTTATCTGG	TACACTTGAG	780
GTTATGCCAT	CAGCCAGTCA	TTCTGAAAAT	GGACCAAGTC	TCTATGAACC	TATTCACGGT	840
TCAGCACCTG	ATATTGCAGG	TCAAGGAATT	GCCAATCCTA	TTTCCATGAT	TTTATTAGTT	900
GTCATGATGT	TGAGAGATAG	TTTCGGACGT	TATGAGGATA	CAGAGCGTAT	CAAACGTGCT	960
GTTGAGACAA	GTCTGGCGGC	AGGAATTTTA	ACGAGAGATA	TAGGAGGTCA	GGCTTCAACA	1020
AAGGAAATGA	TGGAAGCTAT	TATTGCAAGG	TTATGA			1056

(2) INFORMATION FOR SEQ ID NO:1358:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1383 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1358:

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ATAGTAAAGG AGGAGAAAAGG ATTGAAAGAA AAACAATTTT GGAATCGTAT ATTAGAATTT 60
GCACAAGAAA GACTGACTCG ATCCATGTAT GATTTCTATG CTATTCAAGC TGAAC TCATC 120
AAGGTAGAGG AAAATGTTGC CACTATATTT CTACCTCGCT CTGAAATGGA AATGGTCTGG 180
GAAAAACAAC TAAAAGATAT TATTGTAGTA GCTGGTTTTG AAATTTATGA CGCTGAAATA 240
ACTCCCCACT ATATTTTTCAC CAAACCTCAA GATACGACTA GCTCACAAGT TGAAGAAGCT 300
ACAAATTTAA CTCTTTATAA CTATAGTCCA AAGTTAGTAT CTATTCCCTTA TTCAGATACG 360
GGATTAAAAG AAAAGTATAC CTTTGATAAC TTTATTTCAAG GGGATGGAAA TGTTTGGGCT 420
GTATCAGCCG CTTTAGCTGT CTCTGAAGAT TTGGCTCTGA CCTATAACCC TCTTTTTTATC 480
TATGGAGGAC CAGGCCCTGG TAAGACTCAC TTATTAAACG CTATTGGAAA TGAAATTCTA 540
AAAAATATTC CTAATGCGCG TGTTAAATAT ATCCCTGCCG AAAGCTTTAT TAATGACTTT 600
CTTGATCACC TAAGACTTGG GGAAATGGAA AAGTTTAAAA AGACCTATCG TAGTCTTGAT 660
CTTTTGTTAA TCGATGATAT CCAGTCACTC AGCGGAAAAA AAGTTGCAAC TCAGGAAGAA 720
TTTTTCAATA CCTTTAACGC CCTTCATGAC AAGCAAAAAC AGATTGTCCT AACGAGTGAT 780
CGTAGTCCAA AACATCTAGA AGGGCTCGAG GAGAGGCTTG TCACGCGTTT TAGTTGGGGA 840
TTGACACAAA CTATCACACC CCCTGACTTT GAAACACGTA TTGCCATTTT ACAAAGTAAA 900
ACGGAACATT TAGGCTACAA TTTCCAAAGT GATACTCTAG AATACCTAGC TGGGCAATTT 960
GATTCAAATG TTCGAGATCT TGAGGGGAGCC ATCAACGACA TCACTTTAAT TGCCAGAGTA 1020
AAAAAAATCA AGGATATCAC TATTGATATT GCTGCAGAAG CCATTAGAGC CCGCAAACAA 1080
GATGTTAGCC AAATGCTCGT CATCCCAATT GATAAAATCC AAAGTGAAGT TGGTAACTTT 1140
TATGGTGTTA GTATCAAAGA AATGAAGGGA AGTAGACGCC TTCAAATATAT TGTTTTGGCC 1200
CGTCAAGTAG CCATGTATTT ATCTAGAGAA CTAACAGATA ATAGTCTTCC AAAAAATTGGG 1260
AAGGAATTTG GGGGAAAAGA TCATACCACA GTCATTTCATG CCCATGCCAA AATAAAATCT 1320
TTGATTGATC AAGACGATAA TTTACGTTTA GAAATTGAAT CAATCAAAAA GAAAATCAAA 1380
TAA
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(2) INFORMATION FOR SEQ ID NO:1359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1359:

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GTGGTAAAGG AGCAGATCAT GACCTACACA ATCTTAATCG TAGAGGATGA ATATCTGGTA 60
AGACAAGGTT TGAATAAACT GGTCAATGTA GCAGCCTACG ATATGGAAAT CATTGGTCAG 120
GCTGAAAAATG GAAGGCAGGC TTGGGAATTG ATCCAAAAGC AGGTGCCAGA TATCATTTTA 180
ACCGATATCA ACATGCCTCA TCTAAATGGC ATCCAGTTGG CCAGTCTGGT ACGAGAAACC 240
TATCCTCAGG TTCATTTGGT CTTTTTAACA GGTTACGATG ATTTTGATTA TGCCTTGTCT 300
GCTGTCAAAC TAGGTGTGGA CGACTACCTG CTCAAACCCT TTTCTCGTCA GGATATTGAG 360
GAAATGTTGG GGAAATCAA ACAAAAAC TA GACAAGGAAG AGAAAGAAGA GCAGTTACAA 420
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GATTTATTGA	CTAATAGGTT	TGAAGGAAAC	ATGGCCCAGA	AAATCCAGTC	TCATCTGGCT	480
GATAGCCAAAT	TTAGTTTAAA	GTCTTTAGCC	AGTGACTTAG	GTTTTAGTCC	GACCTATCTG	540
AGTTCCTTGA	TTAAGAAAGA	GTTGGGCTTG	CCTTTTCAGG	ATTATCTGGT	GAGAGAACGT	600
GTTAAACAAG	CCAAGCTCTT	GCTTTTAACT	ACAGATCTGA	AGATTTATGA	GATCGCAGAG	660
AAGGTTGGTT	TTGAAGATAT	GAACTATTTT	ACCCAACGTT	TTAAGCAGAT	TGCAGGTGTG	720
ACACCTCGTC	AGTTTAAAGAA	GGGAGAAGAC	CGATGA			756

(2) INFORMATION FOR SEQ ID NO:1360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1360:

GAGAAAAAGG	AAACAATGAT	TTTTACATAT	AACAAAGAAC	ATGTCGGTGA	TGTCCTTATG	60
GTCATCGTGA	AAAATAGCGG	AGATGCTAAA	CTGAATGTGG	AACGCAAAGA	CAAGGTAGCC	120
CGTGTTTTCC	TCAAAGAAAA	TGGGGAAACA	GTAGCTTGGA	ACATTTTTGA	GGTTTCGAGC	180
TTGTTTGAAA	TTGCAGAGCG	CGGTCAAGTC	TTTTTTATCAG	ATGAGCAAGT	CGCTCGTTTG	240
AACCAAGAAT	TACAGGCGGA	AGGTTTACAA	GAAGAAATTG	TTAATGATAA	GGAACCTAAG	300
TTTGTTGTTG	GTGAAATTGT	CGAGATGGTA	GCTCATCCAG	ACAGTGACCA	CCTCAACATC	360
TGCCAAGTTG	CAGTCGCAAG	TGACAAAGATA	GTGCAAATCG	TTGCAGGAGC	ACCTAATGCG	420
CGTGTTGGGT	TGAAAACCAT	TGTGGCTCTT	CCTGGTGCCA	TGATGCCAAA	AGGGAATTTT	480
ATTTTCCCAG	GCGAACTTCG	TGGTGAAAAG	AGTTTTGGGA	TGATGTGTAG	TCCTCGTGAA	540
TTGCATTTGC	CAAATGCTCC	GCAAAAACGT	GGGGTGCTTG	AATTATCAGA	AGACCAAGTT	600
GTGGAACAC	CGTTCGACCC	AGCGAAACAC	TGGACTGCCT	AG		642

(2) INFORMATION FOR SEQ ID NO:1361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1361:

CTAAGAAAGG	AGCCAAGCAT	GGCAAAGGGC	GAGGGAAAGG	TCGTCGCACA	AAATAAAAAG	60
GCACGCCACG	ACTATACAAT	CGTAGATACG	CTAGAGGCAG	GGATGGTCCT	GACTGGAAC	120
GAAATCAAGA	GTGTACGAGC	TGCTCGAATT	AATCTCAAGG	ATGGCTTTGC	TCAAGTGAAA	180
AATGGAGAAG	TTTGGCTGAG	CAATGTTTCAT	ATCGCGCCTT	ACGAAGAGGG	CAATATCTGG	240
AACCAGGAAC	CAGAACGTCG	TCGTAAACTC	CTGCTCCATA	AAAAGCAAAT	TCAAAAATTG	300
GAACAAGAGA	CCAAAGGGAC	AGGAATGACC	TTAGTTCCCC	TTAAGGTCTA	TATAAAGAT	360
GGCTACGCTA	AGCTTCTTTT	AGGACTTGCC	AAAGGGAAGC	ATGACTATGA	CAAACGGGAG	420
TCTATCAAAC	GTCGTGAGCA	AAATCGAGAT	ATCGCGCGTG	TGATGAAAGC	TGTTAATCAG	480
CGATAA						486

(2) INFORMATION FOR SEQ ID NO:1362:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2034 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2034

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1362:

AAAAGAAAGG	AGTGGAGCAT	GAATCTACAT	CAACCCTTG	ATGTCTTGCC	TGGTGTGGGA	60
CCAAAGTCAG	CAGAAAAATA	CGCCAAACTA	GGAATTGAAA	ACTTGCAAGA	TCTCTTGCTC	120
TACTTTCCTT	TCCGTTATGA	AGACTTCAAA	ACCAAGCAGG	TGCTGGAGCT	GGAAGACGGT	180
GAGAAGGCAG	TTCTTTCTGG	TCAGGTAGTG	ACTCCTGCTA	GTGTCCAGTA	TTATGGTTTC	240
AAGCGCAATC	GCCTGCGTTT	TAGTCTCAAG	CAGGGAGAGG	TCGTTTTTGC	GGTGAATTTT	300
TTTAACCAGC	CCTATCTGGC	TGATAAAATA	GAGTTGGGAG	CAACCCTTGC	TGTCTTTGGA	360
AAATGGGACC	GCGCTAAGGC	TAGTCTGAAT	GGGATGAAGG	TTCTGGCTCA	GGTAGAAGAT	420
GACCTCCAGC	CTGTTTATCG	TCTGGCTCAG	GGAATCAGTC	AGGCCAGTCT	GGTTAAGGTC	480
ATCAAGACGG	CTTTTGATCA	GGGACTGGAC	CTCTTGATAG	AAGAAAATCT	GCCCCAGTCT	540
TTACTAGACA	AATACAACT	CATGTCCCGT	TGTCAGGCAG	TCCGAGCTAT	GCATTTTCCA	600
AAGGATTTGG	CAGAATACAA	GCAGGCTCTT	CGCCGTATAA	AGTTTGAGGA	ACTCTTTTAT	660
TTCCAAATGC	AGCTGCAGAT	GCTCAAATCT	GAAAATAGAG	TTCAGGGAAG	TGGTCTGGTT	720
CTGAATTGGT	CTCAGGAAAA	AGTGACAGCA	GTTAAAGTAA	GTCTTCCTTT	TGCCCTGACC	780
CAAGCTCAGG	AAAAGAGTTT	GCAGGAAATT	TTAAGTCCGA	CCACCACATG		840
AATCGTCTCC	TACAAGGGGA	TGTGGGGAGT	GGAAAAACGG	TAGTCGCTGG	CTTGGCCATG	900
TTTGCGGCAG	TGACAGCAGG	TTATCAGGCT	GCCCTAATGG	TACCAACAGA	AATCCTCGCA	960

GAGCAACACT	TTGAGAGTTT	ACAGAACCTT	TTTCCCAATT	TGAAACTGGC	TCTCTTGACA	1020
GGTTCCTTGA	AAGCTGCAGA	AAAGAGAGAG	GTCCTTGGAGA	CCATTGCCAA	GGGTGAGGCT	1080
GATTTGATTA	TCGGAACCTCA	CGCTCTGATA	CAAGATGGGG	TGGAGTATGC	TCGTCTTGGT	1140
TTGATTATTA	TCGATGAGCA	GCACCGTTTT	GGTGTAGGGC	AAAGGCGTAT	TTTACGGGAA	1200
AAAGGTGACA	ATCCAGATGT	CCTCATGATG	ACGGCGACTC	CCATTCCACG	GACGCTTGCC	1260
ATCACAGCCT	TTGGAGATAT	GGATGTTTCC	ATTATCGACC	AGATGCCAGC	AGGTCGGAAG	1320
CCTATTGTGA	CGCGCTGGAT	CAAACATGAG	CAACTACCTC	AGGTCCTGAC	TTGGTTAGAG	1380
GGGGAAAATC	AAAAAGGTTT	CCAAGCCTAT	GTCATCTCTC	CTTTGATTGA	AGAATCAGAA	1440
GCTCTAGATT	TGAAAAATGC	CATTGCCTTA	TCAGAGGAGT	TGACGACTCA	TTTTGCAGGC	1500
AAGGCAGAGG	TGGCTCTTCT	ACATGGTAGG	ATGAAGAGTG	ACGAAAAAGA	CCAGATCATG	1560
CAGGATTTCA	AGGAGAGAAA	GACGGATATT	CTGGTTTCGA	CGACGTTTAT	TGAGGTTGGG	1620
GTCAACGTTT	CCAAATGCGAC	TGTCATGATT	ATCATGGATG	CCGATCGCTT	CGGGCTCAGC	1680
CAGCTTCACC	AGCTTAGAGG	TCGTGTCGGT	CGGGGGGACA	AGCAGTCCTA	CGCTGTTCTC	1740
GTTGCCAATC	CCAAGACGGA	TTCTGGGAAA	GACCGCATGC	GCATCATGAC	AGAAACGACC	1800
AATGGATTTG	TCCTTGCGGA	GGAAGATTTG	AAAATGCGTG	GTTCTGGTGA	GATTTTTTGA	1860
ACCAGACAGT	CAGGACTTCC	AGAGTTCCAA	GTGGCTGATA	TTATCGAAGA	TTTTCCGATT	1920
TTAGAAGAAG	CAAGAAAGGT	TGCTAGCTAC	ATTAGTTCTA	TAGAACTTG	GCAAGAAGAT	1980
CCAGAGTGGC	GCATGATTGC	CCTTCATCTG	GAAAAGAAAG	AACATCTGGA	TTAA	2034

(2) INFORMATION FOR SEQ ID NO:1363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1363:

TTGATGAAGG	AAATCTTTGA	TAGACGTTAC	CCTGTGACGA	GTTTCTTCCT	CTTAGTGACG	60
ACCTTGGTAT	TTTTACTAAT	GTTGGTCACT	ACAGGCGGAA	ACTTTGACAG	GGCAGATACA	120
TTATTTTCGAT	TTGGAGCCAT	GTATGGGCCA	GCTATTTCGCC	TCTTTCCCGA	GCAGGTTTGG	180
CGTCTCTTGT	CTGCCATTTT	TGTTCATATT	GGGTGGGAAC	ATTTTCATTGT	TAAATATGCTT	240
TCACCTTTATT	ATCTTGGAAG	GCAGGTAGAG	GAGATTTTTCG	GTTCTAAGCA	GTTTTTCTTT	300
CTCTATCTTT	TATCAGGAAT	GATGGGCAAT	CTCTTTGTTT	TTGTATTTAG	TCCTAAATCC	360
TTAGCAGCAG	GCGCCTCTAC	CTCTCTTTAT	GGGCTATTTG	CCGCGATTAT	TGTTCTTCGC	420
TATGCAACTC	GCAATCCTTA	TATCCAACAG	CTAGGGCAAT	CCTATCTGAC	ACTTTTTTGTG	480
GTTAACATTA	TTGGAAGTGT	TCTGATTCCA	GGAATCAGCC	TAGCAGGCCA	TATCGGTGGT	540
GCAGTTGGTG	GCGCATTTCT	AGCAGTTATC	TTTCCAGTTA	GAGGAGAAAA	ACGGATGTAT	600
AACACCAGCC	AGAGATTAGG	AGCGGTAGTC	TTGTTCGTAG	GACTCGCCAT	TTTGCTTTTC	660
TACAAGGGAA	TGGGAATGTG	A				681

(2) INFORMATION FOR SEQ ID NO:1364:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 960 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...960
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1364:

ACGATGAAGG	AAAATTTAAA	AGTTAATATT	CTATGGTTAC	TCCTTTTGTT	AGCTGGCTAT	60
AGCTTGATTA	GTGTACTGGT	TTCAGTCGGA	GTACTTAATC	TATTCTATGT	ACAGATTTTA	120
CAACAAATTG	GAATTAATAT	TATTTTGGCT	GTTGGTCTCA	ACTTAATCGT	TGGTTTTTCA	180
GGACAATTTT	CACTTGGTCA	TGCTGGTTTC	ATGGCGATTG	GTGCCTATGC	AGCAGCTATT	240
ATTGGTTCTA	AATCACCAAC	CTACGGTGCC	TTCTTTGGAG	CTATGCTTGT	AGGGGCTTTG	300
CTTTCAGGAG	CAGTTGCCCT	ACTTGTCTGC	ATTCCAACCT	TGCGCTTGAA	GGGGGACTAT	360
CTTGCGGTAG	CAACTCTAGG	TGTTTCTGAA	ATTATCCGTA	TCTTTATCAT	CAATGGTGGA	420
AGCCTTACAA	ATGGTGCGGC	AGGTATCTTA	GGGATTCCCTA	ACTTTACAAC	TTGGCAAATG	480
GTTTACTTCT	TTGTCGTGAT	TACAACCATT	GCAACCTTGA	ACTTCTTGCG	TAGCCCAATT	540
GGTCGTTCAA	CCCTCTCTGT	TCGTGAAGAT	GAAATCGCTG	CTGAGTCAGT	TGGGGTTAAT	600
ACGACTAAAA	TTAAAATCAT	CGCTTTTGTC	TTTGGTGCCA	TTACTGCAAG	TATTGCTGGG	660
TCACTTCAGG	CAGGATTTAT	CGGGTCTGTT	GTACCGAAAG	ATTACACCTT	CATCAACTCA	720
ATCAACGTTT	TGATTATTGT	TGTATTTGGT	GGACTCGGTT	CCATTACAGG	TGCGATTGTT	780
TCGGCTATTG	TTCTGGGAAT	TTTGAATATG	CTTCTCCAAG	ATGTTGCTAG	TGTGCGTATG	840
ATTATTTACG	CTTTGGCCTT	GGTATTGGTA	ATGATTTTCA	GACCAGGTGG	ACTCCTTGGA	900
ACATGGGAAC	TGAGCCTATC	ACGTTTCTTT	AAAAAATCTA	AGAAGGAGGA	ACAAAACTAA	960

(2) INFORMATION FOR SEQ ID NO:1365:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1365:

AATGAGAAGG	AAAAATGTCA	AACTTTTATA	TTGCAAATAG	GAGAAATTAT	GACAAAAACA	60
TTAAAACGTC	CTGAGGTTTT	ATCACCTGCA	GGGACTTTAG	AGAAGCTAAA	GGTAGCTGTT	120
CAGTATGGAG	CAGATGCTGT	CTTTATCGGT	GGTCAGGCCCT	ATGGTCTTCG	TAGCCGTGCC	180
GGAAACTTTA	CTTTCGAACA	GATGGAAGAA	GGCGTGCAGT	TTGCGGCCAA	GTATGGTGCC	240
AAGGTCTATG	TAGCGGCTAA	TATGGTTATG	CACGAAGGAA	ATGAAGCTGG	TGCTGGTGAG	300
TGGTTCCGTA	AACTGCGTGA	TATCGGGATT	GCAGCAGTTA	TCGTATCTGA	CCCAGCCTTG	360
ATTATGATTG	CAGCTACTGA	AGCACCAGGC	CTTGAAATCC	ACCTTTCTAC	CCAAGCCAGT	420
GCCACTAACT	ATGAAACCCCT	TGAGTTCTGG	AAAGAGCTAG	GCTTGACTCG	TGTCGTTTTA	480
GCGCGTGAGG	TTTCAATGGA	AGAATTAGCT	GAAATCCGCA	AACGTACAGA	TGTTGAAATT	540
GAAGCCTTTG	TCCATGGAGC	TATGTGTATT	TCATACTCTG	GACGTTGTAC	TCTTTCAAAC	600
CACATGAGTA	TGCGTGATGC	CAACCGTGGT	GGATGTTCTC	AGTCATGCCG	TTGGAAATAC	660
GACCTTTACG	ATATGCCATT	TGGGAAAGAA	CGTAAGAGTT	TGCAGGGTGA	GATTCCAGAA	720
GAATTTTCAA	TGTCAGCCGT	TGACATGCTT	ATGATTGACC	ACATTCCAGA	TATGATTGAA	780
AATGGTGTGG	ACAGTCTAAA	AATCGAAGGA	CGTATGAAGT	CTATTCACTA	CGTATCAACA	840
GTAACCAACT	GCTACAAGGC	GGCTGTGGAT	GCCTATCTTG	AAAGTCCTGA	AAAGTTTGAA	900
GCTATCAAAC	AAGACTTGGT	GGACGAGATG	TGGAAGGTTG	CCCAACGTGA	ATTGGCAACA	960
GGTTTCTACT	ACGGTATACC	ATCTGAAAAT	GAGCAGTTGT	TTGGTGCTCG	CCGTAAAATT	1020
CCTGAGTACA	AGTTTGTGCG	TGAAGTGGTT	TCTTATGATG	ATGCGGTACA	AACAGCAACT	1080
ATTCGTCAAC	GAAACGTCAT	TAACGAAGGG	GACCAAGTTG	AGTTTTATGG	TCCAGGTTTC	1140
CGTCATTTTG	AAACCTATAT	TGAAGATTTG	CATGATGCCA	AAGGCAATAA	AATCGACCGC	1200
GCTCCAAATC	CAATGGAAC	ATTGACTATT	AAAGTCCCAC	AACCCGTTCA	ATCAGGAGAC	1260
ATGGTTTCGTG	CATTAAAAGA	AGGACTCATC	AATTTTTATA	AGGAAGATGG	AACCAGCGTC	1320
ACAGTTCGAG	CTTAA					1335

(2) INFORMATION FOR SEQ ID NO:1366:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 462 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1366:

GATGGTGAGG	AAAAGATGAC	AATTCGTTTT	GAAGAAAAGG	TGAGTATAGA	AAACGCTCAA	60
TTTGTATGCC	AGTGGTCCAA	CTCCCTAGGC	AAATCCTTTT	AAGAACAATG	GATGGGACCA	120
AGGATTCCTT	TTCTACTGAC	CCTTCAAGCC	TTGGAAGGAG	TCTTTTCAAT	CTTTGATGAA	180
CAAGAGTTTG	TGGGACTTAT	CCAGAAAATC	AGGCTAGAAG	ACAGCAATCT	TCATATCGGG	240
AGATTTTTTTA	TCAACCCCCA	GAAACAGGAG	CAAGACTTAG	GTAGCCAGGC	TTTAAGGAAA	300

TTTGTTAGTT	TGGCCTTTGA	AAATGAAGAT	ATAGATAGTA	TTTCTCTAAA	TGTTTTTCGAG	360
GCAAAATCAAA	GAGCTCAGAA	TCTTTACCAA	AAAGAAGGAT	TTGAAAATCGT	TCAAATGGTT	420
GAAGCACCTG	TACGAAAATA	TAGTAGATTG	AAACTAGAAT	AG		462

(2) INFORMATION FOR SEQ ID NO:1367:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1305
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1367:

AATTTTCGAGG	ACATAAAGAT	GACAGTTAAA	ATTGCTTTAC	TGGGATTTGG	TACCGTTGCA	60
AGTGGTGTGC	CTTTCCTCCT	AAAGGAAAAAT	GGAGGAAAAA	TCAATCAATC	AGCACATTCA	120
GATATCAAAAG	TTGCTAAGGT	ATTGGTCAAG	GATGAAGATG	AAAAAAATCG	CTTGCTTGCA	180
GCAGGGAATG	ACTTTAACTT	TGTAACCAAT	GTGGATGATA	TTTTATCAGA	CCAGGATATT	240
ACTATCGTAG	TGGAATTGAT	GGGGCGTATT	GAGCCTGCTA	AAACCTTTAT	CACTCGTGCC	300
TTGGAAGCTG	GAAAACACGT	TGTTACTGCT	AACAAGGACC	TTTtagctgt	CCATGGCGCA	360
GAATTGCTAG	AAATCGCTCA	AGCTAACAAG	GTAGCACTTT	ACTACGAAGC	AGCAGTTGCT	420
GGTGGGATTC	CAATTCTTCG	TACTTTAGCA	AATTCCTTGG	CTTCTGATAA	AATTACGCGC	480
GTGCTTGGAG	TAGTCAACGG	AACTTCCAAC	TTCATGGTGA	CCAAGATGGT	GGAAGAAGGC	540
TGGTCTTACG	ATGATGCTCT	TGCGGAAGCA	CAACGTCTAG	GATTTGCAGA	AAGCGATCCG	600
ACGAATGACG	TAGATGGGAT	TGATGCAGCC	TACAAGATGG	TTATTTTGAG	CCAATTTGCC	660
TTTGGCATGA	AGATTGCCTT	TGATGATGTA	GCCCACAAGG	GAATCCGCAA	TATCACACCA	720
GAAGACGTAG	CTGTAGCTCA	AGAGCTTGGT	TACGTAGTGA	AATTGGTTGG	TTCTATTGAG	780
GAAACTTCTT	CAGGTATTGC	TGCAGAAAGT	ACTCCAACCT	TCCTACCTAA	AGCGCACCCA	840
CTTGCTAGTG	TGAATGGCGT	AATGAACGCT	GTCTTTGTAG	AATCTATCGG	TATTGGTGAG	900
TCTATGTACT	ACGGACCAGG	TGCGGGTCAA	AAACCAACTG	CAACAAGTGT	TGTAGCTGAT	960
ATTGTCCGTA	TCGTTTCGTC	TTTGAATGAT	GGTACTATTG	GCAAAGACTT	CAACGAATAT	1020
AGCCGTGACT	TGGTCTTGGC	AAATCCTGAA	GATGTCAAAG	CAAAC TACTA	TTTCTCAATC	1080
TTGGCTCCAG	ACTCAAAAAG	TCAGGCTCTG	AAGTTGGCTG	AAATCTTCAA	TGCTCAAGAT	1140
ATTTTCCTTTA	AGCAAAATCCT	TCAAGATGGC	AAAGAGGGTG	ACAAGGCGCG	TGTCGTTATC	1200
ATCACACACA	AGATTAATAA	AGCCCAGCTT	GAAAATGTCT	CAGCTGAATT	GAAGAAGGTT	1260
TCAGAATTCG	ACCTCTTGAA	TACCTTCAAG	GTGCTAGGAG	AATAA		1305

(2) INFORMATION FOR SEQ ID NO:1368:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 621 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1368:

GAGGTAGAGG	AAATGTCTCA	ATCCAGCTAC	CTGTCGCCCT	TGCTCTGGTT	AAAAAAGAA	60
GCCGATAAGG	AAAAGATGAG	CGCGACCCAG	TGCCAGATAT	TTTCTTTTA	CTATCAAATG	120
TTTGAGCTCT	TATTTGCTAG	AGAAAGCGAC	ATGAAAGACT	TATGTCTGGG	AACGAAAGGT	180
TTTTATTTCT	CGCAGTTAGA	GAAAAATTTG	CTTTCTGGAG	TTTCCCGATT	TCTAAAAAAC	240
TTGGAGGGGA	AAGTAACTCT	CAAGGCTAAC	CAAGAAGTAT	CAGCTCGCAA	AGCCCTTTTT	300
CTAGCCTTGA	CAACTAGCCA	ATCAGATTGG	CAGGAGTTAG	CTCCTGTTTT	TGATTTTTAT	360
CAGACTATCG	GGAGGCTTGA	AAATCCTTCT	CTCTTGAGTT	CTCAGGACAG	ACAACATCTG	420
ATGTGGATTT	ACCAGTCAGC	TTTGGAGAAA	GATTATATTG	TCAACGTTAT	TGGCGACAAG	480
CATTTTGTAT	TGAAAAGACA	ACATGCTACT	AAATTGACAG	CGCGCCAAAC	TCAAACTTTG	540
GAAATTCTGA	GTCAATCAGA	AGACTTGGTC	AATCCTGTCT	ATGTTACATT	AGGAGAAAAG	600
GGGGTGCTCT	TGCTTGATT A					621

(2) INFORMATION FOR SEQ ID NO:1369:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 477 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1369:

TCAAAGAGG	AAATCATGAA	AAAAAGAGCA	ATAGTGGCAG	TCATTGTACT	GCTTTTAATT	60
GGGCTGGATC	AGTTGGTCAA	ATCCTATATC	GTCCAGCAGA	TTCCACTGGG	TGAAGTGCGC	120
TCCTGGATTC	CCAATTTTCGT	TAGCTTGACC	TACCTGCAAA	ATCGAGGTGC	AGCCTTTTCT	180
ATCTTACAAG	ATCAGCAGCT	GTTATTCGCT	GTCATTACTC	TGGTTGTCGT	GATAGGTGCC	240
ATTTGGTATT	TACATAAACA	CATGGAGGAC	TCATTCTGGA	TGGTCTTGGG	TTTGACTTTG	300
ATAATCGCGG	GTGGTCTTGG	AAACTTTATT	GACAGGGCCA	GTCAGGGGCTT	TGTTGTGGAT	360

ATGTTCCACC	TTGACTTTAT	CAACTTTGCA	ATTTTCAATG	TGGCAGATAG	CTATCTGACG	420
GTTGGAGTGA	TTATTTTATT	GATTGCAATG	CTAAAAGAGG	AAATAAATGG	AAATTAA	477

(2) INFORMATION FOR SEQ ID NO:1370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1370:

AAAAAAGAGG	ACATTAATAT	GGTTGTTAAG	ACAGTTGTTG	AAGCACAAGA	TATTTTTGAC	60
AAAGCTTGGG	AAGGCTTCAA	AGGCGTAGAT	TGGAAAGAAA	AAGCAAGTGT	ATCACGCTTT	120
GTACAAGCTA	ACTACACACC	TTATGATGGA	GACGAAAGCT	TCCTTGACAG	ACCAACAGAG	180
CGTTCAC TTC	ACATCAAGAA	AATTGTAGAA	GAAACTAAAG	CACACTACGA	AGAAACTCGT	240
TTCCCAATGG	AACTTCGTCC	AACATCTATC	GCTGATATCC	CTGCTGGATT	TATCGACAAA	300
GAAAAATGAAG	TTATCTTTGG	TATCCAAAAT	GATGAACTCT	TCAAATTGAA	CTTCATGCCA	360
AAAGGTGGTA	TCCGTATGGC	TGAAACTACT	TTAAAAGAAA	ATGGATACGA	ACCAGACCCA	420
GCTGTTCACG	AAATCTTCAC	TAAATATGTA	ACAACAGTTA	ACGACGGTAT	TTTCCGTGCC	480
TACACTTCAA	ATATTCGTCG	CGCTCGTCAT	GCACACACTG	TAACTGGTCT	TCCAGATGCA	540
TACTCACGCG	GACGTATCAT	CGGTGTTTAC	GCACGTCTTG	CTCTTTACGG	TGCAGACTAC	600
TTGATGCAAG	AAAAAGTAAA	CGACTGGAAT	GCAATCAAAG	AAATCGATGA	AGAAACAATC	660
CGTCTTCGTG	AAGAAGTAAA	CCTTCAATAC	CAAGCATTGC	AACAAGTTGT	TCGCCTGGGT	720
GACCTTTACG	GGGTTGATGT	TCGCAAACCA	GCGATGAACG	TGAAAGAAGC	AATCCAATGG	780
GTTAACATTG	CTTTCATGGC	TGTCTGCCGT	GTGATTAACG	GTGCTGCTAC	ATCTCTAGGT	840
CGTGATACAA	TCGTATTGGA	CATCTTTGCA	GAACGTGACC	TTGCTCGTGG	TACATTTACT	900
GAATCAGAAA	TCCAAGAATT	CGTTGATGAT	TTTCGTTATGA	AACTTCGTAC	AGTTAAATTT	960
GCTCGTACCA	AAGCTTATGA	CCAATTGTAC	TCAGGTGACC	CAACCTTTAT	CACAACTTCT	1020
ATGGCTGGTA	TGGGTAACGA	CGGTCGTCAC	CGTGTTACTA	AGATGGACTA	CCGTTTCTTG	1080
AACACTCTTG	ACAACATCGG	TAACTCACCA	GAACCAAACCT	TGACAGTTCT	TTGGACTGAC	1140
AAATTGCCAT	ACAACCTCCG	TCGCTACTGT	ATGCACATGA	GCCACAAACA	CTCTTCTATC	1200
CAATACGAAG	GTGTAACAAC	AATGGCTAAA	GACGGATATG	GTGAAATGAG	CTGTATCTCA	1260
TGCTGTGTGT	CTCCACTTGA	TCCAGAAAAT	GAAGAACAAC	GCCACAACAT	CCAGTACTTC	1320
GGTGCTCGTG	TAAACGTTCT	TAAAGCCCTT	CTTACTGGTT	TGAATGGTGG	TTACGACGAT	1380
GTTACAAAAG	ACTACAAAAGT	ATTTGATATC	GAACCAATCC	GTGACGAAGT	TCTTGAATTT	1440
GAATCAGTTA	AAGCGAACTT	TGAAAAATCT	CTTGACTGGT	TGACTGACAC	TTACGTAGAT	1500
GCCTTGAAAC	TCATCCACTA	CATGACTGAT	AGGTACAAC	ACGAAGCTGT	TCAAATGGCC	1560
TTCTTGCCAA	CTAAACAACG	TGCCAACATG	GGATTCCGTA	TCTGTGGATT	TGCTAACACT	1620
GTTGATACAT	TGTCAGCTAT	CAAATACGCT	ACAGTTAAAC	CAATCCGTGA	CGAAGATGGC	1680
TACATCTACG	ATTACGAAAC	AATCGGTGAC	TACCCACGCT	GGGGTGAAGA	TGACCCACGT	1740
TCAACGAAT	TGGCAGAAATG	GTTGATCGAA	GCTTACACAA	CTCGTCTACG	TAGCCACAAA	1800
CTATACAAAAG	ACGCAGAAAGC	TACAGTATCA	CTTTTGACAA	TCACATCTAA	CGTTGCTTAC	1860

TCTAAACAAA	CTGGTAACTC	ACCAGTTCAC	AAAGGTGTAT	ACCTCAACGA	AGATGGTTCT	1920
GTGAAC TTGT	CTAAACTTGA	ATTCTTCTCA	CCAGGTGCTA	ACCCATCTAA	CAAAGCTAAA	1980
GGTGGTTGGT	TGCAAAACTT	GAAC TCACTT	TCTAGCCTTG	ACTTTAGTTA	TGCAGCTGAC	2040
GGTATCTCAT	TGACTACACA	AGTATCACCT	CGCGCTCTTG	GTAAGACTCG	TGATGAACAA	2100
GTTGATAACT	TGGTAACAAT	CCTTGATGGT	TACTTCGAAA	ACGGTGGACA	ACACGTTAAC	2160
TTGAACGTTA	TGGACTTGAA	CGATGTTTAC	GAAAAAATCA	TGTCAGGCGA	AGACGTTATC	2220
GTACGTATCT	CTGGATACTG	TGTAAACACT	AAATACCTCA	CTCCAGAACA	AAAAACTGAA	2280
TTGACACAAC	GTGTCTTCCA	CGAAGTTCTT	TCAATGGATG	ACGCCTTGGA	TGCATTGAGC	2340
TAA						2343

(2) INFORMATION FOR SEQ ID NO:1371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1371:

AAGGGAGAGG	ATGAACCTAT	GAGAAAATTT	AAAATCTTTT	TATTTATCGA	AGCCTGTCTT	60
CTGACAGGAG	CTCTGATTTT	GATGGTATCA	GAGCATTTTT	CGCGTTTTCT	GCTGATACTA	120
TTCCTCTTTT	TGCTTTTGAT	TCGCTACTAC	ACTGGTAAAG	AGGGAAATAA	TCTTCTTTTA	180
GTAGCGGCAA	CCATTCTCTT	CTTTTTTCATC	GTTATGCTCA	ATCCTTTTGT	GATTCTAGCT	240
ATTTTTGTTG	CGGTTATCTA	TAGCCTCTTT	CTTCTTTACC	CGATGATGAA	CCAGGAAAAA	300
GAGCAGACCA	ATTTGGTTTT	TGAAGAGGTC	GTGACGGTTA	AGAAGGAGAA	AAATCGTTGG	360
TTTGGAATC	TTCATCATTT	TTCAAGCTAC	CAGACTTGCC	AATTCGATGA	TATCAATCTC	420
TTTCGCTTCA	TGGGCAAGGA	CACTATTTCAT	CTGGAGAGGG	TCATCTTAAC	CAATCATGAC	480
AATGTCATTA	TCCTCAGAAA	GATGGTAGGA	ACGACCAAAA	TCATCGTACC	TGTAGATGTG	540
GAAGTCAGTC	TCAGCGTTAA	CTGTCTCTAT	GGGGATTTGA	CTTTTTTCAA	CCAGCCCAAG	600
CGAGCCCTCC	GCAATGAACA	CTATCATCAA	GAAACAAAAG	ACTATCTCAA	GAGTAACAAG	660
AGTGTC AAGA	TTTTCTTGAC	CACTATGATT	GGTGATGTGG	AGGTGGTTAG	AGGATGA	717

(2) INFORMATION FOR SEQ ID NO:1372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1372:

TTAGCGGAGG	AAAGGTATTG	TACTATGATA	ATTCAACTAA	GTGATTTAGG	TCAAGTTCAC	60
CTTGTTTGTA	GCAAGATAGA	TATGAGGCAG	GGAATAGACT	CATTAGCCTA	TGTAGTTAAA	120
ACCCACTTTG	AATTGGATCC	TTTCTCCGGT	CAAGTCTTTC	TCTTTTGTGG	TGGACGTAAA	180
GACCGCTTTA	AAGCCCTTTA	CTGGGATGGT	CAAGGATTTT	GGCTACTATA	TAAACGCTTT	240
GAGAACGGCA	GACTGACTTG	GCCCAGTACA	GAAAAGGATG	TCAAAGCTCT	CACACCTGAA	300
CAAGTAGACT	GGCTTATGAA	GGGCTTTTCT	ATCACTCCAA	AAATAAATCC	ATCAGAAAGT	360
CGTGATTTC	ATTGA					375

(2) INFORMATION FOR SEQ ID NO:1373:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1373:

TACAAGGAGG	AAAGCATGGA	AGAATCAAAA	GAATTAAATG	CCGTCATTGA	TGTGATTATG	60
CTAGCGGGGA	CTATTCTCCT	TAAAAGTGGC	TCAGAAATCC	ATCGTGTAGA	AGATACCATG	120
ATTCGAATCG	CGATTGCGAG	GGGATTGTGG	ATTGCAATGT	CCTTGCCATG	CCTGCCGCTA	180
TCTTTTCTC	TATTGAAAAT	ACCAATATTT	CGCGCATGA			219

(2) INFORMATION FOR SEQ ID NO:1374:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1788 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1374:

GAAAAGGAGG	ATGATCTAAT	GGAAGAAAAA	GTATCATTGA	AAGTCAGGGT	TCAAAAAC TA	60
GGGACATCGC	TTTCAAATAT	GGTTATGCCC	AATATTGGAG	CATTTATTGC	TTGGGGAGTA	120
TTGACTGCCC	TTTTTATCGC	TGATGGTTAT	CTGCCAAATG	AACAGTTAGC	TACTGTTGTT	180
GGTCCTATGT	TAACGTATTT	ATTGCCAATC	CTGATTGGTT	ACACAGGTGG	ATATATGATC	240
CATGGCCAAAC	GTGGTGCCGT	TGTAGGAGCT	ATTGCTACTG	TTGGTGCAAT	CACAGGTTCT	300
AGTGTTCCTA	TGTTTATCGG	AGCTATGGTA	ATGGGCCCAC	TGGGAGGATG	GACTATCAAG	360
AAATTTGATG	AGAAGTTCCA	GGAAAAAATT	CGTCCCGGAT	TTGAAATGTT	AGTTAATAAC	420
TTCTCAGCTG	GTCTCGTTGG	TTTTGCATTA	TTGCTTTTGG	CTTCTACGC	AATCGGTCCA	480
GTCGTATCGA	CTCTTACTGG	AGCTGTTGGG	AATGGTGTTG	AGGCTATTGT	CAATGCTCAC	540
CTCCTTCCTA	TGGCTAATAT	TATCATCGAA	CCGGCTAAAG	TCCTTTTCCT	CAATAATGCC	600
CTCAATCATG	GCATTTTAC	TCCTCTGGGA	GTAGAACAGG	TAGCTCAAGC	TGGTAAGTCA	660
ATTCTCTTCC	TATTGGAAGC	TAATCCTGGA	CCAGGCCTGG	GAATTCTATT	AAC TTATGCT	720
GTATTCGGTA	AAGGTTC TGC	TAAATCTTCT	TCTTGGGGGG	CAATGGTTAT	TCATTTCTTC	780
GGAGGGGATTC	ATGAAATTTA	CTTTCCTTAT	GTTATGATGA	AGCCTACTCT	ATTTTTAGCT	840
GCTATGGCAG	GAGGTATCTC	TGGAAC TTTT	ACTTTTCAAC	TCTTAGACGC	TGGTCTTAAA	900
TCTCCAGCTT	CACCAGGTTC	TATTATTGCG	ATTATGGCTA	CGGCGCCAAA	AGGTGTTTGG	960
CCCCATCTAA	ATGTTCTTTT	AGGTGTTTTA	GTGGCAGCAG	TTGTTTCTTT	CCTTG TAGCA	1020
GCCCTTATTC	TTCATGCAGA	CAAGTCAACT	GAGGATTCGC	TCGAAGCTGC	TCAGGCGGCT	1080
ACCCAAGCAG	CTAAGGCTCA	GTCTAAAGGT	CAGTTAGTAT	CAACTTCTGT	TGATGCAGTT	1140
GTTTCGACAG	ACTCAGTGGA	AAAAATCATT	TTCGCCTGCG	ATGCTGGTAT	GGGAAGCTCT	1200
GCTATGGGAG	CTAGTATTCT	TCGAGATAAG	GTTAAAAAAG	CAGGTCTAGA	GATTCCAGTA	1260
TCTAATCAGG	CAATCTCAAA	TTTGCTTGAT	ACACCAAAAA	CATTAATTGT	TACTCAGGAA	1320
GAAGTGACAC	CAAGAGCTAA	AGACAAGAGT	CCAAGTGCTA	TTCAATGTTT	TGTTGATAAT	1380
TTCTTAGCGT	CCCCTCGTTA	TGATGAAATT	GTAGCTTCAT	TAACAGGAGC	TTCTCCAATA	1440
GCAGAAATTG	AAGGAGATAT	ACCAACTTCA	GCACCAAGTAG	ATAGTCAGGA	AATTGACCTT	1500
AACCATATTG	ATGCTGTAGT	AGTTGCTTAT	GGTAAAGCAC	AGGGAAGTGC	AACTATGGGC	1560
TGTGAAACGA	TTCGGGCTAT	CTTTAGAAAC	AAGAATATTC	GTATTCCAGT	TTCTACTGCC	1620
AAAATTTTCA	AATTAGGTGA	ATTTAATTCT	AAAAATATAA	TGATTGTAAC	AACTATTTCT	1680
TTACAGGCAG	AAGTGCAGCA	AGCAGCACCG	AATTCTCAAT	TTCTTATTGT	GGATAGTTTA	1740
GTAACAACAC	CAGAAATATGA	CAAAATGGCT	GCTAGAATGT	ACAAATAG		1788

(2) INFORMATION FOR SEQ ID NO:1375:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 336 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...336
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1375:

AATGAGGAGG	AATTTATGGA	AATTATTGTT	CCAGATCAAA	TTATCATGGG	TTTAATTTTA	60
TATGCTGGCG	ATGCGAAACA	ACATATTTAT	AAAGCATTAG	ATTACATAAA	GAACGGTACA	120
TGTGAACGAT	GTGAAGAAGA	AATCCAGTTA	GCTGATGCCG	CCTTATTAGA	AGCTCATAAT	180
CTACAAACAA	AATTCTTGGC	ACAGGAAGCG	TCTGGTACAA	AGACAGAAAT	TACAGCTCTC	240
TTTGTTCATT	CACAAGATCA	TTCATGACT	AGTATGACGG	AGATTAATTT	AATCAAAGAA	300
ATTATTAGTT	TGAGAAAAGA	ACTTCATAAA	AAATAA			336

(2) INFORMATION FOR SEQ ID NO:1376:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1110 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1110
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1376:

TCGGGGGAGG	AGGAATCGTT	GACTTTGCAA	GCAGAGATTA	TCAAGAACAC	CAAGCAGCCA	60
AGTGGAATGA	GCAAATTGAC	CAGCTTCTTA	AAGATGGACA	TATCACAAGT	CTTCAGGCTG	120
AGACGGAAAA	AATTAGCTAC	AGCTAAGCAA	AAAAATATCA	TCACCCTATT	TAACAATCTC	180
TTTTCTAGCG	GTTTTCATCT	GGTGGAGACT	ATCTCCTTTT	TAGATAGGAG	TGCTTTGTTG	240
GACAAGCAGT	GTGTGACCCA	GATGCGTGTG	GGCTTGCTCT	AGGGGAAATC	ATTCTCAGAA	300
ATGATGGAAA	GTTTGGGATG	TTCAAGTGCT	ATTGTCACTC	AGTTATCCCT	AGCTGAAGTT	360
CATGGCAATC	TCCACCTGAG	TTTGGGAAAG	ATAGAAGAAT	ATCTGGACAA	TCTGGCTAAG	420
GTCAAGAAAA	AATTGATTGA	AGTAGCGACC	TATCCCTTGA	TTTTGCTGGG	TTTTCTTCTC	480
TTAATTATGC	TGGGGCTACG	GAATTACCTG	CTCCCACAAC	TGGATAGTAG	CAATATTGCC	540
ACCCAAATTA	TCGGTAATCT	GCCCCAAATT	TTTCTAGGCA	TGGTAGGGCT	TGTTTCCGTG	600
CTTGCCCTTT	TAGCACTCAC	TTTTTATAAA	AGAAGTTCTA	AGATGAGTGT	CTTTTCTATC	660
TTAGCACGCC	TTCCCTTTAT	TGGAATCTTT	GTGCAGACCT	ACTTGACAGC	CTATTATGCA	720
CGTGAATGGG	GGAATATGAT	TTACAGGGA	ATGGAGTTGA	CGCAGATTTT	TCAAATGATG	780
CAGGAACAAG	GTTCCCAGCT	CTTTAAAGAA	GTCGGTCAAG	ATCTGGCTCA	AACCCTGAAA	840
AATGGCCGTG	AATTTTCTCA	GACGATAGGA	ACCTATCCCT	TCTTTAGGAA	GGAATTGAGT	900
CTCATCATAG	AGTATGGGGA	AGTTAAGTCC	AAGCTGGGTA	GTGAGTTGGA	AATCTATGCT	960

GAAAAAACTT GGGGAAGCCTT TTTTACCCGA GTCAACCGCA CCATGAATTT GGTGCAGCCA	1020
CTGGTTTTTA TCTTTGTGGC ACTGATTATC GTTTTACTTT ATGCGGCAAT GTCATGCCC	1080
ATGTATCAAA ATATGGAGGT AAATTTTAA	1110

(2) INFORMATION FOR SEQ ID NO:1377:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 820 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...820
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1377:

TTTTTGGGAC CATTTCTTGG TTAATAGTCT TGTCGAAATN GAACAATTTA AGGCCGGAAA	60
TCTAGACGTT CGAATGATTA ATGATATCAA CCAGATTCAG AACGTTGTCA TGATGACCTT	120
CCAAATTCTT TTCAGACTTC CCCTCTTGTT CATCGGTTTCG TTTATCCTAG CGGTTCAAAC	180
CTTACCTTCT CTGTGGTGGG TGATTGTTCT CATGGTAGTC TTGATTTTGT GTTTGACTGC	240
TGTCATGATG GGAATGATGG GGCCTCGTTT TGCCAAGTTT CAAACCCTTC TTGAGCGCAT	300
CAATGCCATT GCCAAGGAAA ATTTACGTGG CGTTCGTGTG GTCAAGTCCT TTGTCCAAGA	360
AAAAGAGCAA TTTGCTAAGT TTACAGAGAT CTCAGACGAG CTTTTTGGTC AAAACCTTTA	420
CATTGTTTAT GCCTTTTCAG TAGTGGAACC CTTTATGATG TTGTTTGGTT ACGGGGCGGT	480
CTTCTCTCT ATTTGGCTGG TCGCGGGAAT GGTTCACTCG GATCCGTCTG TTGTTGGTTC	540
CATCGCTTCT TTTGTTAATT ACCTAAGCCA GATTATCTTT ACCATTGTGA TGGTTGGATT	600
TTTGGGAAAAT TCTGTCAGCC GTGCCATGAT TTCCATGCGT CGTATTCGAG AAATTCTTGA	660
CGCAGAGCCA GCTATGACCT TCAAGGATAT CCCAGATGAA GAGTTGGTTG GAAGCCCTAG	720
CTTTGAAAAT GTGACCTTTA CCTATCCCAT GGACAAGGAA CCGATGCTGA AAGATGTGAG	780
CTTTACTATT GAACCTTGTC AAATGGTTGG TGAGTATGA	820

(2) INFORMATION FOR SEQ ID NO:1378:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 882 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1378:

TTGAGCTGGG	AGCGCAAGGT	GTTGCGATTG	AAGACAGTCT	GGACTATGTG	GGAAATGTTG	60
ACCGCTTCGG	CGAGATTTTC	CCCAGAGGTC	GAGCAGCAAG	AAGAAATCGT	AGTGACAGCC	120
TACTACCCCTG	ACACGGTGGA	TGTGACAGTG	GTTGAGGCGG	ACTTGCAGGC	TCGCATATCA	180
GAATTGACGG	ATTTTATGGA	TTTGGGAGAG	TTAAAAATAG	GTACGACTGC	CTTGGCTGAG	240
GAAGACTGGG	CAGATAACTG	GAAGAAATAC	TATGAGCCAG	CTCGTATCAC	TCATGATTTG	300
ACCATCGTTC	CCTCTTGAC	AGACTATGAG	GCGACTGCGG	GAGAAAAAAT	TATCAAGCTG	360
GATCCTGGCA	TGGCTTTTGG	TACTGGAACC	CACCCAAC TA	CCAAGATGAG	CCTTTTTGCC	420
TTGGAACAGG	TTCTTCGTGG	TGGCGAAACG	GTGCTAGATG	TGGGGACTGG	TTCAGGGGTT	480
CTCTCTATTG	CCAGCTCGCT	TCTGGGGGCT	AAAGAAATTT	TCGCCTATGA	CCTGGATGAT	540
GTGGCGGTTT	GTGTGGCTCA	GGAAAAATAT	GAGCTCAACC	CTGGCATGGA	AAATATCCAT	600
GTAGCGGCTG	GAGATTTGCT	TAAGGGTGTG	GAAATTGAGG	CAGATGTCAT	CGTGGCTAAT	660
ATCTTGGCGG	ATATTCTCAT	TCATCTGACG	GAGGATGCTT	ATCGCTTGGT	AAAGGATGAA	720
GGCTACCTGA	TCATGAGTGG	CATTATCAAG	GACAAGTGGG	ACATGGTGCG	CCAGTCGGCT	780
GAGTCAGCTG	GATTTTTCCT	CGAAACTCAC	ATGGTTCAAG	GGGAATGGAA	TACCTGTGTC	840
TTTAAGAAAA	CCAAGGATAT	CTCTGGTGTG	ATTGGAGGCT	AG		882

(2) INFORMATION FOR SEQ ID NO:1379:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1379:

AATAATAGGG	ATTTTAAGGA	GTTTGATATG	TATAACCTAT	TATTAACCAT	TTTATTAGTA	60
TTATCTGTTG	TGATTGTGAT	TGCAATTTTC	ATGCAACCAA	CCAAAAACCA	ATCCAGCAAT	120
GTATTTGATG	CCAGTTCAGG	TGATTTGTTT	GAACGCAGTA	AAGCTCGCGG	TTTTGAAGCT	180
GTAATGCAGC	GTTTGACAGG	GATTTTAGTC	TTTTTCTGGC	TAGCCATTGC	CTTAGCATTG	240
ACGGTATTAT	CAAGTAGATA	A				261

(2) INFORMATION FOR SEQ ID NO:1380:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1380:

ACCATAAGGG	AGGTGGTAGG	GATGGTAGAA	CCAAACCTAG	AAAGCCTTAT	AAAAGATCTT	60
TACAAATCATG	CTCGACATGA	TTTGAGTGAA	GATTTAGTTG	CTGCTCTCCT	AGAGACTACT	120
AAAAAACTGC	CTACTACAAA	TGAGCAATTG	CAGGCAGTTC	GTCTCTCAGG	CCTGGTCAAT	180
CGTGAATTGC	TCCTAAATCC	CAAACATCCA	GCACCTGAGT	TGCTCAACTT	GGCTCGCTTT	240
GTCAAAAGAG	AAGAAGCCAA	GTACAGAGGA	ACTGCGACTT	CTGCGCTTAT	GTATGAGGAA	300
CTTTTAAAA	TGCTTTGA					318

(2) INFORMATION FOR SEQ ID NO:1381:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1302 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1381:

GTAGAAAGGG	AGAAAATGTA	TAAAGTATTA	TTAGTAGATG	ATGAGTACAT	GGTGACAGAA	60
GGTCTGAAGC	GTTTGATTCC	CTTTGATAAG	TGGGATATGG	AGGTTGTCGC	AACAGCCAGT	120
CATGCCGATG	AAGCTCTAGA	ATATGTTTCAG	GAAAATCCTG	TCGATGTCAT	CATTTCCGAT	180
GTCAATATGC	CAGACAAAAC	AGGGCTTGAT	ATGATTTCGG	AGATGAAAAG	GATCTTACCA	240
GATGCTGCCT	ATATCCTGCT	CTCAGGTTAT	CAGGAGTTTG	ATTATGTAAA	AAGAGCAATG	300
AACCTTAGTG	TGGTGGACTA	TTTGGTCAAG	CCTGTTGATA	AGGTAGAGCT	GGGAAATCTG	360
CTGGAGAAGA	TTGCAGGTCA	GCTCGGCGAG	AGAGGGAAGA	AAAGTCAGAC	TCTTAGTCAA	420

GAATTAGACG	AGGCTGGATT	TGTTAGTTAT	TTAGGGGATA	AGGAGAATTG	GTGGATAGGT	480
CTATCCAAGG	AAAAACAAGG	TTCCTTCACC	ATTCCCTACT	ATGTCTTGGG	CCAAGACTGG	540
CAGATTTTCA	TTTCTGGCCA	ACCTCTAGAT	GGTTTAGTCG	TTACACCTTT	TGAAGCTCCT	600
TATCAAGAAC	ACTTTGAACG	CTGGAAGCTG	AATGCTGAGA	AAACCCCTCT	TTACGGTTCT	660
GTAAATTTGC	AGCAGTCTGA	GAGTCTCTTT	GCCTATTACG	AACCGATTTA	TAGGGTTATC	720
ATTCAGGGAA	ATCTCAATCA	AATCGTAGAA	GAGTTAAATC	TCTTGAGAGAA	GGTAGTTCCT	780
GAAAATACGC	CGCGTGTTC	GATTACTAAA	CAGCTTTTTA	TTCAGTTTGT	CATGGATGTT	840
TTCCATTTAT	TTGAACATCT	CAAAGCTGAT	GACCTGACAG	ACATCGTCAA	AACCATTTCAT	900
GCTATTCAAT	CCTTCGATGA	ATTGGTTTCT	TATATCAAGG	AAACTCTGAT	CAGCTTTTTTC	960
GGTCAATACC	GTATCAATGA	AAATGTGGTC	AGTGTGCTGG	AAGTCATTGG	TCGTGATTAC	1020
CAAAAAGAGC	TTTCCCTCAA	GGATATCAGT	AAGGCCCTCT	TTATCAATCC	TGTCTATCTA	1080
GGGCAGTTGA	TTAAGCGTGA	AACCGATTCT	ACCTTTGCAG	AGTTACTAAA	TAAACAACGT	1140
ATTAAGGCTG	CCCAGCAGCT	CTTGCTTTCA	ACTAGTGACA	GCATCGAAGA	TATTTGTTAT	1200
GCTGTTGGTT	ACAGTAACCT	TGGATATTTT	TATAAAGTTT	TCCGAAAATT	GTGCGGAAAA	1260
TCGCCAAAAG	CCTACCGAAA	ACAGGTAGAA	ACTATACTAT	AA		1302

(2) INFORMATION FOR SEQ ID NO:1382:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 969 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...969
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1382:

AAAAGGAGGG	AATTCATGTT	TGTTGCGAGA	GATACTAGGG	GAGAATTGGT	AAATGTGTTA	60
GAGGATAAAC	TTGAGAAGCA	AGCATAACCC	TGCCCAGCTT	GTGGAGGCCA	GATCCATTTG	120
CGTCAAGGAC	CAAGTGATCG	GACGCATTTT	GCCCATAAAT	CCTTAAAAGA	CTGTGATTTT	180
TTCTTTGAAA	ATGAAAGTCC	AGAACACATA	GCCAATAAGG	AATCCCTCTA	TCACTGGTTG	240
AAAAAAGAGA	CAAAGGTTCA	ATTAGAGTAC	CCGCTTTCAG	AACTTAAACA	GATTGCGGAT	300
GTATTTGTAA	ATGGCAATCT	AGCTCTAGAA	GTTTCAGTGTA	GTCCCTTGCC	TCAGAAAGTC	360
CTTAAAGAGC	GAAGTGAGGG	CTATCGTAGT	CAGGGTTACC	AAGTACTGTG	GTTGCTGGGT	420
CAAAAACCTGT	GGCTCAAGGA	GCGTTTGACT	CGTCTACAGC	AAGGTTTTCT	GTATTTTCAGT	480
CAAAACATGG	GCTTTTATGT	TTGGGAATTA	GACAAGGAAA	AACAAGTTTT	AAGACTCAAA	540
TACCTGATTT	ACCAGGATCT	CCGCGGTAAA	CTCCATTATC	AAATCAAGGA	ATTTTCCTAT	600
GGTCAAGGTA	GTTTATTGGA	AATATTGCGT	CTTCCCTATA	AGAGACAAAA	AATATCTCAT	660
TTTACAGTTT	CTGAGGACAA	GGACATCTGT	CGCTATATTC	GGCAACAAC	TTATTATCAA	720
AATCTCTTTT	GGATGAAAGA	ACAAGCAGAA	GCCTATCAAA	AGGGAGAAAA	TATCCTGACT	780
TATGGACTGA	AAGAATGGTA	TCCACAAATT	CGACCAATAG	TGGGCAAATT	TTTCCAGATT	840
GAACAAGACT	TGACTAGCTA	TTATCGGAAC	TTTTTATACCT	ATTACCAAAA	AAATCCTCAA	900
AATGATTGGC	AAAAGCTTTA	TCCACCAGCC	TTTTATCAGC	AATATTTCTT	GAAAAATATG	960
GTAGAATAG						969

(2) INFORMATION FOR SEQ ID NO:1383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1719 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1383:

AATGGGAGGG	ATAAGATGAC	TGAATTAGAT	AAACGTCACC	GCAGTAGCAT	CTATGACAGC	60
ATGGTTAAAT	CACCTAACCG	TGCTATGCTT	CGTGCGACTG	GTATGACAGA	TAAGGACTTT	120
GAAACATCGA	TTGTGGGAGT	GATTTTCGACT	TGGGCGGAAA	ATACACCATG	TAACATTTCAC	180
TTGCATGATT	TCGGGAAACT	GGCTAAAGAA	GGTGTCAAAT	CTGCAGGCGC	TTGGCCTGTA	240
CAGTTTGGAA	CCATTACCGT	AGCGGACGGG	ATCGCTATGG	GAACGCCTGG	TATGCGTTTC	300
TCTCTAACAT	CTCGTGACAT	CATCGCGGAC	TCCATCGAGG	CGGCTATGAG	TGGTCACAAC	360
GTGGATGCCT	TCGTCGCTAT	CGGTGGCTGT	GACAAGAACA	TGCCTGGATC	TATGATTGCT	420
ATTGCTAATA	TGGATATCCC	AGCTATTTTC	GCCTATGGTG	GAAC TATTGC	ACCGGGAAAT	480
CTTGATGGTA	AAGATATCGA	CTTGGTTTCT	GTCTTTGAAG	GTATCGGAAA	ATGGAACCAC	540
GGTGACATGA	CAGCTGAGGA	CGTGAAACGT	CTTGAATGTA	ATGCCTGCCC	TGGCCCTGGT	600
GGTTGTGGTG	GTATGTATAC	TGCTAATACC	ATGGCAACTG	CTATCGAAGT	TCTAGGGATG	660
AGTTTGGCCAG	GGTCATCCCT	TCACCCAGCT	GAATCAGCTG	ATAAGAAAGA	AGATATCGAA	720
GCAGCAGGAC	GTGCTGTTGT	TAAGATGTTG	GAAC TTGGTC	TCAAACCATC	AGATATCTTG	780
ACTCGTGAAG	CCTTTGAAGA	TGCTATTACT	GTAACGATGG	CTCTCGGTGG	TTCTACAAAC	840
GCCACTCTTC	ACTTGCTCGC	CATTGCCCAT	GCCGCAAATG	TTGACTTGTC	ACTTGAGGAC	900
TTCAATACGA	TTCAAGAACG	TGTGCCCTCAC	TTGGCCGACT	TGAAACCATC	TGGTCAGTAT	960
GTCTTCCAAG	ACCTCTACGA	AGTCGGTGGT	GTCCCTGCGG	TTATGAAGTA	CTTGTTGGCA	1020
AATGGTTTCC	TTCACGGAGA	TCGCATCACA	TGTACTGGTA	AGACTGTAGC	TGAAAAC TTG	1080
GCTGACTTTG	CAGACTTGAC	TCCAGGCCAA	AAAGTTATCA	TGCCACTTGA	AAATCCAAAA	1140
CGTGCGGATG	GTCCGCTTAT	CATCTTGAAC	GGGAACCTTG	CTCCTGACGG	TGCAGTTGCC	1200
AAGGTATCAG	GTGTTAAAGT	GCGTCGTCAC	GTTGGGCCAG	CTAAGGTCTT	TGACTCAGAA	1260
GAAGATGCGA	TTCAGGCCGT	TCTGACAGAT	GAAATCGTTG	ATGGCGATGT	AGTCGTTGTT	1320
CGTTTTGTGT	GACCTAAAGG	TGGTCCTGGT	ATGCCTGAGA	TGCTGTCACT	TTCTTCAATG	1380
ATTGTTGGTA	AAGGTCAGGG	AGATAAGGTG	GCCCTCTTGA	CGGACGGACG	TTTCTCTGGT	1440
GGTACTTATG	GTCTGGTTGT	TGGACATATC	GCTCCTGAAG	CTCAGGATGG	TGGACCAATT	1500
GCCTATCTCC	GTACCGGCGA	TATCGTTACG	GTTGACCAAG	ATACCAAAGA	AATTTCCATG	1560
GCCGTATCCG	AAGAAGAACT	TGAAAAACGC	AAGGCAGAAA	CAACCTTGCC	ACCAC TT TAC	1620
AGCCGTGGTG	TCCTCGGTAA	ATATGCCCAC	ATCGTATCAT	CTGCTTCACG	CGGAGCCGTG	1680
ACAGACTTCT	GGAATATGGA	CAAGTCAGGT	AAAAAATAA			1719

(2) INFORMATION FOR SEQ ID NO:1384:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1384:

CTACGAGGGG ATATAGAAAA CAAGACCCTA CTAATAAGAA TAATCTGGGA CAACTGCACC	60
AGATTCACAA CTAATACTCT TCGAAAATCT CTTCAAACCG CGTCAACGTC GCCTTGCCGT	120
AGATATGTGT TCCTGACTTT GTCAGTCTTA TCTACAACCT CAAAACAGTG TTTTGAGCAG	180
CCTACGGCTA GTTTCCTAGC TTGCTCTTTG ATTTTCATTG AGTATAAAAT ACAAGAAGAT	240
AACTTCTTGA AAAAATAA	258

(2) INFORMATION FOR SEQ ID NO:1385:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 729 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1385:

CTAAAGGGGG AGCGCTACAT GTCTAATTCA TTTGTCAAGT TGTTAGTCTC TCAATTATTT	60
GCAAATTTAG CAGATATTTT CTTTAGAGTA ACAATCATTG CTAACATATA CATTATTTCA	120
AAATCAGTAA TTGCCACATC ACTAGTTCCT ATCTTAATAG GAATATCCTC TTTTGTGCG	180
AGTCTTTTAG TTCCGTTGGT TACTAAAAGG TTAGCGCTAA ATAGGGTTTT ATCTTTATCT	240
CAATTTGGAA AGACTATATT ATTGGCGATA CTGGTAGGAA TGTTTACCGT AATGCAATCC	300
GTAGCGCCTT TGGTGACCTA TCTATTTGTT GTTGCAATTT CCATACTAGA TGGTTTTGCA	360
GCACCCGTTT CCTATGCTAT TGTGCCACGC TATGCGACCG ATTTGGGTAA GGCTAATTCA	420
GCCTTATCAA TGA CTGGTGA AGCTGTTCAA TTGATAGGTT GGGGATTAGG TGGACTCTTG	480

TTTGCAACAA	TTGGTCTGTT	ACCTACCACG	TTTATCATTT	TAGTCTTGTA	TATCATTTCT	540
AGCTTTCTGA	TGTTATTTCT	TCCTAACGCT	GAAGTGGAGG	TGTTAGAGTC	AGAAACTAAT	600
CTTGAAATTT	TGCTCAAAGG	TTGGAAGTTA	GTTGCTAGAA	ATCCTAGATT	AAGACTTTTG	660
TATCAGCAAA	TTTATTGGAA	ATTTTTTCAA	ATACGATTTG	GGTTTCTTCC	ATTATACTTG	720
TTTTTGTA						729

(2) INFORMATION FOR SEQ ID NO:1386:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...630
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1386:

CTGAAAAGTT	TGCTTCAACC	ATCACCCAAG	GTGAGTCATG	AGCCAGAGCA	GGTTTATCAA	60
GTGGCGCGTG	ATGGCATTGC	CAAGCAGGAT	CATCTAGCCT	ATCTCAAACC	TATGTCTTAT	120
CAAAATACCT	ATGCTGTAGC	TGTTCCGAAA	AAGATTGCTC	AAGAATATGG	CTTGAAGACC	180
ATTTTCGATT	TGAAAAAAGT	GGAAGGGCAG	CTGAAGGCAG	GCTTTACGCT	TGAGTTTAAC	240
GACCGTGAAG	ATGGAAATAA	GGGCTTGCAA	TCAATGTATG	GTCTCAATCT	CAATGTGGCG	300
ACTATGCAGC	CAGCTCTTCG	TTATCAGGCA	ATTCAAGTCAG	GGGATATTCA	AATCACGGAT	360
GCCTATTCTGA	CTGATGCGGA	ATTGGAGCGT	TATGATTTAC	AGGTCTTGGA	AGATGACAAG	420
CAACTCTTCC	CACCTTATCA	AGGGGCTCCA	CTCATGAAAG	AAGCTCTTCT	CAAGAAACAC	480
CCAGAGTTGG	AAAGAGTTCT	TAATACATTG	GCTGGTAAGA	TTACAGAAAG	CCAGATGAGC	540
CAGCTCAACT	ACCAAGTCGG	TGTTGAAGGC	AAGTCAGCAA	AGCAAGTAGC	CAAGGAGTTT	600
CTCCAAGAAC	AAGGTTTGTT	GAAGAAATGA				630

(2) INFORMATION FOR SEQ ID NO:1387:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 705 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1387:

AACTCTTTAC	TCCTTATATC	CTTTATATTG	TCCCTTATAT	GGTGCTTGAA	AAATATGAAG	60
ATAATGTTTA	AGAATTTTAA	CAATATTTTG	CTAAAGAGAA	AGATTGTTTT	ACTACTTCGT	120
ATAGTTCTGA	TGATGATTTT	GATAAACTAT	CTATTGTCAA	CAGCGGTTCA	AAAGCAGGAT	180
GCTGTTATCT	TTTTCAAGAG	AGAATTGATT	TCAATTTTTT	CCTATAATGA	CTATTCTGAA	240
GCGAATTTAG	AAATCCCCAA	ACTCTTGTTA	AACCTTTTCGC	TTTTTCATGGT	AGGATGGCTC	300
TCTGTCAATTT	TACTTGAAAG	TGATTGGGCA	GACCATTACC	ATCACCTGAT	TCGCTATCAA	360
TCAAGCTCCT	TTTTTCGATTA	TACAAGGAAA	CGATTGGTTG	TCATTTCTAA	ATTTTTTACT	420
CAAGATTTAC	TTGTCTGGTT	CCTTGGTTTA	CTTCCGCTAG	GAATTCATTT	CAAAACAGTC	480
GCACTTTTCT	TTTTACTTGC	TCAGTTAATG	ATGTTGTACT	TACTACTGTC	TTATCTGATA	540
GCACTGATTA	GTGCGGGCGC	TGGTTTTTCC	TTTTTCTCT	ATTTTTTAGC	ATTTGTGGGA	600
CAAGAATGGA	TGATGGATCA	TATTGTAACA	GTGTATTTAC	TACTCTTAAG	CTTATTAGTT	660
ATGTTGATTG	TTAGTCGCTT	GGAAGAGAAA	TTTAAGAAAG	GATAA		705

(2) INFORMATION FOR SEQ ID NO:1388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1388:

AAATATTTAC	TAGAAGCGAA	AAAAACAAAG	ATTATCGATT	GGGATTTTGC	AGACACTTGC	60
TGGGAAAAGG	AGCTTAGAAA	ATACCAATAT	GTGGCTGCTA	ACTATTTGAA	AGCAATGCAG	120
TCTTATCTAA	AGGAAACCGA	TTTGCCTAAG	CTAGAGCAGT	TAGTCGTGAC	AAAATCCTGG	180
TGGGACACGG	TAGATATCCT	AGATCGAGTA	GTAGGGAGTT	TGGTGTATGA	ACACCCTGAA	240
CTAGAAGAAA	TAATCTTAAT	ACTCTTCGAA	AATCTCTTCA	AACCACGTCA	GCTCTATCTG	300
CAACCTCAAA	ACAGTGTTTT	GAGCAATCTG	CGGCTAGCTT	CCTAG		345

(2) INFORMATION FOR SEQ ID NO:1389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1389:

GGTGGCTTAC	TTAAAAAAGT	TAAAAGAGTT	AGAGGAAAGG	GACGAAGCCC	TAGAGCGAGA	60
AAGGCAGAAA	CAGTTAGAGA	AATGGTTTCA	GGAGGATTTT	GACTAGATTT	TCTTCTTGAA	120
ACAGCACGTT	TAGCTCGCTC	GACTTACTAT	TATCAGTTGA	AACAACTGGA	TGGGGTTGAT	180
AAAGATAAAG	AGATTAAAAAC	CGAAATTCAG	GCCATTTATA	ATGAACATAA	AGGCAACTAT	240
GGCTATCGTC	GAATCCATTT	AGAACTAAGA	AATCGTGGTT	TTGTGGTGAA	TCATAAGAAA	300
GTTCAACGTC	TGATGAAAGT	TCTTGGTTTA	ACAGCTCGAA	TTCGTCGGAA	ACGAAAGTAT	360
TCCTCCTACC	AAGGAGAGAT	TGGCAAGAAA	GCAGAGAATC	TCATTCAACG	TCAGTTTGAA	420
GCAACCAAAC	CAATGGAAAA	GTGCTATACG	GATGTGACAG	AGTTTGCCAT	TCCAAATAGC	480
ACACAGAAAC	TCTATTTATC	GCCTGTTTTA	GATGGCTTTA	ACAGCGAAAT	TTCGCCTATA	540
ATCTTTCAAC	TTACCAAAC	TTAG				564

(2) INFORMATION FOR SEQ ID NO:1390:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 666 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1390:

AGTAGAAGTT	TACGGTGTTG	TAGACCACCA	CCGTGTGCTA	ACTTTGAAAC	TGCAAGCCCA	60
CTTTACATGC	GTTTGGAGCC	AGTTGGATCA	GCGTCTTCAA	TCGTTTACCG	TATGTTCAAA	120
GAACATGGTG	TAGCTGTTCC	TAAAGAGATT	GCAGGTTTGA	TGCTTTCAGG	TTTGATTTCA	180
GATACCCCTT	TTTTGAAAATC	ACCAACAACA	CACCCAACAG	ATAAAATCAT	TGCTCCTGAA	240
TTGGCTGAAT	TGGCTGGTGT	AAACTTGGAA	GAATATGGTT	TGGCAATGTT	GAAAGCTGGT	300
ACCAACTTGG	CTAGCAAATC	TGCTGAAGAA	TTGATTGACA	TCGATGCTAA	GACTTTTGAA	360

CTCAACGGAA	ATAATGTCCG	TGTTGCCCAA	GTGAACACAG	TTGACATCGC	TGAAGTTTTG	420
GAACGCCAAG	CAGAAATTGA	AGCTGCAATG	CAAGCTGCCA	ACGAATCAAA	CGGCTACTCT	480
GACTTTGTCT	TGATGATTAC	AGATATCGTC	AACTCAAAC	CAGAAATATT	GGCTCTTGGT	540
GCCAATATGG	ACAAGGTCGA	AGCGGCTTTC	AATTTCAAAC	TTGAAAACAA	TCATGCCTTC	600
CTTGCTGGTG	CCGTTTCACG	TAAGAAACAA	GTGGTACCTC	AATTAAC	TGAAGCTTTAAT	660
ACGTAA						666

(2) INFORMATION FOR SEQ ID NO:1391:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 189 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...189
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1391:

CTACTATTAC	TCTTAACATT	TTATCCTCCA	CTAACAACTC	AAGCTCCCTT	ACATTATATC	60
GACCAGCCCC	ATGGAAAGAT	TATAGCTAGA	CTAATCAATG	ATATAATACA	TACTAGAATA	120
CAAAATATTT	TTATATTCAT	ACTTTTCTC	CTATCTTTAT	TTTCTACCTA	CATAGTACCT	180
CTTATTTAA						189

(2) INFORMATION FOR SEQ ID NO:1392:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1392:

GCTATATTAC	TCTTTCCTAA	CCTCCTTTTT	TCATATGTGG	ATAAAATCTC	TTGTCTATCC	60
CTTCCCCCAT	TGTCACCCAT	TATAGTCATT	TCGTGTCTCT	TTTTCCCCTT	TTTAATGCAA	120
GGGAAATTAC	TCTCCTTAGA	TGATAATCCA	AAAGCTAGAA	AGGTATCTCA	AACCTCTCTA	180
CTCTCCCAGA	CTAGTTTACA	ACTAAAAGGA	AAAGATTCTA	TTTTATGA		228

(2) INFORMATION FOR SEQ ID NO:1393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1393:

GTATGGTTAC	TGACTTCGTC	AGTTCTATCC	ACAACCTCAA	AACGGTGTTT	TGAGCTGACT	60
TCGTCAGTTC	TATCCACAAC	CTCAAAACAG	TGTTTTGAGC	TGACTTCATC	AGTTCTATCT	120
GCAACCTCAA	AACGGTGTTT	TGAGCAACCT	GCGGCTAGTT	TCCTAGTTTG	CTCTTTGATT	180
TTCATTGAGT	ATTATTAA					198

(2) INFORMATION FOR SEQ ID NO:1394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1394:

GTATGGTTAC	TGACTTCGTC	AGTTTCATCT	ACAACCTCAA	AACCATGTTT	TGAGCTGACT	60
TCGTCAGTTC	TATCCACAAC	CTCAAAACAG	TGTTTTGAGC	AACCTGCGGC	TAGCTTCCTA	120
GTTTGCTCTT	TGATTTTCAT	TGAGTATAAA	ATCCTAGTTT	TTCAAAGATT	TCTGAGAAGT	180
TTTGGCTGA						189

(2) INFORMATION FOR SEQ ID NO:1395:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...225
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1395:

GTATGGTTAC	TGACTTCGTC	AGTTCTATCC	ACAACCTCAA	AACAGTGTTT	TGAGCTGACT	60
TCGTCAGTCT	TATCTACAGG	TTCAAAGCAG	TGTTTTGAGC	AATCTGCGGT	TAGCTTCCTA	120
GTTTGCTCTT	TGATTTTCAT	TGAGTATAAA	TCATTCAACG	TAAATGAAAA	AAATTTCTTA	180
ACGAAAGATA	GAGATAAATC	GAAATCAGTA	GATCGTATAA	AGTGA		225

(2) INFORMATION FOR SEQ ID NO:1396:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1308 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1308
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1396:

GTCATTCTAC	TCAAATCTAC	GTTAGAAAGG	ACTGCTATGC	CAGACAATCT	CGCGCTTCGC	60
ATGCGCCCTA	AAACCATCGA	CCAGGTCATC	GGTCAGGAGC	ATCTGGTTCGG	ACCTGGAAAA	120
ATCATCCGCC	GCATGGTGGA	AGCCAACCGC	CTGTCCCTCCA	TGATTCTATA	TGGCCCTCCT	180
GGAATCGGCA	AAACAGTAT	TGCCCTCTGCC	ATCGCTGGAA	CGACCAAGTA	TGCCCTTTCGA	240
ACTTTCAATG	CAACAGTTGA	TAGTAAAAAG	CGACTGCAAG	AAATCTCGGA	AGAAGCTAAA	300
TTTCTGGTG	GTCTCGTCCT	ATTGCTAGAC	GAAATTCATC	GACTAGATAA	GACCAAGCAA	360
GACTTCCTCT	TGCCTCTCTT	GGAAAGTGGA	CTGGTCATCA	TGATTGGAGC	AACGACTGAA	420
AATCCTTTCT	TCTCTGTCAC	TCCTGCCATT	CGTAGCCGAG	TTCAAATTTT	CGAGTTGGAA	480
CCTCTGTCTA	ACCAAGACGT	CAAAGAGGCC	CTGCAGATAG	CTCTAAGTAA	CCCTGAACGT	540
GGTTTTGATT	TTCCAATAGA	ACTAGATGAG	GATGCGCTGG	ATTTTCATCGC	AACCTCTACA	600
AACGGAGACC	TTCGCTCTGC	CTTTAACTCA	CTGGACTTGG	CTGTTCTCTC	TACCCCTGAG	660
AATGACGAGG	GCATTGCGCA	CATCACCTTA	GACATCATGG	AAAATAGTCT	TCAGAGAAGC	720
TACATCACTA	TGGACAAGGA	TGGAGACGGT	CACTATGATG	TTCTATCTGC	CCTGCAAAAG	780
TCTATTTCGT	GCTCAGATGT	GGATGCCAGT	CTCCACTATA	CTGCCCGCTT	GATTGAGGCT	840
GGGGATCTGC	CTAGTCTCGC	TCGTGCTTGG	ACTGTTATCG	CCTATGAAGA	TATCGGCTTA	900
GCCAATCCTG	AGGCCCAGAT	TCATACCGTG	ACTGCTCTGG	ATGCTGCCCA	GAAGATTGGG	960
TTCCCAGAAG	CCCGCATTTCT	CATTGCCAAT	GTCTGTGATTG	ATTTGGCCCT	TTCTCCAAAA	1020
TCCAACTCAG	CCTATGTAGC	TATGGATAAG	GCACTTGCTG	ACCTCAAAAC	ATCAGGGCAC	1080
TTGCCTATTC	CGCGACACCT	GCGTGATGGG	CACTACAGTG	GAAGCAAGGA	ACTGGGGAAT	1140
GCCCAAGACT	ATCTCTATCC	ACACAACCTAT	CCTGGAAATT	GGGTCAAGCA	AGACTATCTG	1200
CCAGAAAAAA	TTCGTAAATCA	TCACTATTTT	CAAGCAGAAG	ATACTGGTAA	ATATGAACGG	1260
GCTTTGGCTC	AAAGAAAAGGA	AGCTATCGAC	CATTTGCGAA	AAATCTGA		1308

(2) INFORMATION FOR SEQ ID NO:1397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1397:

AGCATTCTAC	TAAAAACATT	GGATGAAGAT	ATTCTTCTTG	GTTGTATCCT	TCCTTGGA	60
CCAGAAGCCT	TTGAAAAACT	CAAAGCATA	GGGGATGGCC	GTGAAGAACT	TATGACTGAT	120
GTACGTGGTA	CTAGCTGTTT	TGTTATCAAG	TTTGAAAAAG	CAGGTGAACA	ATTGGCTGCC	180
AAGCTTTGGG	AAGAAGGTAA	AATGGTCTAC	GCCTCATATG	CTTCAATGAC	AAAACGATTG	240
AAACTCGCTA	TGAGAGCAAG	GTGTAATGGT	GTCTATGGTC	GATAA		285

(2) INFORMATION FOR SEQ ID NO:1398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1356 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

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(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1398:

GATCAGAGTT	TAACATATGTC	AGAAAAATCA	CAATGGGGGT	CGAAACTTGG	CTTTATTCTA	60
GCATCTGCTG	GCTCGGTCAT	CGGGCTTGGT	TCCGTTTGGA	AGTTTCCCTA	CATGACTGCT	120
GCTAATGGCG	GTGGAGGCTT	TTTACTAATC	TTTCTCATTT	CCACTATTTT	AATCGATTTC	180
CCTCTCCTGC	TGGCTGAGTT	TGCCCTTGCC	CGTAGTGCCTG	GCGTTTCCGC	TATCAAAACC	240
TTTGAAAAAC	TGGGCAAGAA	TAACAAGTAC	AACTTTATCG	GTTGGATTGG	CGCCTTTGCC	300
CTCTTTATCC	TCTTATCTTT	TTACAGTGTT	ATCGGAGGAT	GGATTCTAGT	CTATCTAGGT	360
ATTGAGTTTG	GGAAATTGTT	CCAACCTGGT	GGAACGGGTG	ATTATGCTCA	GTTATTTACT	420
TCAATCATTT	CAAATCCAGC	CATTGCCCTA	GGAGCTCAAG	CGACCTTTAT	CCTATTGAAT	480
ATCTTCATTG	TATCACGTGG	GGTTCAAAAA	GGGATTGAAA	GAGCTTCGAA	AGTCATGATG	540
CCCCTGCTCT	TTATCATCTT	TGTCGTCATC	ATCGAACGCT	CTCTCAGTTT	GCCAAATGCC	600
ATGGAAGGGG	TTCTTTACTT	CCTCAAACCA	GATTTTTTCAA	AACTGACTAG	CGCTGGTCTC	660
CTCTATGCTC	TGAGACAATC	TTTCTTTGCC	CTCTCACTAG	GGGTTACAGC	CATGTTGACC	720
TATGCTTCTT	ACTTGGACAA	GAAAACCAAT	CTGGTCCAGT	CAAGAATCTC	CATCGTAGCC	780
ATGAATATCT	CGGTATCCAT	CATGGCAGGT	CTAGCCATTT	TCCAAGCTCG	GTCCCCCTTC	840
AATATCCAGT	CTGAAGGGGG	ACCGAGCTTG	GTCTTTATCG	TCTTGCCCTCA	ACTCTTTGAC	900
AAGATGCCTT	TTGGAACCAT	TTTCTATGTC	CTCTTCCTCT	TTGCGACTGT	CACTTCCTCT	960
GTCGTTATGC	TGGAATCAA	TGTAGACAAT	ATCACCAATC	AGGACAACAG	CAAGCGTGCT	1020
AAATGGAGTG	TTATTTTAGG	AATTTTGACC	TTTGTCTTTG	GCATTCCCTC	AGCCCTATCT	1080
TACGGTGTCA	TGGCGGATGT	TCACATTTT	GGTAAAGCCT	TCTTTGACGC	TATGGACTTC	1140
TTGGTTTCCA	ATCTCCTCAT	GCCATTTGGA	GCTCTCTTCC	TTTCACTTTT	TACAGGCTAT	1200
ATCTTTAAAA	AGGCTCTTGC	AATGGAGGAA	CTCCATCTCG	ATGAAAGAGC	ATGGAAACAA	1260
GGACTGTTCC	AAGTCTGGCT	CTTCCTTCTT	CGTTTCGTCA	TTCCAATCAT	CATCTGTGGT	1320
CTTCATCGCC	CAATTTATGT	AATCAAAAGG	ACTTGA			1356

(2) INFORMATION FOR SEQ ID NO:1399:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1399:

ACGGAGAGTT	TACGGAAAAG	TAAGATGAGT	GTATTGGATG	AAGAGTATCT	AAAAAATACA	60
CGAAAAGTTT	ATAATGATTT	TTGTAATCAA	GCTGATAACT	ATAGAACATC	AAAAGATTTT	120
ATTGATAATA	TTCCAATAGA	ATATTTAGCT	AGATATAGAG	AAATTATATT	AGCTGAGCAT	180
GATAGTTGTG	TCAAAAATGA	TGAAGCGGTA	AGGAATTTTG	TTACCTCAGT	ATTGTTGTCT	240
GCATTTGTAT	CGGCGATGGT	ATCAGCTATG	ATATCATTAG	AAATACAAAC	ATATAAATTT	300
GTAATACCGT	TCATAATTGG	TATGATTTGG	ACAGTAGTTG	TATTTCTTAT	GATCAATTGG	360
AATTATATAG	GCAAATACTA	A				381

(2) INFORMATION FOR SEQ ID NO:1400:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1400:

AACAGGAGTT	TGAAAATGAA	AAGACCACTT	GAGATGGCAC	ATGATTTTTT	GGCTGAGGTC	60
GTGACAAAAG	AGGATGTCGT	AGTGGATGCG	ACTATGGGAA	ATGGTCATGA	CACGCTTTTT	120
TTAGCCAAGC	TAGCCAAGCA	AGTCTATGCC	TTTGATATTC	AGAAGCAAGC	CTTGGAAAAG	180
ACCCAAGAGC	GTTTGCAATCA	GGCTGACTTG	ACAAATGCCC	AGTTAATCTT	GCAAGGCCAT	240
GAGACACTGG	ACCAGTTTGT	GATAAAAAGCT	AAGGCAGGGA	TTTTTAATCT	GGGCTATTTG	300
CCGTCAGCTG	ATAAGTCTGT	CATCACCCGA	CCGCAGACAA	CGATTGAGGC	ATTAGAAAAG	360
CTATGTGGCT	TACTTGTCAA	AGGTGGACGA	ATTGCTATTA	TGATTTACTA	TGGTCATGAA	420
GGAGGCGATC	TCGAGAGAGA	TGCTGTCTTG	GATTTTGTGA	TCCAGTTGAA	CCAACAAGAG	480
TACACAGCTG	CCATTTACCG	AACTTTAAAC	CAAGTCAACA	ACCCGCCGTT	TTTAGTGATG	540
ATTGAAAAAT	TAGAGAGATA	CAGACATGGA	TAA			573

(2) INFORMATION FOR SEQ ID NO:1401:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 618 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...618
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1401:

GTGTTAATAC	TTTTCAAAAA	TCTCTTCAAA	CCACGTCAGC	TTCGCCTTGC	CGTATATATG	60
TTACTGACTT	CGTCAGTTCT	ATCTGCCACC	TCAAAACGGT	GTTTTGAGCT	GACTTCGTCA	120
GTTCTATCTG	CCACCTCAAA	ACGGTGTTTT	GAGCTGACTT	CGTCAGTTCT	ATCTGCCACC	180
TCAAAACGGT	GTTTTGAGCT	GACTTCGTCA	GTTCTATCTG	CCACCTCAAA	ACGGTGTTTT	240
GAGCTGACTT	CGTCAGTTCT	ATCTGCCACC	TCAAAACGGT	GTTTTGAGCT	GACTTCGTCA	300
GTTCTATCTG	CCACCTCAAA	ACGGTGTTTT	GAGCTGACTT	CGTCAGTTCT	ATCTGCCACC	360
TCAAAACGGT	GTTTTGAGCT	GACTTCGTCA	GTTCTATCTG	CCACCTCAAA	ACGGTGTTTT	420
GAGCTGACTT	CGTCAGTTCT	ATCTGCCACC	TCAAAACGGT	GTTTTGAGCT	GACTTCGTCA	480
GTTCTATCTG	CCACCTCAAA	ACGGTGTTTT	GAGCTGACTT	CGTCAGTTCT	ATCTGCCACC	540
TCAAAACGGT	GTTTTGAGCA	TCATGCGACT	AGCTTCTTAG	TTTGCTCTTT	GATTTTCATT	600
GAGTATAAAA	ACAGATGA					618

(2) INFORMATION FOR SEQ ID NO:1402:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1407 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1407
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1402:

AAAGGGATAC	TCATGAGTAA	AAAAAGACGA	AATCGTCATA	AAAAAGAAGG	TCAAGAACCG	60
CAATTTGATT	TTGATGAAGC	AAAAGAGCTA	ACAGTTGGTC	AAGCTATTCG	TAAAAATGAA	120
GAAGTGGAAG	CAGGAGTCTT	GCCTGAGGAT	TCCATTTTGG	ACAAGTATGT	TAAGCAACAC	180
AGAGATGAAA	TTGAGGCGGA	TAAGTTTGCG	ACTCGTCAAT	ACAAAAAAGA	GGAGTTCGTT	240
GAAACTCAGA	GTCTGGATGA	TTTAATTCAA	GAGATGCGTG	AGGCTGTAGA	GAAGTCAGAA	300

GCTTCTTCGG	AGGAAGTTCC	ATCTTCTGAA	GACATCTTAC	TACCCTTGCC	TCTGGACGAT	360
GAGGAGCAAG	GCTTGGATCC	TCTATTGCTA	GATGATGAAA	ATCCAACAGA	AATGACTGAA	420
GAAGTGGAAG	AGGAGCAAAA	CCTTTCTCGT	CTGGATCAAG	AGGACTCAGA	AAAGAAAAGT	480
AAAAAAGGCT	TTATTTTGAC	CGTTTTGGCG	CTTGATATCAG	TAATTATTTG	TGTCAGTGCT	540
TATTATGTCT	ACCGTCAAGT	GAATCGCTCG	ACCAAGGAAA	TTGAAACTTC	TCAATCAACT	600
ACAGCCAATC	AATCAGATGT	GGATGATTTT	AATACACTTT	ATGACGCCTT	TTACACAGAT	660
AGCAATAAAA	CGGCTTTGAA	AAATAGCCAG	TTTGATAAAC	TGAGTCAACT	CAAAACCTTG	720
CTTGATAAGC	TGGAAGGTAG	TCGTGAACAT	ACACTTGCCA	AATCTAAATA	TGATAGTCTA	780
GCAACGCAAA	TCAAGGCTAT	TCAAGATGTC	AATGCACAA	TTGAAAAATC	AGCTATTGTG	840
GATGGTGTGT	TGGATACCCA	TGCCAAAGCT	AAATCGGATG	CTAAATTTAC	AGATATTAAA	900
ACTGGGAATA	CGGAGCTTGA	TAAAGTGCTA	GATAAGGCTA	TCAGTCTTGG	TAAGAGCCAG	960
CAAACAAGTA	CTTTTAGCTC	AAGTTCAAGT	CAAAC TAGCA	GCTCAAGCTC	TAGTCAAGCA	1020
AGCTCAAATA	CGACAAGTGA	GCCAAAACCA	AGTAGTTCAA	ATGAGACTAG	AAGTAGTCGC	1080
AGTGAAGTCA	ATATGGGTCT	CTCGAGTGCA	GGGGTTGCTG	TTCAAAGAAG	TGCCAGTCGT	1140
GTTGCCCTATA	ATCAGTCTGC	TATTGATGAT	AGTAATAACT	CTGCCTGGGA	TTTTGCGGAT	1200
GGTGTCTTGG	AACAAATTCT	AGCGACTTCA	CGTTCACGTG	GCTATATCAC	TGGAGACCAA	1260
TATATCCTTG	AACGTGTCAA	TATCGTTAAC	GGCAATGGTT	ATTACAACCT	CTATAAGCCA	1320
GATGTAACCT	ATCTCTTTAC	CCTTAAC TGT	AAGACAGGCT	ACTTTGTGCG	AAATGGCGCT	1380
GGTCATGCGG	ATGACTTGGA	CTACTAA				1407

(2) INFORMATION FOR SEQ ID NO:1403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1403:

GAACCTGTAC	TTGCGACTTT	GACAATTCCA	GAAGGTTATA	CCTTGGATCA	GATTGCTCAA	60
ACTGTGGGTC	AATTGCAAGG	TGACTTCAAA	GAGTCTTTGA	CAGCGGAGGC	TTTCTTGGCT	120
AAAGTTCAAG	ATGAGACGTT	TATCAGTCAA	GCAGTAGCGA	AATATCCTAC	TTTACTGGAA	180
AGTTTGCC TG	TAAAAGACAG	CGGTGCGCGT	TATCGTTTGG	AAGGATACCT	TTTCCCAGCT	240
ACATACTCTA	TCAAGGAAAG	CACAACTATT	GAGAGCTTGA	TTGATGAGAT	GTTAGCTGCT	300
ATGGATAAGA	ACCTATCTCC	TTACTATAGT	ACTATCAAAT	CTAAAAACTT	GACTGTCAAT	360
GAGTTGTTGA	CCATTGCTTC	CTTGGTCGAA	AAAGAAGGTG	CCAAGACAGA	AGATCGTAAG	420
CTCATTGCAG	GTGTATTCTA	CAATCGTTTG	AATCGTGATA	TGCCACTTCA	AAGTAATATT	480
GCAATCTTGT	ATGCCCAAGG	AAAAC TGGGG	CAAAATATCA	GTCTAGCTGA	GGATGTTGCG	540
ATTGATACCA	ACATTGATTC	ACCTTATAAT	GTTTATAAAA	ATGTAGGTCT	CATGCCTGGT	600
CCAGTCGATA	GTCCAAGTCT	GGATGCGATT	GAGTCAAGCA	TCAATCAAAC	TAAGAGCGAT	660
AACCTCTACT	TTGTAGCAGA	TGTCACAGAA	GGCAAGGTCT	ACTATGCTAA	CAATCAAGAA	720
GACCACGACC	GCAATGTCCG	TGAACATGTC	AACAGCAAAT	TAAACTAA		768

(2) INFORMATION FOR SEQ ID NO:1404:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 669 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...669
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1404:

CAGTTTTAC	TTATGTTGA	AATTTTTAAA	TCCTATCAAT	TTAATCAAGA	AAAGGCTCAT	60
GATTATGGT	TTATAGAAAA	TAGCGAAGTC	TGGACATATA	GTTGCCAGAT	TTTGCAAGGT	120
GACTTTGTCA	TGACTGTGTC	CATCACTGCT	GATAATGTGA	ACTTTCAAGT	CTTTGACCAA	180
GAGACTGGTG	ACCTCTATCC	TCACGTTTCA	TGAGGGGAAG	TTTTGTTCGGA		240
AATGTCCGTG	AGGCTTGTCT	GGAGATTCTT	TACCAGATTTC	GGAAGGCTTG	TTTTGATGTG	300
CAAGATTTTA	TCTGTCATCA	GAATAAGCGT	ATCATGACTC	AAGTTCAGGA	AAAGTATGGA	360
AACCAGTTGG	AGTATCTGTG	GGAAAAATCG	CCTGATACAG	CTGTATTGCG	CCATGAAGGC	420
AATCAAAAAGT	GGTATGCCGT	CTTGATGAAA	ATCTCTTGGA	ATAAGCTGGA	AAAGGGCAGA	480
GAAGGACAAG	TGGAAGCAGT	CAACCTCAAG	CATGACCAAG	TAGCTAATTT	GCTTTCACAA	540
AAGGGGATTT	ATCCAGCCTT	CCATATGAGC	AAGCGCTACT	GGATTAGTGT	GTCCCTTGAT	600
GATACTTTAT	CAGATGAAGA	AGTACTGGAA	TTGATAGAAA	AAAGTTGGAA	CTTAACCTCT	660
AAAAAATGA						669

(2) INFORMATION FOR SEQ ID NO:1405:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 597 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1405:

ACTGTTTCAC	TCCCGAATGC	TAAAATCGTT	CTTGATCGCT	TTCACATTGT	ACAACATCTT	60
AGCCGTGCTA	TGAGTCGTGT	GCGTGTCCTA	ATCATGAATC	AGTTTCATCG	AAAATCCCAT	120
GAATACAAGG	CTATCAAGCA	CTACTGGAAG	CTCATACAAC	AGGATAGCCG	TAAACTGAGT	180
GATAAACGTT	TTTATCGTCC	TACTTTTCGT	ATGCACTTAA	CCAATAAAGA	GATTTTAAAC	240
AAGCTTTTGA	GTTATTCGGA	AGACTTGAAA	CACCACTATC	AGCTCTATCA	GCTCTTGCTT	300
TTTCACTTCC	AGAATAAGGA	ACCAGAGAAA	TTTTTCGAAC	TTATTGAGGA	CAATCTAAAG	360
CAGGCTCATC	CTCTTTTCA	GACTGTCTTT	AAAACCTTTC	TAAAGGACAA	AGAGAAAATC	420
GTCAACGCC	TTCAACTACA	CTATTCTAAC	GCCAAATTGG	AAGCGACCAA	TAATCTCATC	480
AAACTTATCA	AGCGCAATGC	CTTTGGTTTT	CGGAACTTTG	AAAACTTCAA	AAAACGGATT	540
TTTATCGCTT	TGAACATCAA	AAAAGAAAGG	ACGAAATTTG	TCCTTTCTCA	AGCTTAG	597

(2) INFORMATION FOR SEQ ID NO:1406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1406:

GATGTTGGTT	TGGAAAGTCG	TAAATTAGCT	GTTAGTGGAA	AAATTAAGCA	TTATGTGGTT	60
GATAATGACA	ATGTTGTGAC	TCCCTTGATT	CATAATAATC	GTGATATTGT	TACATTTACA	120
GGTAATTCAC	GCTTTAAACA	CCGTTCTCGT	GGCTATTTTG	AAAGTCCAAT	GAATGATATT	180
CCTAACTTTA	ATATTGGTAA	ACAAGCTATC	TTGGATAAAC	ATGGTTATCG	TGATCCGAAA	240
TTGGATAAAG	TGCGATTCTT	TAAGAAACAG	GCTCTGCCTC	GATCTTCTAG	TCAACCAAGC	300
GCTGAACCAA	TGGAAAATAT	TGCCTTAGGA	AAACAGGTTA	CTCAAAGTTC	GACAGTTTTT	360
GGAGGAGATG	CTAGAAGAGC	TGTGGATGGC	AAAGTCGATG	GTAAGTATGG	TCACAATTCT	420
GTCATCATA	CAAACCTCCA	ATCTAAGCCT	TGGTGGCAAG	TAGATTTGGC	TAAAGAAGAA	480
ACCATTCGCC	AAATCAATAT	TTACAACCGA	ACAGACACTG	CCCAGGATAG	ATTGGCAAAC	540
TTTGATGTCA	TTCTTTTAGA	CAGTTCTGGT	AAAGAAATTG	AGTGA		585

(2) INFORMATION FOR SEQ ID NO:1407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1407:

TTCTGGTCAC	TATCAGGCTG	CGGCAATAAC	TTGAGTTACA	CAAAAGAGCG	TGCTGAAAAA	60
TACCTTTACT	CGCTTCCAAT	TTCCAACAAT	CCCCTCGTCC	TTGTCAGCAA	CAAGAAAAAT	120
CCTTTGACTT	CTCTTGACCA	GATCGCTGGT	AAAACAACAC	AAGAGGATAC	CGGAAC TTCT	180
AACGCTCAAT	TCATCAATAA	CTGGAATCAG	AAACACACTG	ATAATCCCGC	TACAATTAAAT	240
TTTTCTGGTG	AGGATATTGG	TAAACGAATC	CTAGACCTTG	CTAACGGAGA	GTTTGATTTC	300
CTAGTTTTTG	ACAAGGTATC	CGTTCAAAAG	ATTATCAAGG	ACCGTGGTTT	AGACCTCTCA	360
GTCGTTGATT	TACCTTCTGC	AGATAGCCCC	AGCAATTATA	TCATTTTCTC	AAGCGACCAA	420
AAAGAGTTTA	AAGAGCAATT	TGATAAAGCG	CTCAAAGAAC	TCTATCAAGA	CGGAACCCCTT	480
GAAAACTCA	GCAATACCTA	TCTAGGTGGT	TCTTACCTCC	CAGATCAATC	TCAGTTACAA	540
TAA						543

(2) INFORMATION FOR SEQ ID NO:1408:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1408:

TCCATACCAC	TTGAAGGTTC	GTCAAAAAAG	ACAAATGGAG	AATTCTTGCA	CATAACAGAT	60
GCTATTGCAA	GCCTTTGCTT	TCGCCCTCCT	GATAAACTCA	TCGGATGCCT	TTCAATAAAT	120
TCGTCCAGGC	ATAAATCTTT	TAAAATGATT	TTCGCCTTTT	CTTCATCAAA	ATTCTTTACT	180
CCTAATCTAA	GCTCGTTGAA	TACTTCATCT	GTGAATAATT	GA		222

(2) INFORMATION FOR SEQ ID NO:1409:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 378 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...378
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1409:

CCGCTCGCAC TCAGCCAAGT TGC GCGTGGT CAGAAAAATT CACAAGTAAG AGGGAAAAAG	60
ATGGCAGAAA AAATGGAAAA AACAGGTCAA ATACTACAGA TGCAACTTAA ACGGTTTTTCG	120
CGTGTGGAAA AAGCTTTTTTA CTTTTCCATT GCTGTAACCA CTCTTATTGT AGCCATTAGT	180
ATTATTTTTTA TGCAGACCAA GCTCTTGCAA GTGCAGAATG ATTTGACAAA AATCAATGCG	240
CAGATAGAGG AAAAGAAGAC CGAATTGGAC GATGCCAAGC AAGAGGTCAA TGA ACTATTA	300
CGTGCAGAAC GTTTGAAAGA AATTGCCAAT TCACACGATT TGCAATTAAA CAATGAAAAT	360
ATTATAATAG CGGAGTAA	378

(2) INFORMATION FOR SEQ ID NO:1410:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...249
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1410:

GTCCNGCAGN AATTTGNTTT NNNNNNGCTT TTTTNGGAAT NACGTCTGCT TAGCAAGNAA	60
CGTATCACAG GAGCTCTTCC AACTAATAAG TACATCATCG AACAAAGGTGG ACGTGCAATT	120
CTTTTCTCTC ACCTTGACG TGTGAAAGAA GAAGCTGATA AAGCTGGTAA ATCACTTGCT	180
CCTGTAGCAG CAGACTTGGC AGCAAACTT GGTCAAGATG TTGTTTTCCC AGGTGTCACT	240
CGTGGTTAG	249

(2) INFORMATION FOR SEQ ID NO:1411:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 585 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...585
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1411:

GAACTAGGTT	TGCATCAAGC	TCAAACGTGA	AAAGAAAATA	ATCGTGTTTC	CTATATAGAT	60
GGAAAACACG	CGACGCAAAA	AACGGAGAAAT	TTGACTCCTG	ATGAGGTTAG	CAAGCGTGAA	120
GGAATCAACG	CCGAACAAAT	CGTCATCAAG	ATTACGGATC	AAGGTTATGT	GACCTCTCAT	180
GGAGACCATT	ATCATTACTA	TAATGGCAAG	GTCCCTTATG	ATGCCATCAT	CAGTGAAGAG	240
CTCCTCATGA	AAGATCCGAA	TTATCAGTTG	AAGGATTCAG	ACATTGTCAA	TGAAATCAAG	300
GGTGTTTATG	TCATTAAAGT	AAACGGTAAA	TACTATGTTT	ACCTTAAGGA	TGCAGCTCAT	360
GCGGATAATG	TCCGTACAAA	AGAAGAAATC	AATCGGCAAA	AACAAGAACA	TAGTCAGCAT	420
CGTGAAGGAG	GGACTTCAGC	AAACGATGGT	GCGGTAGCCT	TTGCACGTTT	ACAGGGACGC	480
TACACCACAG	ATGATGGTTA	TATCTTCAAT	GCATCTGATA	TCATCGAAGA	TACGGGGCGA	540
TGCCTATATC	GTTCCCTCATG	GAGATCATT	CCATTACATT	CCTAA		585

(2) INFORMATION FOR SEQ ID NO:1412:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1524 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1524
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1412:

AAAAGACAAC	TACTATATCA	AGGTGCCAGC	TATCCTAGAC	GATGGAGGAG	ATGCCTAATG	60
ACTTTTAACA	ATAAACTAT	TGAAGAGTTG	CACAATCTCC	TTGTCTCTAA	GGAAATTTCT	120

GCAACAGAAAT	TGACCCAAGC	AACACTTGAA	AATATCAAGT	CTCGTGAGGA	AGCTCTCAAT	180
TCATTTGTCA	CCATCGCTGA	GGAGCAAGCT	CTTGTTCAAG	CTAAAGCCAT	TGATGAAGCT	240
GGAATTGATG	CTGACAATGT	CCTTTCAGGA	ATTCCACTTG	CTGTTAAGGA	TAACATCTCT	300
ACAGACGGTA	TTCTCACAAC	TGCTGCCTCA	AAAATGCTCT	ACAACTATGA	GCCAATCTTT	360
GATGCGACAG	CTGTTGCCAA	TGCAAAAACC	AAGGGCATGA	TTGTCGTTGG	AAAGACCAAC	420
ATGGACGAAT	TTGCTATGGG	TGGTTCAGGT	GAAACTTCAT	ACTACGGAGC	AACTAAAAAC	480
GCTTGGGACC	ACAGCAAGGT	TCCTGGTGGG	TCATCAAGTG	GTTCTGCCGC	AGCTGTAGCC	540
TCAGGACAAG	TTCGCTTGTC	ACTTGGTTCT	GATACTGGTG	GTTCCATCCG	CCAACCTGCT	600
GCCTTCAACG	GAATCGTTGG	TCTCAAACCA	ACCTACGGAA	CAGTTTCACG	TTTCGGTCTC	660
ATTGCCTTTG	GTAGCTCATT	AGACCAGATT	GGATCTTTTG	CTCCTACTGT	TAAGGAAAAT	720
GCCCTCTTGC	TCAACGCTAT	TGCCAGCGAA	GATGCTAAAG	ACTCTACTTC	TGCTCCTGTC	780
CGCATCGCCG	ACTTTACTTC	AAAAATCGGC	CAAGACATCA	AGGGTATGAA	AATCGCTTTG	840
CCTAAGGAAT	ACCTCGGTGA	AGGAATTAAC	CCAGAGGTTA	AGGAAACCAT	TCTAAATGCC	900
GCTAAACACT	TTGAAAAATT	GGGTGCTATT	GTCGAAGAAG	TCAGCCTTCC	TCACTCTAAA	960
TACGGAGTTG	CCGTATACTA	CATCATCGCT	TCATCAGAAG	CTTCATCAAA	CTTGCAACGC	1020
TTCGACGGTA	TCCGTTACGG	CTATCGCGCA	GAAGATGCAA	CCAACCTTGA	TGAAATCTAT	1080
GTAAACAGCC	GAAGCCAAGG	TTTTGGTGAA	GAAGTGAAGC	GCCGTATCAT	GCTGGGTACT	1140
TTCAGTCTTT	CATCAGGTTA	CTACGATGCC	TACTACAAGA	AGGCTGGACA	GGTCCGTACA	1200
CTTATCATTC	AAGATTTCGA	AAAAGTCTTC	GCGGATTACG	ATTTGATTTT	GGGTCCAAC	1260
GCTCCAAGTG	TTGCCTATGA	CTTGATTCT	CTCAACCATG	ACCCAGTTGC	CATGTACTTA	1320
GCCGACCTAT	TGACCATACC	TGTAAACTTG	GCAGGACTGC	CTGGAATTTT	GATTCCTGCT	1380
GGATTCTCTC	AAGGTCTACC	TGTCGGACTC	CAATTGATTG	GTCCCAAGTA	CTCTGAGGAA	1440
ACCATTTACC	AAGCTGCTGC	TGCTTTTGAA	GCAACAACAG	ACTACCACAA	ACAACAACCC	1500
GTGATTTTGT	GAGGTGACAA	CTAA				1524

(2) INFORMATION FOR SEQ ID NO:1413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1413:

GATTTTAAAC	TTTCCAGATA	TGACGACAGA	AGGTCCTTCC	CTCTTGGGGG	AGCTGTTGCT	60
GTCACTTTGA	TAACCAAAGG	CGTGAACCCA	TTTTTAGCGA	CAC TTGTTGC	TGTAGGAGCA	120
GGTTGTTTGG	CTGGAATGGC	AGCAGGCCTT	CTTTATACAA	AAGGAAAGAT	CCCAACCTTG	180
CTCTCAGGGA	TTTTGGTGAT	GACTTCTCGT	CACTCAATCA	TGCTCTTGAT	TATGGGACGT	240
GCAAAATTTAG	GCCTGCTTGG	AACCAAGCAA	ATTCAGGATG	TTTTGCCTTT	TGATTCCGGAT	300
TTGAATCAAC	TCTTGACAGG	TCTCATCTTT	GTGAGCATTG	TTATTGCTCT	CATGCTCTTT	360
TTCTTGGACA	CTAAACTCGG	ACAAGCCTAT	ATTGCTACAG	GGGATAATCC	TGATATGGCT	420
AGAAGTTTCG	GGATTCATAC	TGGACGCATG	GAGCTCATGG	GCTTGGTCTT	ATCAAATGGT	480

GTGATTGCC	TTGCAGGTGC	CCTCATTGCT	CAGCAAGAAG	GCTATGCCGA	TGTGTCTCGA	540
GGGATCGGG	TTATCGTTGT	GGGACTTGCA	AGTTTGATTA	TTGGAGAAGT	TATTTTCAAG	600
AGTTTGAGCT	TGGCAGAGCG	TTTGGTTACT	ATCGTTGTAG	GTTCTATCGC	TTATCAATTT	660
TTAGTGTGGG	CAGTTATCGC	ACTTGGCTTT	AATACAAGTT	ACCTTCGTTT	ATACAGTGCC	720
TTGATTTTAG	CAGTCTGCCT	CATGATTCCA	ACATTTAAGC	AAACAATCTT	GAAAGGAGCC	780
AAGTTAAGCA	AATGA					795

(2) INFORMATION FOR SEQ ID NO:1414:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1221 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1221
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1414:

CTGAGTAAAC	TGGTTGATGT	TGTTATGATT	CAATCTCTAT	TTAAGTTGGA	AAATAGTCAA	60
AGTCTTTTGG	ATGAGTATGA	GATGATGATT	GTGGATGAGT	GTCACCATAT	CTCTGCCTTG	120
ATGTTTGAAA	AAGTTGTTGC	TCAGCTTAGA	GGGAAGTATC	TTTACGGTTT	GACGGCTACG	180
CCTGAGCGTA	AGAATGGTCA	TGAGCCTATT	GTTTTTCAGA	GAATTGGTGA	GATACTCCAT	240
ACTGCTGATA	AGAGGGAAAC	GGATTTTAAA	CGGCAATTGC	AATTAAGATT	CACTTCCTTTT	300
GGTCATTTGG	AGATTGAAAA	GACCAAAGCA	AGTAATTTTA	TACAGCTCAG	TGATTGGATT	360
GCTACAGACT	CAGCGAGGAA	TCAGTTGATT	CTCAAGGATA	TTCTAGCCCA	AGTGGCAGAA	420
GGACGGAATA	TCTTGGGTTT	AGTTAATCGA	ATTCAACAGA	TAGATGTCTT	TGAAAAGTTA	480
TTGAAAGAGA	AAGAGGTTGA	TGACTGTTAC	ATTATTAGCG	GAAAAACCAA	AGTCCGAGAA	540
AGAACGAGTT	TACTGGAGAC	GTTAGAACAG	TTAGATAAAG	GGTTTGTTTT	GTTGTCTACT	600
GGAAAATACA	TTGGCGAAGA	TTTTGACTTA	CCTCAGTTGG	ACACGCTTAT	CTTGGCAGCA	660
CCCTTTTCTT	GGAAAAATAA	TTTAATTCAG	TATGCAGGTC	GGATTCATAG	AAACTACAAG	720
GATAAGTCTT	TGGTGCGTAT	TTTCGATTAT	GTGGATATTC	ATGTTCCCTTA	TTTAGAAAAG	780
ATGTTTCAGA	AACGACAAGT	AGCTTATCGA	AAGATGGATT	ATCGTGTCAT	CGAGGGTGAG	840
GAGAAACAAAT	TCGTTTATGT	TGATAGTAGA	TATGAGAAGG	TGTTGAGAGA	GGACTTAGCA	900
GGGGAAAGAC	AGGAATGTCT	GCTTATTTTA	CCTTATGTGC	ACCAGACAAA	ACTGATGAAT	960
TTTCTAAAAAG	AATTTAGGAT	TAGTCAAAT	GAGATATGTA	TACCAGAGAC	GGTTGCAAAT	1020
AAAGCATGGC	TAGACCAGTT	GAAGAGCCAG	AAAAATTAAAG	TGTCTTTTAC	TCAATCAAAA	1080
ATAGTAACGC	CTATTCTTTT	GGTGAATAAG	ACTATTGTTT	GGTATGGTGC	AATGCCATTA	1140
TTAGGGAAAG	TAGATGAGAT	GACCATATTA	CGTTTGGAAT	CAGCTAGTAT	AGTTTCTGAA	1200
CTAGTGGCAG	GTTTACGATA	G				1221

(2) INFORMATION FOR SEQ ID NO:1415:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 918 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...918
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1415:

ATGGACAAAC	TGGAGCAAGT	AAAATCTTGC	GTAATCTCTT	TGTGCCACCA	ACATTTGTTC	60
AAGCAGATGG	TAAAAACTTT	GGCGATATGG	TCAAAGAGAA	ATTGGTCACT	TATGGGGATG	120
AATGGAAGGA	TGTTAATCTT	GCAGATTCTC	AGGATGGTCT	TTACAATACA	GAAAAAGGCA	180
AGGCTGAGAT	TTGCTAAAGC	TAAATCAGCC	TTACAAGCAG	AAGGAGTCCA	ATTCCCAATT	240
CATTTGGATA	TGCCAGTTGA	CCAAACAGCA	ACTACAAAAG	TTCAGCGCGT	CCAATCTATG	300
AAACAATCCT	TGGAAGCAAC	TTTAGGAGCT	GATAATGTCA	TTATTGATAT	TCAACAATA	360
CAAAAAGACG	AAGTAAACAA	TATTACATAT	TTTGCTGAAA	ATGCTGCTGG	CGAAGACTGG	420
GATTTATCAG	ATAATGTCGG	TTGGGGTCCA	GACTTTGCCG	ATCCATCAAC	CTACCTTGAT	480
ATCATCAAAC	CATCTGTAGG	AGAAAAGTACT	AAAACATATT	TAGGGTTTGA	CTCAGGGGAA	540
GATAATGTAG	CTGCTAAAAA	AGTAGGTCTA	TATGACTACG	AAAAATTGGT	TACTGAGGCT	600
GGTGATGAGA	CTACAGATGT	TGCTAAACGC	TATGATAAAT	ACGCTGCAGC	CCAAGCTTGG	660
TTGACAGATA	GTGCTTTGAT	TATTCCAAC	ACATCTCGTA	CAGGGCGTCC	AATCTTGTCT	720
AAGATGGTAC	CATTTACAAT	ACCATTTGCA	TTGTCAGGAA	ATAAAGGTAC	AAGTGAACCA	780
GTCTTGATATA	AATACTTGA	ACTTCAAGAC	AAGGCAGTCA	CTGTAGATGA	ATACCAAAAA	840
GCTCAGGAAA	AATGGATGAA	AGAAAAAGAA	GAGTCTAATA	AAAAGGCTCA	AGAAGATCTC	900
GCAAAACATG	TGAAATAA					918

(2) INFORMATION FOR SEQ ID NO:1416:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 900 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1416:

GGCTTTTTTTT	GTTACAATAT	CTGTATGCAA	TTCACATTTA	CATTACCCGC	CTCTCTACCT	60
CAAATGACGG	TAAAGCAATT	ACTTGAGGAA	CAACTCCTCA	TCCCTAGAAA	AATCCGTCAT	120
TTTTTTGAGAA	TCAAGAAACA	TATTTTGATA	AATCAAGAAG	AAGTCCACTG	GAACGAAATC	180
GTAAATCCTG	GAGATGTTTG	CCAGTTGACT	TTTGACGAGG	AAGATTATTC	CCAAAAGACG	240
ATCCCTTGGG	GCAACCCAGA	CTTAGTGACG	GAAGTTTATC	AAGATCAACA	CTTGATTATT	300
GTAAACAAAC	CAGAGGGGAT	GAAAACGCAT	GGTAATCAAC	CAAACGAAAT	TGCCCTTCTT	360
AACCATGTCA	GTACCTATGT	TGGCCAAACC	TGCTATGTCG	TTCATCGTCT	GGACATGGAA	420
ACCAGTGGCT	TAGTTCCTCT	TGCCAAAAAT	CCTTTTATCC	TGCCCATTCCT	CAATCGCTTA	480
TTGGAGAAAA	AAGAGATTTT	TAGAGAATAT	TGGGCTCTAG	TTGATGGAAA	TATCAACAGA	540
AAAGAACTTG	TTTTTCAGAGA	CAAAATTGGA	CGTGATCGCC	ATGATCGTAG	AAAAAGAATA	600
GTTGATGCAA	AAAATGGGCA	ATATGCTGAA	ACGTATGTAA	GCAGATTAAA	GCAATTCTCA	660
AACAAGACTT	CCTTGGCTCA	TTGCAAGCTA	AAGACAGGGC	GAACCCATCA	GATTCGTGTG	720
CACCTTTCGC	ATCATAACTT	CCCTATTTTG	GGCGACCTC	TCTATAACAG	CAATTCAAAG	780
ACAAGTCGGC	TTATGCTTCA	TGCCTTTCGA	CTTTCCTTTA	CCCATCCACT	TACATTAGAA	840
AAATTAAACT	TCACTGCCCT	CTCAAATACT	TTTGAAACAG	AATTAAAAAA	GAATGGATGA	900

(2) INFORMATION FOR SEQ ID NO:1417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1417:

CCCGTTTTTTT	GGTATAATAA	GAAGAATAAA	TTGAAAGAAG	GAATTCCAAA	AATGGGAAAA	60
ATTGAAGTTA	TTAATCACCC	ACTGATTCAA	CACAAAATTGT	CAATCTTGCG	TCGTACAGAT	120
ACTTCTACAA	AAGCTTTTTCG	TGAGCTAGTA	GATGAGATTG	CAATGTTGAT	GGGGTATGAA	180
GTACTTCGTG	ATCTTCCACT	AGAAGATGTG	GAAATCGAAA	CACCAATTAC	AAAAACAGTT	240
CAAAAACAAT	TGGCAGGTAA	GAAATTGGCC	ATCGTCCCAA	TCTTGCGTGC	AGGTATCGGG	300
ATGGTTGATG	GTCTCTTGAG	CTTGGTTCCA	GCTGCTAAAG	TTGGCCACAT	CGGTATGTAC	360
CGTGATGAAG	AAACACTTCA	ACCAGTTGAA	TACTTGGTGA	AATTGCCTGA	GGACATTGAC	420
CAACGTCAAA	TTTTTGTAGT	AGACCCAATG	TTGGCAACAG	GTGGCTCAGC	AATCTTGGCT	480
GTTGATTCTC	TTAAAAAACG	TGGCGCATCA	AATATCAAAT	TTGTCTGCCT	TGTATCTGCT	540
CCAGAGGGTG	TAAAAGCCCT	TCAAGAAGCT	CATCCAGATG	TAGAAATCTT	TACAGCAGCC	600
TTGGATGAAC	GTTTGAACGA	ACACGGTTAT	ATCGTTCCAG	GTCTTGAGAG	TGCTGGAGAC	660
CGCTTGTTTCG	GTACAAAATA	A				681

(2) INFORMATION FOR SEQ ID NO:1418:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1418:

TACCGAAAAC	TAGTTAGGGG	GCTAGAGGAG	GAGCCCGAAG	GTGGCGACCG	TTGCAAGGTT	60
TGTTTTGACT	ACCGACTGGA	TAAAACAGCG	CAAGTGGCTA	TGGACTTGGG	CTTTGACTAC	120
TTTGGTTCAG	CCTTGACCAT	CAGTCCTCAT	AAGAATTCTC	AACTATCAA	TAGCATCGGA	180
ATCGATGTGC	AAAAAATTTA	CACGCCCCAC	TATTTTCCCA	ACGATTTCAA	GAAAAATCAA	240
GGCTACAAAC	GTTCAGTAGA	GATGTGTGAG	GAGTATGATA	TCTATCGTCA	ATGTTATTGT	300
GGCTGCGTCT	ATGCAGCCCA	AGCCCGAAT	ATTGACCTGG	TTTAA		345

(2) INFORMATION FOR SEQ ID NO:1419:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1419:

ATATGCTTTT	GCAACTGCAA	CACCGTCAGA	TGCTGCGATT	CCTTTAAGCA	TTTCTGTCAT	60
TTCCCTTATG	CCAATCCTTC	TTTTTCCATT	GTTTCTGAGA	TTGCAGCGAT	AGCGTCATCT	120
GCATCTGCAC	CTTCAGCTGA	GATAGTTACG	TCAGCACCTT	GGCCAACACC	AAGACTCATA	180
ACACCCATAA	TTGATTTAAG	GTTAACTGAT	TTACCTTTGT	ACTCAAGAGT	GATATCTGAA	240
GCAAATTTGC	TAGCAGTTTG	TACCAACAAT	GTTGCTGGAC	GTGCGTGA		288

(2) INFORMATION FOR SEQ ID NO:1420:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...315
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1420:

AACAGCTTTT	GGATAAGGTG	TTGCTCTATG	ACAATTCATC	TATCTAGCCT	AGGACAGGTC	60
TATCTCGTAT	GTGGGAAAAC	GGATATGAGG	CAAGGCATTG	ATTCAGTGGC	TTATCTGGTT	120
AAAACCCACT	TTGAATTAGA	TCCTTTCTCA	GGTCAAGTTT	TTCTCTTTTG	TGGTGGACGT	180
AAAGACCGCT	TTAAAGCCCT	TTACTGGGAT	GGTCAAGGAT	TTTGGCTACT	ATATAAACGC	240
TTTGAGAACG	GCAGACTGAC	TTGGCTAAGT	ACAGAAAAGG	ATGTCAAAGC	TCTCGCACCT	300
GAACAAGTAG	ACTAG					315

(2) INFORMATION FOR SEQ ID NO:1421:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 987 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...987
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1421:

AGGAGAAAAC	TCATGGAAGT	TTTTGAAAGT	CTCAAAGCCA	ACCTTGTTGG	TAAAAATGCT	60
CGTATCGTTC	TCCCTGAAGG	GGAAGAGCCT	CGTATTCCTC	AAGCAACAAA	ACGCTTAGTA	120
AAAGAAACAG	AAGTGATTCC	TGTTTTGCTT	GGAAATCCTG	AAAAAATTAA	AATTTATCTT	180
GAAATTGAAG	GAATCATGGA	TGGTTATGAG	GTCAATCGACC	CTCAACATTA	TCCTCAATTT	240
GAAGAAATGG	TTTCTGCCTT	GGTGGAGCGT	CGCAAGGGCA	AAATGACTGA	AGAAGATGTA	300

CGCAAGGTTT	TGGTTGAAGA	TGTCAACTAC	TTTGGTGTGA	TGTTGGTTTA	CTTGGGCTTG	360
GTTGATGGAA	TGGTGTTCAGG	AGCGATTAC	TCAACAGCTT	CAACAGTTCG	CCCAGCTCTA	420
CAAATCATCA	AAACTCGTCC	AAATGTAAC	CGTACTTCAG	GAGCCTTCCT	CATGGTTCGT	480
GGTACGGAAC	GTTACCTATT	TGGAGACTGT	GCCATTAATA	TCAATCCAGA	TGCGGAAGCC	540
TTGGCTGAAA	TTGCCATCAA	CTCAGCAATC	ACAGCTAAGA	TGTTTGGCAT	CGAACCTAAA	600
ATTGCCATGT	TGAGCTATTC	TACTAAAGGT	TCAGGGTTTG	GTGAAAGCGT	TGATAAGGTC	660
GTTGAAGCAA	CTAAAATTGC	TCACGACTTG	CGTCCTGACC	TTGAAATCGA	TGGTGAGTTG	720
CAATTTGATG	CGGCCTTTGT	TCCCGAAACT	GCAGCTCTGA	AAGCTCCGGG	AAGTACAGTA	780
GCTGGTCAAG	CAAATGTCTT	CATCTTCCCA	GGTATCGAGG	CAGGAAATAT	CGGTTACAAG	840
ATGGCTGAAC	GCAATGGGTGG	CTTTGCGGCT	GTAGGACCTG	TTTTGCAAGG	TTTAAACAAG	900
CCAGTTAATG	ATCTTTCTCG	TGGATGTAAT	GCAGATGATG	TTTACAAGTT	GACCCTCATC	960
ACAGCAGCTC	AAGCAGTTCA	TCAATAG				987

(2) INFORMATION FOR SEQ ID NO:1422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1422:

AAGGGAAAAAC	TTATGGTATT	AGATTATTTTC	TTTGACAAAA	ACCTTGTTGTT	TTGCTTAGAA	60
GCGGATAATC	AAGAACAAC	CTTTGATCAG	GTTGCAACTT	TATTGGAAGA	ACGAGAAATT	120
GTCACCTCAA	CTTATCGTGA	AGCCTTGATC	ACGCGTGAAA	AGTCATTTCC	AACTGGTTTA	180
GATATGGAAT	TTCTAGGAAA	GGACTTGCCA	AATGTAGCGA	TTCCTCATAC	AGATATTGTT	240
CATAATCTAG	CTGAGAAAGT	GGTGGTTGTT	CGATTAGAAA	AACCAGTAAC	TTTTCACAA	300
ATGATAGCTC	CTGATAAGGA	AGTAGAAGTA	TCCTTGCTCT	TCTTTATCAT	CAATAACTCA	360
AGTTCAAGTC	AAACAAATAT	TCTGGCTCAG	TTGATGGACT	TTTTCACAGG	AAATGGACAT	420
CTTGAAGACC	TATCAAAAAT	TTCCGAACCA	GAAAACTTT	ATGCTTACAT	TGCTGAAGCA	480
ACCGCTTAA						489

(2) INFORMATION FOR SEQ ID NO:1423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1423:

```
GGAATGAAAC TGCTTGTGTG CGGTTCTGGT GGTCGTGAGC ATGCGATTGC TAAAAAGTTA      60
CTTGAATCAA AAGACGTGGA AAAAGTCTTT GTAGCTCCTG GGAATGATGG GATGACTCTG      120

GATGGTTTGG AATTGGTAAA TATCTCTATT TCCGAACATT CTAAATTGAT TGACTTCGCA      180
AAGACCAATG ATGTTGCTTG GACCTTTATC GGTCAGATG ATGCCCTTGC TGCTGGCATC      240
GTGGATGATT TTAACCAAGC TGGACTTAAG GCCTTTGGTC CGACTAGGGC TGCAGCGGAG      300
CTGGAGTGGT CCAAGGATTT CGCCAAGGAA ATCATGGTCA AATACGGCGT TCCGACAGCA      360
ATATATGGCA CATTTTCAGA TTTCGAGGAA GCCAAGGCCT ATATCGAAAA GCATGGTGCG      420
CCTATCGTAG TCAAGGCGGA TGGCTTGGCA CTTGGGAAGG GTGTCGTCGT TGCTGAGACG      480
GTTGAGCAAG CGGTCGAAGC CGCTCATGAG ATGCTTTTGG ACAATAAATT TGGTGACTCA      540
GGTGCGCGCG TGTTATTGA GGAATTCCTT GAAGGAGAGG AATTTTCACT CTTTGCCCTTT      600
GTCAATGGTG ATAAGTTCTA CATCATGCCA ACGGCTCAGG ACCACAAACG TGCCTATGAT      660
GGCGACAAAG GGCCTAACAC GGGTGGTATG GGTGCCTATG CGCCAGTTCC ACACTTACCA      720
CAGAGTGTAG TTGATACAGC GGTGACACC ATTGTCAAGC CAGTTCTAGA AGGGGTGATT      780
AAAGAAGGTC GTCCTTATCT GGGAGTTCTT TACGCAGGGC TTATCCTGAC AGCTGATGGA      840
CCGAAGTCAT CGAGTTCAAC GCTCGGTTCT GAGATCCAGA AACTCAGCTT ATCTTGCCTC      900
GCTTAA                                           906
```

(2) INFORMATION FOR SEQ ID NO:1424:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 636 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1424:

```
ACGATGAAAC TTGAAATTAT AAATGGACAG AAAATTTATG GGAAAAGACC TATTTTAAAT      60
CAGTTGAATT TGGTGTTCAT ATCAGGAAAA ATTTATGGAC TTAAAGGTGA TAATGGATCT      120
GGCAAGACGG TTCTTTTAAA GGTACTTGCT GGTATATTA AGCTTGACAA AGGAAAAGTT      180
```

CTTCAAGATG	GTAAAGTTTA	CGGGATAAAA	AATCATTATA	TTCAGGATGC	AGGAATTTT	240
ATTGAAAAAG	TCGAGTTTTT	ATCTCATTTA	TCCCTGAGAG	AAAATTTGGA	ACTGTTAAGG	300
TATTTTTTCAT	CTAAAGTTAC	GGAAAAAAGA	ATTGCCCTATT	GGATTCAATA	CTATGATTTA	360
CAGGAATTTG	AAGACGTTGA	ATACCGGCAT	TTATCCTTGG	GAACAAAGCA	AAAAATGGCC	420
TTGATTCAAG	CCTTTATTTT	CTCTCCTTCT	ATACTCTTTC	TCGATGAACC	TATGAATGCT	480
TTGGATGAGA	AGAGTGTGAG	GTTAACCAAA	CAGGTCATTT	TATCTTACCT	GAAAAAGAA	540
AATGGTCTGG	TTATCCTGAC	GTCGCACATA	TCGGAAGATA	TTTCAGACCT	TTGTACAGAT	600
GTATTAGTTG	TCGAAAATGG	ACATATACAA	ATGTAA			636

(2) INFORMATION FOR SEQ ID NO:1425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1425:

CAGCGACTTT	GGTCAGTGCT	AAAACAGGGG	AAATTCTGGC	AACAACGCAA	CGACCCGACC	60
TTTGATGCAG	ATACAAAAGA	AGGCATTACA	GAGGACTTTG	TTTGGCGTGA	TATCCTTTTAC	120
CAAAGTAACT	ATGAGCCAGG	TTCCACTATG	AAAGTGATGA	TGTTGGCTGC	TGCTATTGAT	180
AATAATACCT	TTCCAGGAGG	AGAAGTCTTT	AATAGTAGTG	AGTTAAAAAT	TGCAGATGCC	240
ACGATTCGAG	ATTGGGACGT	TAATGAAGGA	TTGACTGGTG	GCAGAATGAT	GACTTTTTTCT	300
CAAGGTTTTG	CACACTCAAG	TAACGTTGGG	ATGACCCTCC	TTGAGCAAAA	GATGGGAGAT	360
GCTACCTGGC	TTGATTATCT	TAATCGTTTT	AAATTTGGAG	TTCCGACCCG	TTTCGGTTTTG	420
ACGGATGAGT	ATGCTGGTCA	GCTTCCTGCG	GATAATATTG	TCAACATTGC	GCAAAGTTCA	480
TTTGGACAAG	GGATTTTCAGT	GACCCAGACA	CAAATGATTC	GTGCCTTTTAC	AGCTATTGCT	540
AATGACGGTG	TCATGCTGGA	GCCTAAATTT	ATTAGTGCCA	TTTATGATCC	AAATGATCAA	600
ACTGCTCGGA	AATCTCAAAA	AGAAATTGTG	GGAAATCCTG	TTTCTAAAAG	TGCAGCTAGT	660
CTAACTCGGA	CTAACATGGT	TTTGGTAGGG	ACGGATCCCG	TTTATGGAAC	CATGTATAAC	720
CACAGCACAG	GCAAGCCAAC	TGTAACCTGT	CCTGGGCAAA	ATGTAGCCCT	CAAGTCTGGT	780
ACGGCTCAGA	TTGCTGACGA	GAAAAATGGT	GGTTATCTAG	TCGGGGTAAC	CGACTATATT	840
TTCTCGGCTG	TATCGATGAG	TCCGGCTGAA	AATCCTGATT	TTATCTTGTA	TGTGACGGTC	900
CAACAACCTG	AACATTATTC	AGGTATTTCAG	TTGGGAGAAT	TTGCCAATCC	TATCTTGGAG	960
CGGGCTTCAG	CTATGAAAGA	CTCTCTCAAT	CTTCAAACAA	CAGCTAAAGC	TTTGGAGCAA	1020
GTAAGTCAAC	AAAGTCCTTA	TCCTATGCCT	AGTGTCAGG	ATATTTTACC	TGGTGATTTA	1080
GCAGAAGAAT	TGCGTCGCAA	TCTTGTAACAA	CCCATCGTTG	TGGGAACAGG	AACGAAGATT	1140
AAAAACAGTT	CTGCTGAAGA	AGGGAAGAAT	CTTGCCCCGA	ATCAGCAAGT	CCTTATCTTA	1200
TCTGATAAAG	TAGAGGAAGT	TCCAGATATG	TATGGTTGGA	CAAAGGAGAC	TGCTGAGACC	1260
CTTGCTAAGT	GGCTCAATAT	AGAACTTGAA	TTTCAAGGTT	CGGGTTCTAC	TGTGCAGAAG	1320
CAAGATGTTT	GTGCTAACAC	AGCTATCAAG	GACATTAAAA	AAATTACATT	AACTTTAGGA	1380
GAATAA						1386

(2) INFORMATION FOR SEQ ID NO:1426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1602 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1426:

CATAGACTTTT	GGGCTCTACT	AGGTAAAGTA	GAGCTTTTTTG	TTATGCACTA	TGAACATTCT	60
AGAAAGGGAA	ATCATATGAT	AAAAATCAAT	CATCTAACCA	TCACACAAAA	CAAAGATTTA	120
CGAGATCTTG	TATCTGACCT	AACCATGACC	ATCCAAGACG	GGGAAAAGGT	TGCTATTATT	180
GGTGAAGAAG	GAAATGGCAA	ATCAACCTTA	CTTAAAATTT	TAATGGGGGA	AGCTTTGTCT	240
GATTTCACTA	TCAAGGGAAA	CATCCAATCT	GACTATCAGT	CACTGGCCTA	CATTCCCTCA	300
AAACTTCCCG	AGGAGCTGAA	AAAGAAAAC	TTACACGACT	ACTTCTTTTT	AGATTCTATT	360
GATTTAGACT	ACAGTATCCT	CTATCGTTTG	GCGGAGGAAT	TGCATTTTGA	TAGCAATCGT	420
TTCGCAAGTG	ACCAAGAGAT	TGGCAGTCTA	TCAGGGGGCG	AAGCTTTGAA	AATTCAGCTT	480
ATCCATGAGT	TAGCCAAACC	CTTTGAGATT	CTATTTTTAG	ATGAACCTTC	AAATGACCTA	540
GACCTTGAGA	CAGTTGATTG	GTTAAAAGGC	CAAATTCAAA	AGACCAGGCA	AACCGTTATT	600
TTCATTTCCC	ATGATGAAGA	CTTTCTTTCT	GAAACGGCAG	ACACTATTGT	TCACCTGCGA	660
CTGGTCAAAC	ACCGTAAAGA	AGCGGAAACG	CTAGTAGAGC	ATTTAGACTA	TGATAGCTAT	720
AGTGAGCAGA	GAAAGGCTAA	TTTTGCCAAA	CAAAGTCAGC	AAGCTGCTAA	CAACCAAAGA	780
GCCTACGATA	AAACCATGGA	AAAACATCGG	AGAGTTAAGC	AAAATGTAGA	AACTGCGCTT	840
CGAGCTACCA	AAGATAGTAC	TGCCGGTCGC	CTATTGGCTA	AAAAGATGAA	AACTGTCCCTC	900
TCACAAGAAA	AACGCTACGA	AAAGACAGCT	CAGTCCATGA	CTCAAAAGCC	ACTTGAAGAG	960
GAACAAATCC	AACTTTTCTT	TTCAGACATC	CAACCATTAC	CAGCTTCTAA	AGTCTTAGTC	1020
CAACTGGAAA	AAGAAAATTT	GTCCATTGAC	GACCGAGTTT	TGGTTCAAAA	ACTACAACCTA	1080
ACTGTCCGTG	GGCAAGAAAA	AATCGGTATT	ATCGGGCCAA	ATGGTGTTGG	GAAATCAACT	1140
CTGTTAGCCA	AATTAAAGCA	ACTTCTGAAT	GATAAAAAGAG	AGATTTCCCT	TGGTTTTATG	1200
CCACAAGATT	ACCACAAAAA	ACTGCAATTG	GATTTATCAC	CAATAGCTTA	TATCAGCAAA	1260
ACTGGGGAAA	AAGAGGAACT	TCAGAAAATC	CACCTCTACC	TAGCCAGTCT	CAATTTTCAGT	1320
TATCCAGAAA	TGCAGCATCA	AATTCGCTCC	TTATCTGGCG	GACAACAGGG	AAAACCTCTG	1380
CTTTTGATC	TAGTCCTGCG	CAAACCAAAC	TTTCTCCTGC	TGGATGAACC	CACACGAAAC	1440
TTTTCTCCCA	CTTCTCAACC	CCAAATCAAA	AAACTCTTTG	CAACCTATCC	AGGCGGTCTC	1500
ATCACTGTTT	CGCATGACCG	TCGTTTCTTA	AAAGAAGTCT	GCTCGATCAT	CTATCGCATG	1560
ACAGAACACG	GTTTGGAGTT	AGTTAATTTA	GAAGATTTAT	AA		1602

(2) INFORMATION FOR SEQ ID NO:1427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1427:

AAGGAGAAAC	TTATGCGAGA	ACATCGTCCA	ATCATTGCTC	TTGATTTTCC	TAGTTTTGAG	60
GCGGTCAAGG	AATTTTTAGC	TCTTTTTCCA	GCAGAAGAAA	GCCTTTATCT	CAAGGTAGGG	120
ATGGAGCTTT	ATTACGCAGC	GGGGCCTGAG	ATTGTGTCCCT	ACTTAAAAGG	TTTGGGTCAT	180
AGTGTCTTTT	TGGATCTCAA	ACTTCATGAC	ATTCCTAATA	CAGTCAAGTC	AGCCATGAAG	240
GTCTTGCTCTC	AGCTTGGTGT	CGATATGACT	AATGTCCATG	CGGCTGGTGG	TGTAGAGATG	300
ATGAAGGCGG	CGCGTGAAGG	TCTTGCGAGT	CAAGCTAAAT	TGATCGCTGT	AACGCAGCTG	360
ACATCAACGT	CAGAAGCCCA	GATGCAGGAG	TTTCAAAATA	TCCAAACCAG	TCTGCAAGAG	420
TCTGTGATTT	ACTATGCCAA	GAAGACAGCT	GAAGCTGGCT	TGGATGGTGT	TGTTTGCTCG	480
GCTCAGGAAG	TACAAGTCAT	CAAGCAGGCT	ACCAATCCAG	ATTTTATCTG	TCTGACACCA	540
GGGATTTCGTC	CAGCTGGTGC	TGCAGTTGGA	GATCAAAAAC	GAGTCATGAC	ACCTGCTGAT	600
GCCTATCAAA	TCGGCAGTGA	CTTCTTCACC	ACGGAGGTTT	GGGCC		645

(2) INFORMATION FOR SEQ ID NO:1428:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 750 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1428:

AGGGACATTT	GGTTCGAAAT	GAAATCAATA	ATTGATGTAA	AAAATCTTTC	TTTTCGCTAT	60
AAAGAAAATC	AGAACTACTA	CGATGTGAAG	GATATTACGT	TTCACGTGAA	ACGTGGAGAA	120
TGGCTTTCGA	TTGTAGGGCA	TAATGGTAGT	GGTAAATCAA	CGACGGTTCG	ATTAATTGAT	180

GGCTTACTGG	AAGCAGAATC	CGGAGAGATT	GTAATTGATG	GCCAACGTTT	GA	240
AATGTTTGGA	ATATACGTCG	TCAAATCGGT	ATGGTTTTTC	AAAATCCAGA	CAATCAATTT	300
GTTGGAGCGA	CTGTTGAAGA	TGATGTTGCT	TTTGGTTTTG	AAAATCAGGG	ACTTTCTCGT	360
CAAGAAATGA	AAAAGAGAGT	GGAAGAAGCT	CTGGCTTTAG	TTGGCATGTT	GGACTTTAAA	420
AAGAGAGAGC	CAGCGCGTCT	ATCAGGTGGC	CAAAAGCAAC	GTGTGGCCAT	TGCAGGTGTT	480
GTAGCCCTAA	GACCAGCTAT	TTTAATCTTA	GATGAAGCAA	CGAGTATGTT	GGATCCTGAG	540
GGGCGTAGAG	AACTTATTGG	GACAGTAAAA	GGAATTCGAA	AAGACTATGA	TATGACAGTC	600
ATTTCTATTA	CCCATGATTT	GGAAGAAATC	GCCATGAGTG	ATCGCCTTTT	GGTTCTGAGA	660
AAAAGGGAAA	TTGAATCAAC	TAGTAGTCCA	AGGGAGCTTT	TCTCTCGAAA	TGATTTAGAT	720
ACAAATTGGA	TTAGACGATC	CTTTTGCTAA				750

(2) INFORMATION FOR SEQ ID NO:1429:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 186 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...186
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1429:

CAAGCAATTT	GCTACGTGGA	TCCAATCGGT	GAACAATCGA	ATCCCCTGGG	ATATAACGCC	60
CTAAAATCAT	ACTATCCATT	TAGCGACTCC	TTGAACTCCT	CTATCTTAAC	CGGTAATCGT	120
TTAAATGACA	CGCCTCTATC	AGCCAATCGT	TTACAAAAGG	CCGTAATTTT	AGGTACTCCC	180
AACTGA						186

(2) INFORMATION FOR SEQ ID NO:1430:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 468 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1430:

TGGCTCGTTT	GTCAAAGAGG	AGGATTTGGC	ATGATACCGA	AATTTAGAGT	GTGGGTAAAA	60
ATAGGAAAAC	GTATGGTTTT	TTCAGATGAC	ATTCTTGCTA	TTGACTACGA	AAACAAAGAA	120
ATAGTGACAC	AACAAGTTTA	TTTTGAGAAT	GGTTTACCAG	ACGATAGAGA	TATCTATTGT	180
TATGATTTTG	ACGAAATCGA	ACTCATGCAA	TCAACAGGAC	TCAAAGACAA	GAACGGCAAG	240
GAAATCTTTG	AAGGCGATAT	TGTACGAACT	ACTAGATTTT	TGGGTAGAGC	TGACGAAATT	300
GGCGGTTTCT	ATGAGTATGA	CAAGGAATTT	ATAGGGATTG	TTAAGCAGCT	TGAGGGTTCT	360
TGGGTAATTG	ATACGGGCAG	TGACGCAGTA	TGTTTATGGA	CTGAAATTGA	AGAAAATGAA	420
ATCATCGGCA	ACATCTATGA	AAATAAGGAG	TTTGGAGGAC	GCAAATGA		468

(2) INFORMATION FOR SEQ ID NO:1431:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1431:

ATGGCAGTTT	GCCTGCAGGT	AGAAGATGCG	GATTTTACAA	AGATAGCCAA	GAAGGCTGGA	60
CTGGGTCCTG	AGGTGGCTCG	GTTATTGTTT	GAGAGAGGGA	TTCAGGACCA	AGAAAGTCTG	120
AAGAAGTTTT	TAGAACCTTC	CTTGGAGGAC	TTACATGATG	CTTATCTGCT	CCATGATATG	180
GACAAGGCAG	TGGAGCGGAT	TCGTCAGGCT	ATTGAAGTAA	GGGAAAATAT	TCTCGTTTAT	240
GGAGACTATG	ATGCGGATGG	CATGACTTCG	GCTTCTATTG	TGAAGGAAAG	TTTGGAACAA	300
CTTGGTGCTG	AGTGCCGAGT	TTACCTGCCA	AATCGTTTTA	CCGATGGCTA	TGGCCCTAAT	360
GCTAGTGTTT	ATAAATACTT	TATCGAGCAA	GAAGGAATTT	CCTTGATTGT	GACGGTGGAC	420
AATGGGGTTG	CTGGTCATGA	GGCTATTGCA	TTGGCTCAGT	CTATGGGAGT	AGATGTCATT	480
GTGACAGACC	ATCATTCCAT	GCCTGAAACC	CTGCCAGATG	CTTATGCTAT	TGTCCATCCT	540
GAACATCCAG	ATGCGGATTA	TCCTTTTAAA	TATTTGGCTG	GTTGTGGAGT	TGCTTTCAAG	600
TTGGCTTGTT	CCCTGTTAGA	AGAAGTGCAA	GTGGAATTGC	TTGATTTGGT	CGCTATTGGA	660
ACTATTGCAG	ATATGGTGAG	TCTGACGGAT	GAAAATCGTA	TCTTAGTTCA	ATATGGTCTG	720
GAAATGTTGG	GTCATACCCA	GCGCATTTGGT	CTGCAAGAAA	TGCTGGACAT	GGCTGGGATT	780
GCTGCCAACG	AAGTAACAGA	AGAAACGGTT	GGTTTCCAGA	TTGCTCCTCG	TTTGAATGCC	840
TTGGGCCGCT	TGGATGATCC	CAATCCTGCC	ATTGATTTGT	TGACTGGATT	TGATGATGAG	900
GAAGCGCATG	AGATTGCCCT	TATGATTAC	CAGAAAAACG	AAGAGCGCAA	GGAAATCGTT	960
CAGTCTATCT	ATGAAGAAAGC	CAAGACCATG	GTGGATCCTG	AGAAGAAGGT	TCAGGTCTTG	1020
GCCAAGGAAAG	GCTGGAATCC	TGGGGTTCTA	GGAATCGTGG	CTGGTCGTTT	ATTGGAAGAA	1080
TTGGGGACAG	ACAGTCATTG	TTCTTAA				1107

(2) INFORMATION FOR SEQ ID NO:1432:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 657 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...657
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1432:

ATCAGAGTTT	GTGAGGAAGA	TTTAAGCATG	TCAAAACACT	ATAAACTTGT	ATTTTATAGC	60
CGTATCTTCT	TGTTTCTAGC	GGCTTTTACG	GGAGTTTATC	TTGAAATTAC	TAGGCATGGT	120
GGTTTTGGGA	TGCTTCTCTA	TTACACGGTT	CTGTCCAACC	TCTTGGTAAC	TATTTTACC	180
CTTTATCTTC	TAAAGGTTAT	GAGCCGTGTA	GGTGAAAATT	GGCAAAGGCC	AAGTCTCTTG	240
CGCTTAAAAG	GTGGGGTCAC	CATGAGTATC	ATGATTACCT	GTGTGATTTA	CCATTTCCCTC	300
TTGGCGCCCA	TTGCGACTAA	TTTCTATACC	CTAGAAAATT	TCCTTTGCCA	CTATATCGTT	360
CCCATCTGGT	TTTAGCGGA	TACCTCTTTT	TTTGACAAAC	AGGGTCAATA	CAAGATTGG	420
GATCCAGCAG	TGTGGACCAT	TTTACCCTTT	CTGTATATGA	TGTTTGCTCT	TTTTAATGGC	480
TTGGTTCTAA	AACTCAATAT	TCCAAATGCC	AAGGATAATC	CTTCCCTTA	CTTCTTTTG	540
AATGTGAACA	AGGGTTGGAA	TGTTGTGTTT	AAGTGGTGTC	TGATTATCTT	TGTTGCCTAT	600
ATGGTAGCAG	GATTTATTTT	CTACTTTATC	AAGCAAATCA	AGAGAAAGTC	ATCCTAA	657

(2) INFORMATION FOR SEQ ID NO:1433:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 621 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...621

GTAGCATCTT	GCTCGACCAA	GCCAGCATT	TCAAAGAAGA	GGTTGTTGAT	TCGCTCTTCA	60
ATCTTGTCGA	TGTTTTGGTT	TTTAAGGACT	GAAATACGGA	TAACGTCTTC	AGGTAGTTTC	120
GAAGTTTCAA	TCGTTTCTGG	CAGGTCGGTT	TTATTAAGTA	GAATAATGCG	ATTGGTATCT	180
TGGCTAATTT	CAAGAAGTTG	TCTGTCTTGC	GCAGTCAGTG	GTTCACTGGC	ATTTAGCACT	240
AGTAGAACCA	AGTTGGCTTC	TTTGAGGGCT	TTTTTCGAAC	GCTCAACACC	GATTTGTTCC	300
ACTATGTCAT	CTGTTTCACG	AATACCGGCT	GTATCAATCA	ATTTGAGAGG	TACACCATTG	360
ATGTTGACGT	ACTCTTCGAT	GACATCTCGT	GTTGTCCCAG	CGATATCTGT	TACGATAGCC	420
TTGTCCTCAC	GCAAGAGGTT	GTTGAGAAGG	CTTGATTTC	CAACGTTGGG	ACGTCCAATG	480
ATAGCCGTTG	AAATTCCTTC	ACGAAGGATT	TTACCACGAC	GTGCTGTCCT	AAGAAGATTG	540
GTTAGTAATT	GCTCAAATC	CATTGTCTTC	TCTCGGACAA	CAGCAGTAGT	GGCTTCCTCA	600
ACATCGTCAT	ACTCAGGATA	G				621

(A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

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(A) NAME/KEY: misc_feature
(B) LOCATION 1...222
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TTTTTGCTCT	GTTGCAACTT	TGACAAGTTT	AGTATATCAT	TATTTTTTAA	TTTTTTTCAT	60
CCAAATCTTG	AATTGGCATC	GAAACGTCTT	GAATTAGCTT	TTTTATTTC	AGCCACCTCT	120
AAATGTTTAA	AAAAATAAT	TTCTAATCAC	TTTTTTACCA	TTCAGGAAGT	TTTAATGACT	180
ATTCAAGATT	TCATAAAATA	TGAACCTAGT	TTTATGGCAT	AA		222

(A) LENGTH: 420 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1435:

ATAAGGTCTT	GTCGAACAAG	GTTATGTTTG	ATGGATCTTC	TATTGAAGGT	TTTGTACGTA	60
TCAATGAGTC	GGATATGTAC	TTGTACCCGG	ACTTGGATAC	ATGGACAGTC	TTCCCTTGGG	120
GAAGATGAAA	ATGGAAGTGT	TGCAGGTCTG	ATCTGTGATG	TCTATACAAC	AGAAGGTGAA	180
CCATTTGCGG	GTGACCCTCG	TGGTAATTTG	AAACGAGCTC	TTCGTCACAT	GGAAGAAGTT	240
GGATTCAAAT	CCTTCAACCT	TGGTCCAGAG	CCAGAATTCT	TCCTATTTAA	GTTGGATGAA	300
AATGGGGACC	CAACACTTGA	AGTGAATGAC	AAGGGTGGCT	ACTTTGATTT	GGCACCTACT	360
GACCTTGCGG	ACAACACACG	TCGTGAGATT	GTGAATGTCT	TGACCCAAAA	TGGGATTTGA	420

(2) INFORMATION FOR SEQ ID NO:1436:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 501 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1436:

GTAAGGTCTT	GGGAGTTGCT	CTCAAGACTT	ATTTTTTGAA	AGGAGAGACA	GAAAAATGGCG	60
ATAGAAAAGC	TATCACCCGG	CATGCAACAG	TATGTGGATA	TTAAAAAGCA	ATATCCAGAT	120
GCTTTTTTGC	TCTTTCGGAT	GGGTGATTTT	TATGAATTAT	TTTATGAGGA	TGCGGTCAAT	180
GCTGCGCAGA	TTCTGGAAAT	TTCCTTAACG	AGTCGCAACA	AGAATGCCGA	CAATCCGATC	240
CCTATGGCGG	GTGTTCCCTA	TCATTCTGCC	CAACAGTATA	TCGATGTCTT	GATTGAGCAG	300
GGTTATAAGG	TGGCTATCGC	AGAGCAGATG	GAAGATCCTA	AACAAGCAGT	TGGGGTTGTT	360
AAACGAGAGG	TTGTTTCAGG	CATTACTCCA	GGGACAGTGG	TCGATAGCAG	TAAGCCGGAC	420
AGTCAGAATA	ATTTTTTGGT	TTCCATAGAC	CGCGAAGGCA	ATCAATTTGG	CCTACCTTAT	480
ATGGATTTGG	TGAACGGGTG	A				501

(2) INFORMATION FOR SEQ ID NO:1437:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1368 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1437:

GTTGAACCTT	GTGGTGGACG	AGCGGCTATC	TCTACTCCAC	TAGGTGAAGG	GGCTATTGGT	60
ATTGTCCGCC	TGAGCGGAAC	AGACAGTTTT	GCTATTGTGC	AAAAGATTTT	TAAAGGAAAA	120
GACTTGAACA	AGGTTGCCAG	CCACACTCTC	AACTACGGTC	ACATTATTGA	TCCTCTGACT	180
GGTAAAGTCA	TGGACGAGGT	TATGGTTGGG	GCTATGAAGT	CTCCAAAGAC	CTTCACTCGT	240
GAGGATATTA	TCGAGATTAA	CACCCACGGT	GGTATTGCGG	TGACCAATGA	GATTCTCCAG	300
CTAGCTATCC	GTGAAGGAGC	TCGGTTGGCA	GAACCTGGTG	AATTTACCAA	ACGTGCCTTT	360
TTAAACGGTC	GCGTAGATTT	GACACAGGCC	GAGGCGGTGA	TGGATATCAT	CCGCGCCAAG	420
ACAGACAAGG	CCATGAACAT	CGCGGTCAAA	CAACTTGATG	GTTCCCTTTC	TGATCTTATC	480
AATAATATCC	GTCAAGAAAT	CCTTAATACA	CTTGCCCAAG	TTGAGGTCAA	TATCGACTAT	540
CCTGAGTATG	ACGATGTTGA	GGAAGCCACT	ACTGCTGTTG	TCCGAGAGAA	GACAATGGAG	600
TTTGAGCAAT	TACTAACCBA	TCTTCTTAGG	ACAGCACGTC	GTGGTAAAAT	CCTTCGTGAA	660
GGAATTTCAA	CGGCTATCAT	TGGACGTCCC	AACGTTGGGA	AATCAAGCCT	TCTCAACAAC	720
CTCTTGCGTG	AGGACAAGGC	TATCGTAACA	GATATCGCTG	GGACAACACG	AGATGTCATC	780
GAAGAGTACG	TCAACATCAA	TGGTGTACCT	CTCAAATTGA	TTGATACAGC	CGGTATTTCGT	840
GAAACAGATG	ACATAGTGGA	ACAAATCGGT	GTTGAGCGTT	CGAAAAAAGC	CCTCAAAGAA	900
GCCAACTTGG	TTCTACTAGT	GCTAAATGCC	AGTGAACCAC	TGACTGCGCA	AGACAGACAA	960
CTTCTTGAAA	TTAGCCAAGA	TACCAATCGC	ATTATTCTAC	TTAATAAAAAC	CGACCTGCCA	1020
GAAACGATTG	AAACTTCGAA	ACTACCTGAA	GACGTTATCC	GTATTTTCAGT	CCTTAAAAAC	1080
CAAAACATCG	ACAAGATTGA	AGAGCGAATC	AACAACCTCT	TCTTTGAAAA	TGCTGGCTTG	1140
GTCGAGCAAG	ATGCTACTTA	CTTGTCAAAC	GCCCGTCACA	TTTCCCTGAT	TGAAAAAGCA	1200
GTTGAAAGCC	TACAAGCCGT	TAATCAAGGT	CTTGAGCTGG	GGATGCCAGT	TGATTTGCTT	1260
CAAGTTGACT	TGACTCGTAC	TTGGGAAATC	CTCGGAGAAA	TCACTGGGGA	TGCTGCCTCA	1320
GATGAACTCA	TCACCCAACT	CTTTAGCCAA	TTCTGTTTGA	GAAAAATAA		1368

(2) INFORMATION FOR SEQ ID NO:1438:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1438:

CCGAACCTTG	TGGTGAAGAC	TGTGTTGTGA	CATACAAAGG	TGGACTTCGT	TTCCACCCAA	60
CTGTAAACCA	AGGGATCTTG	AAATTCCCTCG	GATTTGAACA	AATCTTTAAA	AATGTC'TTGA	120
CTGGACTTCC	TATCGGTGGA	GGTAAAGGTG	GATCAGACTT	CGATCCTAAA	GGTAAAACAG	180
ATGCTGAAGT	GATGCGCTTC	TGCCAAAGCT	TCATGACTGA	ATTGCAAAAA	CACATCGGAC	240
CATCACTTGA	CGTACCTGCT	GGTGATATCG	GTGTTGGTGG	ACGTGAAATT	GGTTACCTTT	300
ACGGTCAATA	CAAACGTC'TT	AACCAATTTG	ATGCTGGTGT	CTTGACTGGT	AAACCTCTTG	360
GATTTGGTGG	GAGCTTGATT	CGTCCAGAAG	CAACTGGTTA	CGGTTTGGTT	TACTATACTG	420
AAGAAATGCT	CAAAGCTAAC	GGTAACAGCT	TTGCTGGTAA	GAAAGTCGTT	ATTTTCAGGTT	480
CTGGTAACGT	TGCTCAATAT	GCTCTTCAAA	AAGCAACTGA	ACTCGGTGCA	ACTGTTATTT	540
CTGTTTCTGA	CTCAAATGGT	TATGTCATCG	ATGAAAATGG	TATCGACTTC	GATCTTTTGG	600
TTGATGTTAA	AGAAAAACGT	CGTGCTCGTT	TGACTGAGTA	TGCAGCTGAA	AAAGCAAC'TG	660
CAACCTACCA	CGAAGGTACT	GTATGGACTT	ACGCTGGAAA	CTATGACATT	GCTCTTCCAT	720
GTGCCACTCA	AAACGAAATC	AACGGTGAAG	CAGCTAAACG	TTTGGTTGCT	CAAGGCGTTA	780
TCTGTGTATC	TGAAGGTGCC	AACATGCCGA	GCGACCTTGA	TGCCATCAAA	GTTTACAAAG	840
AAAATGGTAT	CTTATACGGA	CCTGCAAAAAG	CTGCCAACGC	TGGTGGTGTA	GCCGTTTCAG	900
CTCTTGAAAT	GAGCCAAAAC	AGTCTTCGCC	TCTCATGGAC	TCGTGAAGAA	GTTGATGACC	960
GTCTCAAAGA	CATCATGACA	AACATCTTCA	ACACAGCTAA	AACAACTTCA	GAAACATACG	1020
GTCTTGATAA	AGACTACCTT	GCAGGAGCTA	ACATTGCTGC	CTTTGAAAAAT	GTAGCAAACG	1080
CTATGATTGC	CCAAGGTATT	GTTTAA				1106

(2) INFORMATION FOR SEQ ID NO:1439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1439:

GGCAAGCCTT	GTCAAGCGTA	TCTTGATTGG	TATGCTTTAT	GGGGAATACT	AGGACTGACC	60
CTTCCTAATC	TCTCAGGGAT	TGGGCTACTC	GGGGATTTAT	TCGTTGGAGG	TCTAAAAGCT	120
GTTGCTCCTA	TCCTAGTCTT	TGCCCTCGTT	GCCAATGCCC	TTTCCCAACA	TCAAAAAGGGA	180
CAAGATAGCA	ATATGAAAAC	TGTTGTTTTT	TTGTATATCC	TATGA		225

(2) INFORMATION FOR SEQ ID NO:1440:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...273
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1440:

TTGTTTACTT GCTTCATCAT TCATAGAACT ACTATACCAT ATTTTGTTC GCAGGAAGTC	60
TATTGGAAAG TAAGAAATAT TGAAGCTGAG GCGATTAGAA GAAATTGTGA GCGTGGTGCT	120
ATTTTTTCAG GTAAAATAAA ACATCACGAA GATTCTCAGT TTAAAGGAGA CCACTATGTT	180
GAATGTTATG CTGTTTTAGA TAATACGGTT ATAGCAAGAG ATAGAATAAC AGTCCCTATC	240
GATCCGTTAT GTGGAAAAGA TTTTATAGAG TAG	273

(2) INFORMATION FOR SEQ ID NO:1441:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...195
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1441:

TTTCCTACTT GGCTTATTAT ATCGCTATCA ATCGCTTGGC AACCAGCCAA GGTACAGGC	60
TTGAACGTGA GCTATGTAAG ATTGGACGGG TCTGTTTGG CAATTGTTTT TTAGGGGTG	120
CACCCGCTAG ATATGCTGAC CATTATGACG TCACTTGTCG TCATTGCTGG AGTTTATATT	180
ATTATTAAAG AATAA	195

(2) INFORMATION FOR SEQ ID NO:1442:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 924 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...924
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1442:

AAAAATACTT	GTGGAGGTTT	CATTATGGCA	ATATTTTTC	TGATTTTCT	GATTGTTTGT	60
GTGCTCCTAT	TGGTGATAGT	CACACTGAGT	ACAGTTTATG	TGGTTCGTCA	GCAGTCGGTG	120
GCGATTATTG	AACGCTTTGG	GAAATACCAA	AAGGTTGCTA	ATAGCGGTAT	TCATATTCGC	180
TTGCCTTTTG	GGATTGACTC	GATTGCAGCA	CGGATTCAGT	TGCGCTTGTT	GCAAAGTGAT	240
ATTGTGGTTG	AGACTAAGAC	CAAGGACAAT	GTGTTCGTTA	TGATGAATGT	AGCGACTCAG	300
TACCGTGTCA	ACGAGCAGAG	CGTGACAGAT	GCTTACTATA	AACTCATACG	TCCAGAATCT	360
CAGATTAAAT	CTTATATCGA	AGATGCTCTT	CGCTCTTCTG	TTCCAAAATT	AACCTTGGAT	420
GAATTGTTTG	AGAAAAAAGA	TGAGATTGCC	CTTGAAGTTC	AACACCAAGT	AGCAGAAGAA	480
ATGACCACTT	ACGGCTACAT	TATCGTGAAA	ACCTTGATTA	CCAAGGTCGA	ACCGGATGCA	540
GAAGTTAAGC	AATCCATGAA	TGAAATCAAT	GCGGCGCAAC	GTAAGCGGGT	CGCAGCACAA	600
GAATTGGCGG	AAGCTGACAA	GATTAAAAAT	GTCACTGCAG	CTGAAGCCGA	AGCAGAAAAA	660
GACCGCCTTC	ATGGTGTGGG	GATTGCCCAA	CAACGTAAGG	CGATTGTGGA	TGGATTGGCA	720
GAGTCTATCA	CCGAAC TCA	GGAAGCCAAT	GTGGCATGA	CAGAAGAACA	AATCATGTCT	780
ATCCTCTTGA	CCAACCAGTA	TTTGGATACC	TTGAATACCT	TTGCCCTCTAA	AGGAAATCAA	840
ACCATCTTTT	TACCAAATAC	GCCAAATGGT	GTGGATGATA	TCCGAACACA	AATCTTGTC	900
GCCCTTCGCG	CTGAGAAGAA	ATAA				924

(2) INFORMATION FOR SEQ ID NO:1443:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 243 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1443:

ATGAGAACTT	GTCTTGCCCA	TCGAANATGG	GCGCTTGACC	TTGCTGAGAG	TGTATCAGAC	60
AATATCNTGC	TAAACATTCC	TATCAAGTTC	TTGACGGCTG	AAGAAGAAGC	TGGTCAAGGA	120
TTTGTCTCAG	GAAATGACTG	GCAAATCATG	ACAGAGGAAG	AATACCAAGC	TCAACAAGCA	180
GTAAAGAAAG	AAGAAAACAG	TCCTTTTGCT	GGCTTACAAG	GACTATTTGA	CGGAGATGAA	240
TAA						243

(2) INFORMATION FOR SEQ ID NO:1444:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1444:

CAGCAGACTT	GGCAGCAAAA	CTTGGTCAAG	ATGTTGTTTT	CCCAGGTGTC	ACTCGTGGTT	60
AGCAGTTTGG	ATATTTTGAC	AGAGAAGCGG	ATTGTCGATA	ATCTCATGGC	TTTGACAAG	120
ACCTTGATTT	TCATTGCTCA	CCGCTTGACT	ATTGCTGAGC	GGACAGAGAA	AGTAGTTGTC	180
TTGGATCAGG	GCAAGATTGT	CNNAAAAAGA	NAGCATGCTG	ATTTGCTTGC	ACAGGGTGGC	240
TTTTACGCC	ATNTNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	300
NNNNNNNNN	NNNNNNNT					318

(2) INFORMATION FOR SEQ ID NO:1445:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1445:

CAGCAGACTT	GGCAGCAAAA	CTTGGTCAAG	ATGTTGTTTT	CCCAGGTGTC	ACTCGTGGTG	60
CTGAATTGGA	AGCGGCAATC	AACGCTCTTG	AAGATGGACA	AGTTCTCTTG	GTTGAAAACA	120
CTCGTTACGA	AGATGTTGAC	GGCAAGAAAG	AATCTAAAAA	CGATCCTGAA	CTTGGTAAAT	180
ACTGGGCATC	ACTTGGAGAT	GGTATCTTCG	TAA			213

(2) INFORMATION FOR SEQ ID NO:1446:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 852 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1446:

GGATATTATT	GGAGGGGTTC	TCTAATGGCA	TTTACACTTC	CAGCAAATAA	ACCACAAGTT	60
CCTAAAGATA	CCCCACGAAA	TTTTTTTCATC	TACGGCGAAA	CCATGAGCGG	AAAGTCTTAT	120
CTTGCAAATG	AATTCCCAAA	TCCAATCGTT	TTGAACACAG	ACGGGAATGC	AGAAGCTAAC	180
ACTGTTCCAA	GCAATCAGCT	GATCAATGAA	AAAGATGACA	AGGGACGAAT	TACCAATTCA	240
GTAATTAAGC	AGCTTGGAAG	TATCTTGCTT	GCTCTCCAGA	CACAGAAGCA	CTCTTATGAA	300
ACAGTCGTTA	TTGATGTAA	TGACGATGTT	ATTGAAATGA	TTAAGATTGC	AGTTTGTGAT	360
GAATTAACCC	CAGTTGGTAA	ACCTCGCTTG	AAATCCTTGT	CGGAAATTCC	ATACGGCAAA	420
GGATACGACT	TCTTTAACCA	AGCTATCACA	GAAATTAGTCA	TTGACCTCAA	AGCATTGCCA	480
ATGAATGTTA	TTTACATCAG	CCGTCAGGTA	TCTGAAATATG	ATGACAATGG	CAATGCCACC	540
AAAGACAAGC	CAAGCTTGAA	AGATAAGTAT	GTCAATCTTA	TCAATGGAAA	CTCTGATTTG	600
ATGATCCACA	CTGAAAAACT	CGGCAACAAC	TACAACCGTG	AGGTTGACCG	CAAGCGTAAG	660
ACCTATTATG	CGGACCAGGT	TGATGACAAG	GCCATCTTGA	AAATCTTGGC	AACTATCCGT	720
GGGGCTGTTG	AGCCTGCAAA	GGGCAAGCTA	GCCCCATAAA	AAGAAGCAGC	TAAGACAAC	780
AAACCAGCTA	AGACCGAAAA	AACAAAAGAG	GCACCTAAGA	AAGAAGTTGA	CTCTGATGAT	840
GAATATTTT	AA					852

(2) INFORMATION FOR SEQ ID NO:1447:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...192
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1447:

CTTTTATATT GTTCAATTAC TTTATCAATC ATTTTAAATG ACCTCCACTC TATAATTTGG	60
CATTATATCA CAAGAATAAA GATAGTGTTA AATAAGTTAT ATAAATGCAA AAAAGGAATA	120
TTCCGTTTATA GCAGAGTTGT AACACATTTT TATAAAGAAA TTTATTCCTA CGACTCAGTT	180
TGGCATGCCTT AA	192

(2) INFORMATION FOR SEQ ID NO:1448:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...267
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1448:

GAAATATATT GTAGTGTTTT AGTTTCAATC CGCCATATGA GCGATATTAA GGTAAATATC	60
CCTGGCGAAT GCTTGTATGA CAAGGTATTT GTTCTTTTCAT TTATAATTTA CAACATATCA	120
ATAAATTTAA ATATAGTAAA TGGGATATTT TATATTCAAG CTAAGAAAGA TAGCATCACT	180
TTTGAATGGA AGGCTAAAGA GCAAAC TAGG AAGTTGGCCA TAGATAGCTC AAAACCCTGC	240
TTTGAGGTTG TAGATATAGT AAAATGA	267

(2) INFORMATION FOR SEQ ID NO:1449:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1449:

AGAGGAGAAC	TGATGTCTCA	AGTAAAAGGC	TTGTGTGTTT	TGGATGTAGA	TGGAACCTTA	60
ATCCTAGAAG	AAGTGATTGA	TTTTTTAGGG	AGAGAGGCAG	GTCATGAGGC	GGAAATTTTCG	120
CAGATTACAA	GTCGGGCAAT	GCGAGGAGAG	TTGGTCTTTG	AAAGCAGTTT	AAGAAAAAGA	180
GTGTCCTTGT	TGGAAGGTCT	TCCTATTTTG	GTCTTTGATA	ACGTCTTCAA	CTCAATTCAT	240
CTATCGCTAA	ATGTCCAGA	GTTTCATCTCT	ATTCTCCAAA	AGAATGGCAT	CCTAGTTGAT	300
CTGGTGTCTG	GTGGATTTAC	ACCAATAGTT	GGAGAGATTA	GCAAAATCCC	TTGGTATTGC	360
CTATTTCACT	GCCAACCAGC	TTGA				384

(2) INFORMATION FOR SEQ ID NO:1450:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1450:

AAGCAGCATT	GTGCTAGTCT	AGATTCAGTT	TACTATACTA	AAACGAGTAG	CTTGAAATCA	60
AAAAACCCAC	CCTCACAGGC	AGGTTTATC	TGTATTATTC	AGCTAGATTA	TGCTTTACCT	120
TCTGAACCGA	ATACGTCGAT	ACGTTCTTCA	ACCGATGCTT	GGATAGCTTT	TACACCGTCA	180
GCCAAGAATT	TACGTGGGTC	GAAGAGTTTT	TTCTTGTCGT	ATTCTGCTTC	GTTTGCTTCG	240
TAG						243

(2) INFORMATION FOR SEQ ID NO:1451:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2235 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2235
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1451:

AGAAAAAATT	GTGAGGTAGA	GATGACGATT	TATATTAATA	AGGACGAGAC	CGTTTTTCAT	60
TTGGCAATGA	AAGATAGTAG	TTATATTTTT	AGAAATTTTAG	AAAATGGGGA	ACTTCAACAT	120
CTACATTTTG	GGAAAAGGAT	TCATGTCAAG	GAAAATTATA	ACCAATTGAT	GGCCTATGAA	180
AAAAGAGGAT	TTGAAGTATC	TTTTTCTGAA	GAATTTGAGG	ATATTCAACA	GTC'TATGATA	240
CAAAATGAAT	ATTCTTCATA	TGGGAAAGGA	GATTTTTCGGC	ATCCAGCCTT	TCAAGTTCAA	300
GGAATGAATG	GTAGTAGGAT	AACGACACTA	AAATATCAAG	GTTTTGAACT	TGAAAAAGGG	360
AAAAATCGTC	TTAACTCTCT	ACCTTCAACA	TTTGATGATA	TTGGTCAGTG	TGCGGAAACA	420
TTAACGATTA	TTTTAACAGA	TTCCATATTA	GATTTAACTG	TTAGACTAAA	TTACACAATT	480
TTTCCGGAAT	ACAAATGTCTT	AGTTAGAAAAT	ACGGAATTTT	TAAATAATAG	CAATAATAAG	540
TTGACTCTTT	TGAAAGCAAT	GAGCTTACAG	CTAGATCTAC	CTGATAGTCA	ATATGACTTT	600
ATTCAATTTT	CTGGAGCATG	GCTGAGGGAA	CGTCAGTTAT	ATAGAACTTC	GCTTAGACCA	660
GGTATTCAAG	CAATAGATAG	CTTGAGATAC	TCATCAAGTC	CTCAGCAAAA	TCCTTTCTTT	720
ATGCTATCAA	GGAGGGAAAC	TACAGAGCAT	AGTGGTGAGG	TTTATGGTTT	TAACTTTATC	780
TATTCCTGGAA	ATTTTCAAAA	TATGATTGAA	GTTGACCATT	TTGACACCGC	TAGAGTAACG	840
GTAGGAATAA	ATCCAGTAGA	ATTTTCGTTTT	TTATTAAATC	CTGCCGAAAG	TTTTGTGACA	900
CCAGAAGCAA	TTGTGATCTA	TTCTGATCAA	GGGATGAATC	AGATGAGCCA	ACAACTATCA	960
GATTTTTATC	GACATCATTT	AGTTAATCCT	AATTTTTCTC	AAGCTAGTCG	TCCTATAATA	1020
CTCAATAGTT	GGGAAACATT	TTATTTTGAC	TTGGGTACAG	AAAAAATTTT	AGATTTTAGCA	1080
AAGGCTGCTA	AAGATTTAGG	GATAGAAATTA	TTTGTA CTGG	ATGATGGTTG	GTTTGGTCAT	1140
AGGAAAGATG	ACAAAAGTTC	TCTGGGGGAT	TGGGTAACAG	ATAGAAGTCG	CCTTCCTGAA	1200
GGTATTGGAT	TTCTTG CAGA	TGAAATTCAC	AAAATAGGTT	TACAATTTGG	TTTGTGGTTT	1260
GAGCCTGAAA	TGATTTCTAT	TGATAGTGAT	TTGTACAAGA	ATCATGCCGA	TTGGACTATC	1320
CATTTGTTAG	ACAGAGAGAA	GTCAGTAGGA	AGAAATCAAT	ATGTGTTGGA	TTTGACGAGA	1380
CAGGAAGTTG	TTGATTACCT	TTTTGATTCT	ATTTCTAAAA	TCATAATCAA	AACAAATCTG	1440
GATTATATCA	AATGGGATAT	GAATCGTCAT	ATAACAGATA	TTTATAGTAT	TGAACTTGAT	1500
TCTGAACAGC	AGATGGAATT	TGGTCATCGA	TATATCTTAG	GTCTTTATCA	GTTATTAGAT	1560
CGTTTAATAA	CTAAGTTCCC	TTCAGTTCTA	TTTGAATCTT	GTTCTTCAGG	TGGTGGACGT	1620
TTTGATTTAG	GACTTATGTA	TTATGCACCG	CAAGCGTGGA	CGAGTGATGA	TACGGACCCG	1680
ATAGAAAGAT	TGAAAATTCA	GCATGGAACT	TCTTATGGAT	ATTCTCCATC	AATGATGACA	1740
GCCCATGTTT	CTATTTCTCC	AAATGAACAA	AGTAGAAGAC	AAACGAGTTT	GGACACTAGG	1800
ACAAATGTAG	CTTATTTTAG	TTCTTTTCGGT	TATGAATTAG	ATGTTACGAG	ATTGTCGGTA	1860
GAAGAAAAAG	AACAAGTGAG	AGAACAAATT	CAGTTT TATA	AAAAATATCG	TTCATTGTTT	1920
CAATATGGGG	ATTTCTATAG	GATAAACAGT	CCTTTTAGTT	GTGATTCTGC	TAGTTGGCAA	1980
GTTGTTTCAA	AAGATAAATG	CCAATCGATT	TTATTGTATG	CTCAATTGAA	TAGTAAGTTG	2040
AATCCAGGTT	ATACAAGAGT	TTATTTTAGT	GGTTTAGATA	AAGATAAATG	CTATTCGGTC	2100
TCTGGATTTG	ATGAGTTCTT	TTATGGAGAT	GAATTAATGA	ATGCTGGAAT	AAAAGTCAGT	2160

TTAAGTAATT TAGCACTATG TGTTCCAGAA TATCTTACAA AATTATTTGT TATTGAGGAA	2220
GTTGTATGTA AATAA	2235

(2) INFORMATION FOR SEQ ID NO:1452:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...210
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1452:

CCTAGAAATT GTGTCTTTCT AGACGATATT GAGGACAATA TAATCGTAGC CCCAAAATTA	60
GGAATCAAGA CTTATCAGGT TAAGAAAAGA AGTGATGTTG TTGATATTTT AAACAATTTA	120
TTTAAACTAA AAACCTCTCTA TCTATTAATC CGAGATTCCC CTCTCGGATT TTGTGTTGCT	180
TTCATTAAAT TTACAGGTAA GACTTGCTAG	210

(2) INFORMATION FOR SEQ ID NO:1453:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 405 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...405
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1453:

AAGGAGAATT GGCAGATGGC GACTACTGAG TTGATTGAAC TGGCAATTGA AACCAGCAAA	60
CATGCCTATG TCCCCTATTC TCACTTTCCT ATCGGAGCAG TTTTAGTAGC CAAAGACGGA	120

AATGTTTACA	CGGGAGTGAA	TATCGAAAAT	GTTAGCTATC	CTTTGACCAA	TTGCGGTGAG	180
AGAACAGCTA	TTTTTAAGGC	TATATCTGAA	GGCCAAAGAG	AATTTTCAGA	ATTGATTGTC	240
TATGGTCAAA	CTGAAAAACC	GATTTACCA	TGTGGTGCTT	GTCGCCAAGT	AATGGTCGAA	300
TTTTTTGAAC	AAGATTTAAA	AGTGACCTTA	GTCGCAAAAG	ATAAATCGAC	GGTCGAGATG	360
ACGGTCGGGG	AGTTACTTCC	ATATTCTTTT	ACAGACTTAA	ATTAG		405

(2) INFORMATION FOR SEQ ID NO:1454:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 735 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...735
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1454:

CAGGATTGTT	GGGTAGGGTN	TTCTTATTCA	TCCAAGGCAG	CGGCGACGGT	TCATTTCCGT	60
GCAGACCATG	TGGTCAGCGG	TACGGTATTG	AACTTGATGG	CGCCTGCCTT	GGCTGTTTTTC	120
TTAGTTAAAG	TTCTTTATAA	CAAAGGACAA	ACCGACAACC	TAAGTCAAAC	TTTTGGACGC	180
TTTGATTTC	CAGTCTTGGC	AAATATCCCA	GTGATTGGTG	ATATCTTCTT	CAAGTCAACT	240
AGTCTACTTG	GTTATCTGGC	GATTGCCTTC	TCATTCTTCTG	CTTGGTTTAT	TCTCTTTAAG	300
ACTCAATTTG	GTCTTCGTCT	TCGCTCTGTC	GGTGAACATC	CTCAAGCAGC	GGATACCTTG	360
GGAATCAACG	TCTACAAGAT	GAGATATTTA	GGGATTATTA	TTTCAGGTTT	TCTAGGTGGA	420
ATTGGCGGAG	CGATTTATGC	GCAATCAATC	TCAGTTAACT	TCTCAGTGAC	AACTATTGTT	480
GGACCTGGAT	TTATCGCCCT	TGCTGCGATG	ATCTTTGGGA	AATGGGAATCC	AATCGGTGCT	540
ATGCTTTCTA	GTCTCTTCTT	TGGACTTTCA	CAAAGTTTGG	CTGTTATCGG	TTCTCAATTG	600
CCGTTCTTAC	AAGGAGTGCC	AGCGGTTTAT	CTTCAAATTG	CACCTTATGT	TTTGACAAAT	660
CTTGCTTTAG	CAGCCTTCTT	TGAAAAAGCA	GTCGCACCAA	AAGCAGATGG	TATCAACTAC	720
ATCAAATCAA	AATAA					735

(2) INFORMATION FOR SEQ ID NO:1455:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2640 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1455:

CCA	ACTCGTT	GTGAAGACGG	AAAAGA	AACTC	GTTGCTGAAA	AACACGTAGA	TGAGTTGGTT	60
CAAAA	AGCTC	TAGTTGCCCT	TGAAGAAATG	CGTAAATTGG	ATCAAGAGCA	AGTTGACTAC		120
ATCGTT	GCCA	AAGCATCAGT	AGCAGCTTTG	GATGCCACG	GAGAATTGGC	TTTACATGCC		180
TTTGAAGAAA	CAGGACGTGG	TGTATTTGAA	GACAAAGCAA	CTAAGA	AACTT	GTTTGCCTGT		240
GAACACGTAG	TAAACAACAT	GCGCCACACT	AAGACAGTTG	GCGTTATCGA	AGAAGACGAT			300
GTAACAGGAT	TGACTCTTAT	TGCTGAACCA	GTTGGTGTG	TTTGTGGTAT	TACTCCAACA			360
ACAAACCCAA	CATCAACAGC	AATCTTCAAA	TCATTGATTT	CATTGAAGAC	ACGTAACCCA			420
ATCGTCTTTG	CCTTCCATCC	ATCAGCACAA	GAATCATCTG	CTCATGCAGC	TCGTATCGTC			480
CGCGATGCAG	CTATCGCAGC	TGGTGC	TCCCT	GAAAAC	TGTG	TGCAATGGAT	TACTCAACCA	540
TCTATGGAAG	CAACAAGTGC	CCTTATGAAC	CACGAAGGTG	TTGCGACAAT	CCTTGCAACA			600
GGTGGTAATG	CCATGGTTAA	GGCGGCTTAT	TCATGTGGTA	AACCAGCTCT	TGGGGTAGGT			660
GCCGGAAACG	TTCCAGCTTA	TGTTGAAAAA	TCAGCAAACA	TTCGTCAAGC	AGCACACGAT			720
ATCGTCATGT	CTAAATCATT	TGATAACGGT	ATGGTCTGTG	CATCTGAACA	AGCAGTTATC			780
ATTGATAAAG	AAATTTACGA	TGAATTTGTA	GCAGAGTTCA	AATCTTACCA	CACTTACTTT			840
GTAACAAAAA	AAGAAAAAGC	TCTTCTTGAA	GAGTTC	TGCT	TCGGCGTCAA	AGCAAAACAGC		900
AAAAACTGTG	CTGGTGCAAA	ATTGAACGCT	GACATCGTTG	GTAAACCAGC	AACTTGGATT			960
GCAGAACAAG	CAGGATTTAC	AGTTCAGAA	GGAACAAACA	TTCTTGCTGC	AGAATGTAAA			1020
GAAGTTGGCG	AAAATGAGCC	ATTGACTCGT	GAAAAA	TTGT	CACCAGTTAT	TGCAGTTTTG		1080
AAATCTGAAA	GCCGTGAAGA	TGGTATTACT	AAGGCTCGTC	AAATGGTTGA	ATTTAACGGT			1140
CTTGACACT	CAGCAGCTAT	CCACACAGCT	GACGAAGAAT	TGACTAAAGA	ATTTGGTAAA			1200
GCTGTTAAAG	CTATTCGTGT	TATCTGTAAC	TCACCTTCTA	CTTTTGGTGG	TATCGGGGAC			1260
GTTTACAATG	CCTTCTTGCC	ATCATTGACA	CTTGGATGTG	GTTCTTACGG	ACGCAACTCA			1320
GTTGGGGATA	ACGTTAGTGC	CATTAACCTC	TTGAATATCA	AAAAAGTCGG	AAGACGGAGA			1380
AATAACATGC	AATGGATGAA	ACTTCCTTCA	AAAACATACT	TTGAACGTGA	TTCAATTCAA			1440
TACCTTCAAA	AATGTCGTGA	CGTTGAACGT	GTCATGATCG	TTACTGACCA	TGCCATGGTA			1500
GAGCTTGGTT	TCCTTGATCG	TATCATCGAA	CAACTGGACC	TTCGTCGCAA	TAAGGTTGTT			1560
TACCAAATCT	TTGCGGATGT	AGAACCGGAT	CCAGATATCA	CAACTGTAAA	CCGTGGTACT			1620
GAGATTATGC	GTGCCTTTCAA	ACCAGATACC	ATCATCGCAC	TCGGTGGTGG	GTCTCCAATG			1680
GATGCTGCCA	AAGTAATGTG	GCTCTTCTAC	GAGCAACCAG	AAGTGGACTT	CCGTGACCTT			1740
GTCCAAAAAT	TCATGGATAT	CCGTAAACGT	GCCTTCAAGT	TCCCATTGCT	TGGTAAGAAG			1800
ACTAAATTCA	TCGCGATTCC	AACTACATCT	GGTACAGGAT	CTGAAGTAAC	ACCATTTGCC			1860
GTTATCTCTG	ATAAAGCAAA	CAACCGTAAA	TACCCAATCG	CTGACTACTC	ATTGACACCA			1920
ACTGTGGCAA	TCGTAGATCC	TGCTTTGGTA	TTGACAGTTC	CAGGATTTGT	TGCTGCTGAT			1980
ACTGGTATGG	ACGTATTGAC	TCACGCGACA	GAAGCATACG	TATCACAAAT	GGCTAGTGAC			2040
TACACTGATG	GTTTAGCACT	TCAAGCCATT	AAATTGGTCT	TTGAAAATCT	CGAAAGCTCA			2100
GTTAAGAATG	CAGACTTCCA	CTCACGTGAG	AAAATGCATA	ACGCTTCAAC	AATCGCTGGT			2160
ATGGCCTTTG	CCAATGCCTT	CCTAGGTATT	TCTCACTCAA	TGGCCCATAA	GATTGGTGCG			2220
CAATTCCACA	CAATACACGG	TCGTACAAAT	GCTATCTTGC	TTCCATACGT	TATCCGTTAC			2280
AACGGTACAC	GTCCAGCTAA	GACAGCAACA	TGGCCTAAGT	ACAAC	TACTA	CCGTGCAGAT		2340
GAAAAATACC	AAGATATCGC	ACGCATGCTT	GGACTTCCAG	CTTCTACTCC	AGAAGAAGGG			2400
GTTGAATCTT	ACGCAAAAAGC	TGTCTACGAA	CTCGGTGAAC	GTATTGGGAT	CCAAATGAAT			2460
TTTAGAGACC	AAGGAAATGA	CGAAAAAGAA	TGGAAAGAAC	ATTCTCGTGA	ATTAGCCTTC			2520
CTGGCTTATG	AAGACCAATG	TTCACCAGCT	AACCCACGTC	TTCCAATGGT	AGACCATATG			2580
CAAGAAATCA	TCGAAGATGC	ATACTATGGC	TACAAAGAAA	GACCAGGACG	CCGTAAATAA			2640

(2) INFORMATION FOR SEQ ID NO:1456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 834 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1456:

CAGAGAGGTT	GTTTATTTAT	GAAATCAAAA	AAATGGATAT	TTGTTTTTATG	TAATTTTCTT	60
GCAAGTTTCT	TCCTAGTAGC	TTGCCAGTCA	GGTTCCTAATG	GTTCTCAGTC	AGCTGTTGAG	120
GCCATTAAGC	AAAAGGGGAA	ATTAGTTGTG	GCAACCAGTC	CTGACTATGC	ACCCTTTGAA	180
TTTCAATCAT	TGGTTGATGG	AAAGAACCAG	GTAGTCGGTG	CAGACATCGA	CATGGCTCAG	240
GCTATCGCTG	ATGAACTTGG	GGTTAAGTTG	GAAATCTCAA	GCATGAGTTT	TGACAATGTT	300
TTGACCAGTC	TTCAAACCTGG	TAAGGCTGAC	CTAGCAGTTG	CAGGAATTAG	TGCTACTGAC	360
GAGAGAAAAG	AAGTCTTTGA	TTTTTCAATC	CCATACTATG	AAAACAAGAT	TAGTTTCTTG	420
GTTTCGTAAGG	CTGATGTGGA	AAAATACAAG	GATTTAACTA	GCCTAGAAAAG	TGCTAATATT	480
GCAGCCCAAA	AAGGGACTGT	TCCAGAATCA	ATGGTCAAGG	AACAATTGCC	AAAAGCTCAA	540
TTAACTTCCC	TAACATAATAT	GGGTGAAGCA	GTCAATGAAT	TGCAGGCTGG	AAAAGTAGAT	600
GCTGTTTCATA	TGGATGAGCC	TGTTGCACTT	AGTTATGCTG	CTAAAAACGC	TGGCTTAGCT	660
GTCGCAACTG	TCAGCTTGAA	GATGAAGGAC	GGCGACGCCA	ATGCCGTTGC	TCTTAGAAAA	720
AATAGTGATG	ATTTGAAAGA	AGTGGTAGAC	AAGGTCATCC	AAAAACTTAA	GGATGAAGGA	780
ATTTACCAAA	GCTATCTTGA	AAAAGCAGCA	AGTCTAACTG	AAGTTGAAGA	ATAA	834

(2) INFORMATION FOR SEQ ID NO:1457:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1457:

TGTTTTTCT	GTATTTTAG	GGACATCTGG	CTGGACTTCT	TTTTCAGTCT	TATTAGCTTC	60
GGCTGCTGGC	TTAGACTCAT	CCCCTTGGTT	AGTTGCTTCG	GGCTTTGCTT	CTGTTTCCTT	120
GTCAGACTTA	GGTTTTGCTT	CTGCAGATGG	TGTTTCTGCA	ACCACCTCAC	TTGCTTTTTC	180
CTCTGGTTTA	GCTGCGCTAG	CTGCTTCTGC	AGTTTCAGAT	GCTGTCGCTA	CTCCTTCTGC	240
CTTTTCTAG						249

(2) INFORMATION FOR SEQ ID NO:1458:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...201
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1458:

CTGCCTCTCT	GGACTGCTTT	AAAGGTTTTT	TACTATTCTA	TTATTTCTAC	TAGCACTTGT	60
CAAGTAAAAA	CATGGTCACT	AAAGAACTAT	AAGAGAAAAA	GTAAACCTAG	CGACGCGATG	120
AGCGCTGGGT	CGTTTGGTTT	CGATTGCTCT	CTTCCTCTTG	TTTTTTCTGT	TCTTCTTCTT	180
GTTTTTTCTC	AGCTTCCTTA	G				201

(2) INFORMATION FOR SEQ ID NO:1459:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 671 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...671
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1459:

GCACACTCTG	TGATACTGAT	GGCTCCCCCT	GTAGAACATG	GTACTACCTA	AACAGCAATG	60
GCGCTATGGC	GACAGGATGG	CTCCAAAACA	ATGGTTCATG	GTACTATCTA	AACGCTAATG	120
GTTCAATGGC	AACAGGATGG	CTCCAAAACA	ATGGTTCATG	GTACTATCTA	AACGCTAATG	180
GTTCAATGGC	AACAGGATGG	CTCCAAAACA	ATGGTTCATG	GTACTACCTA	AACGCTAATG	240
GTGATATGGC	GACAGGATGG	CTCCAATACA	ATGGTTCATG	GTACTACCTA	AACGCTAATG	300
GTGATATGGC	GACAGGATGG	CTCCAATACA	ATGGTTCATG	GTACTACCTA	AACGCTAATG	360
GTGATATGGC	GACAGGATGG	CTCCAATACA	ATGGTTCATG	GTACTACCTA	AACAGCAATG	420
GTGCTATGGT	AACAGGATGG	CTCCAAAACA	ATGGCTCATG	GTACTACCTA	AACGCTAACG	480
GTTCAATGGC	AACAGGTTGG	GTGAAAGATG	GAGATACCTG	GTACTATCTT	GAAGCATCAG	540
GTGCTATGAA	AGCAAGCCAA	TGGTTCAAAG	TATCAGATAA	ATGGTACTAT	GTCAATGGCT	600
CAGGTGCCCT	TGCAGTCAAC	ACAACTGTAG	ATGGCTATGG	AGTCAATGCC	AATGGTGAAT	660
GGGTAAACTA	A					671

(2) INFORMATION FOR SEQ ID NO:1460:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 687 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...687
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1460:

AAATCGACCT	GTCTTAAAGG	ATATTACTTG	TTCAATTTTC	AAGGGGCAAA	AATTGCTTTT	60
GTTGGACCAT	CTGGATCAGG	AAAATCAACG	ATTGTGCGTT	TGTTAGAGCG	GTTTTATAAA	120
CCGCTTTCAG	GAGATATTCT	AATGGAGCAA	TCAAGTATAT	ATGATTTTAA	CTTAAAAGAA	180
TGGAGAAGTA	AAATCGCTTG	GGTTTCACAA	AATAATGCAG	TCTTATCTGG	CAGTATTTCGT	240
GACAATCTTT	GTCTCGGTTT	GAATCGCTTA	GTAAGTATG	ATGAATTGAT	GAAAGTGCTA	300
GACTTAGTAT	CACTAGGTGA	TGAGATTCGC	TCCATGAAAG	AGGGACTAGA	TACTGAAGTT	360
GGTGAACGCG	GACGATTCTT	GTGAGGGGGG	CAAAGCCAAA	GACTTCAAAT	AGCTAGAACC	420
TACTTAAAAAG	ATGCTGAAAT	TCTTATATTT	GATGAAGCTA	CTGCTAATCT	TGATGCGGAT	480
TCTGAGTATG	CGATTATCAG	TAGCCTCTAT	TCTGTATTAA	AGGAGAAGAC	GGTTGTGATT	540
ATAGCGCATA	GTTTGTCAAC	GGTAAAAGAT	GTGGATTGTA	TTTTCTTCTT	AGAGGAGGGG	600
AAAATCACTG	GCTCAGGAAC	TCATAAGGAA	CTACTGGAAA	ATCATGAGCG	TTATGCTCGT	660
TTTGTGCAGG	AGCAAATGAT	AGAGTGA				687

(2) INFORMATION FOR SEQ ID NO:1461:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1461:

TTTGGGCACT GTCTCAACGA GAGACTCGGT GAAATTTTAG TACCTGTGAA GATGCAGGTT	60
ACCCGCGACA GGACGGAAAG ACCCCATGGA GCTTTACTGC AGTTTGATAT TGAGTGTCTG	120
TACCACATGT ACAGGATAGG TAGGAGTCTA AGAGATCGGG ACGCCAGTTT CGAAGGAGAC	180
GCTGTTGGGA TACTACCTT GTGTTATGGC CACTCTAACC CAGATAGGTG A	231

(2) INFORMATION FOR SEQ ID NO:1462:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1462:

TTTGGGCACT GTCTCAACGA GAGACTCGGT GAAATTTTAG TACCTGTGAA GATGCAGGTT	60
ACCCGCGACA GGACGGAAAG ACCCCATGGA GCTTTACTGC AGTTTGATAT TGAGTGTCTG	120
TACCACATGT ACAGGATAGG TAGGAGTCTA AGAGATCGGG ACGCCAGTTT CGAAGGAGAC	180
GCTGTTGGGA TACTACCTT GTGTTATGGC CACTCTAACC CAGATAGGTG A	231

(2) INFORMATION FOR SEQ ID NO:1463:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...231
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1463:

TTTGGGCACT GTCTCAACGA GAGACTCGGT GAAATTTTAG TACCTGTGAA GATGCAGGTT	60
ACCCGCGACA GGACGGAAAG ACCCCATGGA GCTTTACTGC AGTTTGATAT TGAGTGTCTG	120
TACCACATGT ACAGGATAGG TAGGAGTCTA AGAGATCGGG ACGCCAGTTT CGAAGGAGAC	180
GCTGTTGGGA TACTACCCTT GTGTTATGGC CACTCTAACC CAGATAGGTG A	231

(2) INFORMATION FOR SEQ ID NO:1464:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...318
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1464:

AAGGTCAACT GGATGATATT GCCAGTCACT TGGATCAAGC TCGCCAGCAG AATGAGGAGT	60
GGATGCCCAA GCAAACACGT GCTGAAGCCA AGAAAGAAAA GGTCAGCGAG CGTGCGCCAT	120
CTACAAAATC AATTAACAGA CCAGTACCAG ATTAGCTATA CTGAAGCACT AGAAAAGGCA	180
CATGAATTGG AAAACCTCAA TCTGGCAGAG CAAGAGGTGC AGGATTTAGA GAAGGCTATT	240
CGCTCATTGG GACCTGTCAA CTTGGAAGCT ATTGACCAGT ACGAAGAAGT TCACAACCGG	300
TCTGGACTTT CTAAATAG	318

(2) INFORMATION FOR SEQ ID NO:1465:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 597 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1465:

AGTTTGA	ACT GC	ACCCCAA	AGTTAG	ACAG AAAAA	ATCTA	ACTTTT	G	GGG	TG	TTTTT	TATT	60
ATGAAAT	TAA	CTTATG	ATGA	TAAAGT	TCAG	ATCTAT	G	AAC	TTAG	AAAAA	ACA	120
TTAGAGA	AGC	TTTCAA	ATAA	ATTTGG	GATA	AATAAT	T	CTA	ATCT	TAGG	TATG	180
TTGATTG	ATC	GTTACG	G	AAT	AGAGT	TCGTC	AAAAA	A	GGGA	AAAAT	CAATA	240
CTATTCT	CCA	GA	ACTAAA	AC	AAGT	TGATAA	AGTT	TTAC	ATG	CAA	ACTGGT	300
CTCA	AAAT	ATGCTC	TCCC	AAATCG	TGGT	ATGCTT	CCAA	ATTGG	CTG	GC	GCAAT	360
ATAAG	AAAA	ACGGGT	ATACTA	TGT	TGAG	AAAA	ACA	AGAGG	GAG	AC	CAGCT	420
AAAA	AT	TAA	AAAT	AGAGT	TTAG	AACG	AC	TTCA	AAG	GA	GAATG	480
AAACGC	CGAA	AGAAAA	CTTG	GGA	AGA	AATG	ACAG	AA	TTAA	AAAG	AGT	540
TTACG	GA	CTG	AGGT	G	CTTA	CTTAA	AAAA	AAG	TTAA	AAAG	AGT	597
TAGAG	CG	GAG	AAAG	G	CA	AA	AG	TTAG	AG	AAATG	GTTT	
CTAG	AG	CG	AG	G	AG	TT	AG	AG	TT	AG	AG	

(2) INFORMATION FOR SEQ ID NO:1466:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 678 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1466:

AAAGA	A	AGACT	GTATG	GATAA	TCGAC	CAATT	GGTTTT	TTTGG	ATTCG	GGTGT	CGGGG	GCTTG	60
ACCGT	T	GTGC	GCGAG	CTCAT	GCGCC	AGCTT	CCCCA	TGAAG	AAATC	GTCTA	TATTG	GAGAT	120
TCGGC	G	CGGG	CGCC	TATGG	CCCCC	GTCC	GCTG	AGCAA	TTCTG	TAATA	TACTT	GGCAG	180
CTGGT	C	AACT	TTCTC	TTGAC	CAAGG	ATGTC	AAAA	TGATTG	TCATT	GCTTG	TAACA	CTGCG	240
ACTGC	G	GTCG	TCTGG	GGAAGA	AATCA	AGGCT	CAACT	AGATA	TTCCT	GTCTT	GGGTG	TAAAT	300
TTGCC	A	GAG	CTTCG	G	CAGC	ATCAAG	TCC	AGTCA	AGGTG	GGAAA	ATCGG	AGTG	360
ATGGA	ACGCC	ATGA	CGGT	A	CAATC	AGAC	ATATAC	CGTC	AGAAAA	TCCAT	GATCT	GGAT	420
CCCCG	AC												

TTACAGGTGG	AGAGCTTGGC	CTGTCCCAAG	TTTGCTCCCT	TGGTTGAGTC	AGGTGCCCTG	480
TCAACCAGTG	TTACCAAGAA	GGTGGTCTAT	GAAACCTGTC	GTCCCTTGGT	TGGAAAGGTG	540
GATAGCCTGA	TTTTGGGCTG	TACTCATTAT	CCACTCCTTC	GCCCTATTAT	CCAAAATGTG	600
ATGGGGCCAA	AGGTTCAGCT	CATCGATAGT	GGGGCAGAGT	GCGTACGGGA	TATCTCAGTT	660
CTTACTCAAT	TATTTTGA					678

(2) INFORMATION FOR SEQ ID NO:1467:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...279
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1467:

TTCGGAGACT	GGAAGGACGT	GGCTCCGCTT	CTTGAAGGTT	TGGTAGAAAA	TCAAGATTAT	60
GTTGTCGAGC	AAGATGCTCG	TAATTCTGCA	GTTCCTTTGC	TAGATAAGCG	TGCTATCAAC	120
GCTCGTATCG	AGCCAGGTGC	TATTATCCGT	GACCAGGTGG	AAATTGGTGA	CAATGCTGTT	180
ATCATGATGG	GAGCTGTTAT	CAATATCGGT	GCTGAAATCG	GTGCTGGAAC	CATGATTGAC	240
ATGGGTGCCA	TCCTTGGTGG	CCGTGCCATC	GTTGGATAA			279

(2) INFORMATION FOR SEQ ID NO:1468:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 414 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...414
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468:

AAAAGATGCT	GCCGGAAGCTG	TGACAGTGTT	GGAAGGGAGA	CAATAATGAA	TCAAGAAGAA	60
TTAGCTAAGA	AAATGTTGCT	TCCATCAAAAG	AATTCTCGTC	TGGAGAAATT	AGGAAAAGGT	120
TTGACCTTTG	CCTGTCTTTC	TTTGATAGTC	ATCCTTGTGG	CCATGATTTT	GGTTTTTCGTA	180
GCGCAAAAAG	GCTTGTCGAC	CTTCTTTGTC	AATGGTGTGA	ATATCTTTGA	CTTTCTTTTG	240
GGAGGAACTT	GGAATCCTTC	TAGTAAAGAA	TTTGGGTGCC	CTTCCTATGA	TTTTGGGTTC	300
CTTTATCGTT	ACCATTCTCT	CAGCCCTTAT	CGCAACACCC	TTTGCTATTG	GTGCAGCAGT	360
TTTTATGACC	GAAGTATCAC	CAAAAGGGGC	GAAGATTTTG	CAACCAGCTA	TTGA	414

(2) INFORMATION FOR SEQ ID NO:1469:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1287 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1287
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1469:

CGCTATCGCT	GCAATCTCAG	AAACAATGGA	AAAAGAAGGA	TTGGCATAAG	GGAAATGACA	60
GAAATGCTTA	AAGGAATCGC	AGCATCTGAC	GGTGTTGCAG	TTGCAAAAGC	ATATCTACTC	120
GTTCAAGCCG	ATTTGTCATT	TGAGACTATT	ACAGTCGAAG	ATACAAACGC	AGAAGAAGCT	180
CGCCTTGATG	CCGCTCTACA	GGCATCACAA	GACGAGCTTT	CTGTTATTCG	CGAGAAAGCA	240
GTAGGTACGC	TCGGTGAAGA	AGCAGCTCAA	GTTTTTGATG	CTCACTTAAT	GGTTCCTGCT	300
GACCCAGAAA	TGATCAGCCA	AATCAAGGAA	ACTATCCGTG	CGAAGAAAAGT	GAATGCAGAA	360
GCAGGTCTGA	AAGAAGTTAC	AGATATGTTT	ATCACTATCT	TTGAAGGCAT	GGAAGACAAC	420
CCATACATGC	AAGAACGCGC	AGCGGATATC	CGCGATGTGA	CAAAACGTGT	ATTGGCAAAC	480
CTTCTTGGTA	AAAAATTGCC	AAACCCAGCT	TCTATCAATG	AAGAAGTGAT	TGTGATTGCA	540
CATGACTTGA	CACCATCTGA	TACAGCTCAA	TTGGACAAAA	ACTTTGTAAA	AGCTTTTGTA	600
ACCAACATCG	GTGGACGTAC	AAGCCACTCA	GCTATCATGG	CACGTACACT	TGAAATTGCA	660
GCTGTATTAG	GTACAAACAA	CATCACTGAA	ATCGTTAAAG	ACGGTGACAT	CCTTGCTGTT	720
AACGGGATCA	CTGGTGAGGT	TATTATCAAC	CCAAGTATG	AACAAGCGGC	AGAATTTAAA	780
GCAGCTGGTG	AAGCTTATGC	GAAACAAAAA	GCTGAATGGG	CGCTCTTGAA	AGATGCTCAA	840
ACAGTGACTG	CTGACGGTAA	ACACTTCGAG	TTGGCTGCTA	ATATCGGTAC	TCCAAAAGAC	900
GTTGAAGGTG	TTAACAACAA	CGGTGCAGAA	GCTGTTGGAC	TTTACCGTAC	AGAGTTCCTG	960
TACATGGATT	CTCAAGACTT	CCCAACTGAA	GATGAGCAGT	ATGAAGCATA	CAAGGCTGTT	1020
CTTGAAGGAA	TGAACGGTAA	ACCTGTTGTC	GTTTCGTACAA	TGGATATCGG	TGGAGATAAG	1080
GAACATCCTT	ACTTCGATAT	GCCTCACGAA	ATGAACCCAT	TCCTTGATT	CCGTGCTCTT	1140
CGTATCTCTA	TCTCTGAGAC	TGGAGATGCT	ATGTTCCGCA	CACAAATCCG	TGCTCCTTCT	1200
TCGTGCGTCT	GTTACGGTCT	AATTGCGTAT	CATGTTCCCA	ATGGTTGCGC	TCTTGAAAGA	1260
ATTCCGTGCA	GCGAAAGCAG	TCTTTGA				1287

(2) INFORMATION FOR SEQ ID NO:1470:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...240
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1470:

CTGGAGAGCT	GGAGATGCTC	TCGGACGAGG	AGAATCCTAG	CTGATATAGA	AGCTAATATG	60
GGCATGGTAA	TCGAAGGAAT	TTCAACGACT	CGAGCAGCCT	ATGAACTAGC	CCAAGAAGCTT	120
GGAGTCTATA	TGCCCATTAC	ACAGGCTATT	TACCAAGTTA	TTTATCACGG	AACCAATATC	180
AAAGATGCCA	TTTATGACAT	CATGAACAAT	GAATTTAAAG	CAGAAAATGA	GTGGTCTTAA	240

(2) INFORMATION FOR SEQ ID NO:1471:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1134 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1134
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1471:

GGAGGTGGCT	GTATGAAAAA	AGTGAAGTTG	GGGGAAGTCT	TATCTCTAAA	AAAAGGCAAG	60
AAAGCCACTG	TACTTGCTGA	ACAAACAAC	CTAAGCCAAC	GTTATATTCA	AATAGATGAT	120
TTAAGAAATA	ATAATAATTT	AAAATTCACT	GAAAGTTTAA	ATATGACTGA	AGCACTTCCA	180
GATGATATTC	TAATAGCATG	GGATGGTGC	AATGCAGGAA	CAGTTGGTTA	TGGATTATCG	240
GGAGCTGTTG	GTAATACAAT	TACGGTCTTA	AAAAAGAATG	AGCGATACAA	AGAAAAAATT	300
ATATCAGATT	ACTTGGGAGT	CTTTTGGGAA	AGTAAATCGC	AGTATTTACG	AGATCATTCA	360
ACAGGTGCAA	CTATTCCTCA	TTTAAACAAG	AATATATTAC	TTGATTTACA	ATTAGAATTG	420
CTAGGTATCG	AAGAACAAGA	GAACATTATC	TGTATTCTTA	ATACGATTAA	AAGGCTTATT	480

ACTAAAAGAA	AATTTAGTT	AGATGAACTA	AACTTGCTCG	TCAAATCCCG	ATTTAACGAG	540
ATGTTTGGGG	AAAATAAAAT	ATTTGAAAGC	ATTGATAACT	TATTTGATAT	TATAGATGGT	600
GATAGGGGCA	AAAATTATCC	TAAATCAGAT	GAGTTGTTTA	GTGAGGAGTA	CTGTTTATTT	660
TTAAATACAA	AGAATGTTAC	TAAAAACGGA	TTTTCATTCG	ATACAAAGCA	ATTTATCACT	720
AAAACAAAGG	ATAAATTACT	TCGAAAAGGC	AACTTGAGC	GTTATGATAT	AGTCTTGACA	780
ACAAGAGGTA	CTGTTGAAA	TGTAGCGTAC	TACGATGAAT	TAATAAAATA	TAAACATTTA	840
CGTATAAATT	CAGGTATGGT	AATATTACGT	CCCAAGACAC	CAAATCTAAA	TCAGAAATTT	900
ATTATCCATG	TTTTAAGAAA	TAATAATTAT	AGTCGAGTGA	TATCAGGAAG	TGCTCAGCCT	960
CAGTTACCAA	TTACAAAATT	AAAAAAAAATA	CTTCTCCCCC	TCCCCCCTACT	AGCCCTCCAA	1020
AATGAGTTCG	CAGACTTTGT	AGTTCAGGTC	GACAAATCAC	AATTGGCAAT	CCAAAAATCT	1080
CTGGAAGAAC	TTGAAACTTT	GAAGAAATCT	CTGATGCAGG	AGTATTTTGG	CTGA	1134

(2) INFORMATION FOR SEQ ID NO:1472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1472:

CATGAAGGCT	GGACTAAAGA	TAGAGTTTCT	CTTGAATACT	GTCTCCCAAG	TCGTACGATA	60
CTTCTTAACT	GGCTAGCACA	ATACAGGAAA	AACGGGTATA	CTATTGTTGA	GAAAAACAAGA	120
GGGAGAGTAC	CTGAGAGCGG	AAAATGCCAT	CCTAAAAAAG	TTAAGAGAAC	TCCGATTGAA	180
GGAGGAAAAA	GAGAAAGAAG	AAAGACAGAA	ATTGTTCAAG	AATTAATTAC	TGAGTTTTCG	240
TTAGATCTTC	TTCTAAAAGC	CATTAAACTA	GCTCGTTTGA	CCTACTACTA	TCACTTGAAA	300
CAGCTAGATA	AAACAGATAA	GGACCAAGAG	CTTAAAGCTG	AAATTCAATC	CATTTTATC	360
GAACACAAGG	GAAATTATGC	TTATCGTCGG	ATTTATTTAG	AACTAAGAAA	TCGTGCTTAT	420
CTGGTAAATT	ATAAAAGAGT	TCAAGGCTTG	ATGAAAGTAC	TCAATTTACA	AGCTAAAATG	480
CGACAGAAAC	GAAAATAA					498

(2) INFORMATION FOR SEQ ID NO:1473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1473:

CATGAAGGCT	GGACTAAAGA	TAGAGTTTCT	CTTGAATACT	GCCTCCCAAG	TCGTACGATA	60
CTTCTTAACT	GGCTAGCACA	ATACAGGAAA	AACGGGTATA	CTATTGTTGA	GAAAACAAGA	120
GAGAGAGTAC	CTGAGATCGG	AGAATGCCAT	CCTAAAAAAG	TTAAGAGAAC	TCCGATTGAA	180
GGAGGAAAAA	GAGAAAGAAG	AAAGACAGAA	ATTGTTCAAG	AATTAATGAC	TGAGTTTTCG	240
TTAGATCTTC	TTCTAAAAGC	CATTAAACTA	GCTCGTTCGA	CCTACTACTA	TCAC TTGAAA	300
CAGCTAGACA	AACCAGATAA	GGACCAAGAG	CTTAAAGCTG	AAATTCAATC	CATTTTTATC	360
GAACACAAGG	GAAATTATGC	TTATCGCTGT	ATTCATTTAG	AACTAAGAAA	TCGTGGTTAT	420
CTGGTAAATC	ATAAAAGAGT	TCAAGGCTTG	ATGAAAGTAC	TCAATTTACA	AGCTAAAATG	480
CGACAGAAAC	GAAAATAA					498

(2) INFORMATION FOR SEQ ID NO:1474:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 498 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1474:

CATGAAGGCT	GGACTAAAGA	TAGAGTTTCT	CTTGAATACG	GTCTCCCAAG	TCGTACGATA	60
CTTCTTAACT	GGCTAGCACA	ATACAGGAAA	AACGGGTATA	CTATTGTTGA	GAAAACAAGA	120
GGGAGAGTAC	CTGAGAGCGG	AGAATGCCAT	CCTAAAAAAG	TTAAGAGAAC	TCCGATTGAA	180
GGAGGAAAAA	GAGAAAGAAG	AAAGACAGAA	ATTGTTCAAG	AATTAATGAC	TGAGTTTTCG	240
TTAGTTCTTC	TTCTAAAAGC	CATTAAACTA	GCTCGTTCGA	CCTACTACTA	TCAC TTGAAA	300
CAGCTAGACA	AAACAGATAA	GGACCAAGAG	CTTAAAGCTG	AAATTCAATC	CATTTTTATC	360
GAACACAAGG	GAAATTATGC	TTATCGCTGT	ATTCATTTAG	AACTAAGAAA	TCGTGCTTAT	420
CTGGTAAATC	ATAAAAGAGT	TCAAGGCTTG	ATAAAAGTAC	TCAATTTACA	AGCTAAAATG	480
CGACAGAAAC	GAAAATAA					498

(2) INFORMATION FOR SEQ ID NO:1475:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1475:

CATGAAGGCT	GGACTAAAGA	TAGAGTTTCT	CTTGAATACG	GTCTCCCAAG	TCGTACGATA	60
CTTCTTAACT	GGCTAGCACA	ATACAGGAAA	AACGGGTATA	CTATTGTTGA	GAAAACAAGA	120
GGGAGAGTAC	CTAAATGGG	ACGTAAGCCA	AAAACGATAC	CTGAAGAGAG	GACAGAATTA	180
GAACATCTTC	AAGCAGAAAA	TGAGTACCTG	AGAGCGGAGA	ATGCCATCCT	AAAAAAGTTA	240
AGAGAACTCC	GATTGAAGGA	GGAAAAAGAG	AAAGAAGAAA	GACAGAAATT	GTTCAAGAAT	300
TAA						303

(2) INFORMATION FOR SEQ ID NO:1476:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1476:

CATGAAGGCT	GGACTAAAGA	TAGAGTTTTT	TTTGAATACG	GTTTCCCAAG	TTGTACGATA	60
ATTTTAACT	GGTAGCACA	ATACAGGAAA	AACGGGTATA	ATATTGTTGA	GAAAACAAGA	120
GGGAGAGTAC	CTAAATGGG	ACGTAAGCCA	AAAACGATAC	CTGAAGAGAG	GACAGAATTA	180
GAACGTTTTC	AAGCAGAAAA	TGAGTACCTG	AGAGCGGAGA	ATGCCATCCT	AAAAAAGTTA	240
AGAGAACTCC	GATTGAAGGA	GGAAAAAGAG	AAAGAAGAAA	GACAGAAATT	GTTCAAGAAT	300
TAA						303

(2) INFORMATION FOR SEQ ID NO:1477:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2379 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1477:

TTTATTTTAT	GGAGAAGTAG	ATTTTTTAGAA	TGCGGAGGGT	TCAATATGGT	TGAGTTTATA	60
AAGTCTAAGA	AAGAAATGAG	TGAGGAGGAT	ATTAAAGCAA	ATTTTCATCAC	TCCTGCTATT	120
GTATCCAAAG	GATGGAAAAA	TGGTGAGCAT	ATCGCTTACG	AAGAATACTT	CACTGATGGT	180
CGAATTGAGG	TTAGAGGAGA	TAAGGCTCGT	CGTAAAGAAG	GAAAAAATC	AGACTATTCA	240
CTGTATTACC	AATTTGGAAC	TCGAATTGCA	ATTGTTGAGG	CAAAGGATAA	TAAACACAGC	300
GTTTCGAGCAG	GATTACAACA	AGCTATTGAA	TATGGAGAGA	TTTTTAGATGT	TCCATTTGTT	360
TATTCTTCGA	ATGGTGATGG	CTTTATTGAA	CACGACCGTA	TCACGAGAGA	AGAACGTGAG	420
CTGGAGTTAG	ACGAATTCCC	TACTCGTGAA	GAATTATTTT	CTCGTATGAC	GAAGGAAAAA	480
GGATTGACGT	ACGAAATTAC	AGAAGCTATC	TCAACTCCAT	ACTATACAGA	CGCCTTCTCA	540
ATGAAAACGC	CACGCTATTA	TCAGCAAATA	GCTATCAACC	GTACTATTGA	AACAGTTGCC	600
AGAGGACAAA	AACGAGTAAT	GTTTGTGATG	GCAACAGGAA	CGGGGAAAAC	GTTTCATGGCT	660
TTTCAAATTA	TTCATCGCCT	TCGAAAAGCT	GGTTTGGCTA	AACGAGTTTT	ATTCTTAGCG	720
GATAGAAACA	TCTTAGTAGA	CCAAACGATG	GCTGAAGACT	TTAGGCCATT	CGAAAAGGTA	780
ATGACGAAAA	TTACACCAAA	ACTTTTGACT	GCTCCTGAAA	AATTAAATTC	TTTTGAAATT	840
TATCTAGGGC	TTTATCAGCA	ACTAACTGGT	GAAGATGGAA	CTGAAACACA	TTATCAAAAA	900
TTTGACAAAG	ACTTCTTTGA	TTTAATCGTA	ATTGATGAAG	CGCACC GTGG	TTCAGCTAAG	960
GAAACAGTA	ACTGGCGTAA	GATAATTGAT	TATTTTCAGTT	CTGCGACACA	GATTGGGATG	1020
ACCGTACTC	CTAAAGAAAC	CAAGAATGCT	TCCAATACGG	AATACTTTGG	TGAGCCAATC	1080
TATACTTATA	GTTTAAAACA	GGGAATCGAG	GATGGTTTTT	TGGCTCCATA	TCGTGTTATG	1140
AGAGTTAATT	TAGATGTAGA	TGTGGATGGT	TATCGTCCAG	AAACTGGAAA	AGTTGATGCT	1200
AACGGACAAT	TAATAGAAGA	TAGGTACTAC	GGCAGGAAAG	ATTTTGATAA	AACCATTGTC	1260
ATTGATGATA	GAACGCAAAG	AGTTGCCAAG	TTTGT'TTCTG	ATTATATGAA	GCAAAACAAT	1320
GCACGATTTG	ATAAAACAAT	TGTTTTTTTGT	GTTGATATTG	ACCATGCCGA	GCGAATGCGT	1380
GCTGCACTTG	TAAAAGAGAA	TCTAGACTTA	GTCCAAGAAG	ACTATCGTTA	TGTCATGCAA	1440
GTAACGGTG	ACAACGCTGA	AGGAAAAGCT	CAACTGGATA	ACTTTATGGA	TGTCAATTCT	1500
AATTTTCCCG	CTATTGTAA	AACGTCTAAA	TTATTAAACGA	CAGGAGTTAA	TGCTAAAACA	1560
TGTCGTTTGA	TTGTTT'TAGA	CTCTAATATC	CAATCCATGA	CTGAATTTAA	ACAAATTATT	1620
GGTCGTGGCA	CACGTCTTTA	TCCTCAAAAG	GGGAAAGAAT	TTTTTACGAT	TATTGATTTT	1680
CGAAATGTTA	CCAATTTGTT	TGCTGACCCT	GATTTTGTATG	GTGATCCAGT	GAAGGTGCTG	1740
GAAACAGGTG	CGAAAACAGT	CAGTGGTTCT	ACGCCCCGTT	TCGTAGGTGA	GGAAGGTGAC	1800
CCAGTAGAAA	AATATATCGT	TACAGACAAG	CAGGTTACCA	TTCTTAATTC	TACTGTTCAA	1860
GTATTGGATG	AAAACGGGAA	ACTGATTACC	GAAAGCCTGA	CCGACTACAC	TCGAAAGAAT	1920

ATCTTAGGTA	GCTACGCCAC	TTTGAACGAT	TTTATCACAG	TTTGGCATA	GGCAGATAAA	1980
AAGAAGCTTA	TCCTAGACGA	ACTTTATAAA	AAAGGAGTTT	ATCTAGATGC	TATTCGAGAG	2040
TCGGAGGGAA	TATCAGAACA	AGAAATCGAT	GATTTTGATT	TACTCCTAAA	ACTTGCCTAT	2100
GGTCAAAAAG	AATTAACCAA	AACGGAACGT	ATCAATAAAC	TCAAACAAAAG	CGGATATTTA	2160
TATAAATATA	GTGAGGAAGC	GCGTGCTGTT	TTGGAAATTT	TACTGAACAA	ATACATGGAT	2220
AAAGGTATTG	GAGAACTCGA	AAGCATTGAA	ACATTAAAAAC	TTCCAGAATT	TCAGATATAT	2280
GGTGGAACCT	TCAAAATCAT	CAATACTTAT	TTTGGAGATA	AAAAACGATA	TTTACAAGCA	2340
ATTAAAGAAT	TGGAGCAAGA	GCTATTTACA	GTAGCTTAA			2379

(2) INFORMATION FOR SEQ ID NO:1478:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 387 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1478:

AAGCATTTAT	GGGTAGTGAG	AATGATTGAT	CATTTTGAGA	TTAAGGTAAA	GGATTTACAA	60
ATTTTCAGAAG	GATTTTATAG	GAGTTTCTC	GCTCCTTTGG	ACTATAAATT	GGCTTTTAAG	120
ACTAGTTCTC	TAATTAGTTT	TCTATCCCCG	AACAGCCCTC	ATCCTGGTGG	TGATTTTGG	180
CTGACTCAGG	GAACACAAGA	TCCTGTTCAT	TTTGCTTTTT	TAGCAGAAAA	TAAGGAAGAA	240
GTTCAGGCTT	GTTATGAGGC	TGGCATAGAG	GCAGGTGGGC	GAGACAAATGG	GGTTCCTGGT	300
TATCGAAGTG	AGCATCCGAT	TTACTATGCT	GCTTTTATGA	TTGACCTGGA	TGGGAACAAT	360
ATAGAGGTGG	TTTGCCATAA	AGAATAA				387

(2) INFORMATION FOR SEQ ID NO:1479:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 591 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1479:

ATGAATTTAT	GGGATATTTT	CTTTACGACT	CAGGCAACCG	AGCCGCCCAA	ATTTGACCTT	60
TTTTGGTATG	TTAGCCTATT	TACGCTCTTA	GCCTTAACCT	TTTATACAGC	CCATCGCTAT	120
CGTGAAAAGA	AGGTTTACCA	ACGATTTTTT	CAAATCTTGC	AGACTGTTCA	GTTAATCCTT	180
CTTTATGGTT	GGTACTGGGT	CAATCATATG	CCACTGTCAG	AAAGCCTACC	CTTTTACCAT	240
TGCCGTATGG	CTATGTTTGT	GGTACTCTTG	CTTCCTGGTC	AGTCCAAATA	TAAACAATAC	300
TTTGCAATTAT	TGGGAACATT	TGGGACATTA	GCAGCCTTTG	TTTATCCAGT	GCCAGATGCT	360
TACCCTTTTT	CACATATCAC	CATTCTATCC	TTTATCTTTG	GTCATTTAGC	ACTCTTGGGG	420
AACTCTCTAG	TTTATCTATT	GAGACAGTAT	AATGCGCGAT	TGCTGGATGT	GAAGGGAATT	480
TTTCTCATGA	CCTTTGCCCT	AAATGCCTTG	ATTTTTGTGG	TCAATTTGGT	GACAGGTGGC	540
GATTACGGAT	TTTTGACAAA	ACCGCCCAT	GGTTGGGGGA	TCACGTTCTA	G	591

(2) INFORMATION FOR SEQ ID NO:1480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1480:

ATGGATTTAT	GGTTTTCTGA	AGTTCATACT	CCAGATGTCA	AATTGTCTCT	GAGAACAGCC	60
AAGCAACTTT	ACGCTGGAAA	AAGTGAATGG	CAGGATATCG	AAGTCTTGGA	TACGCCAGCT	120
TTTGGGAAAA	TACTGATTTT	AAATGGCCAT	GTCTTGTTCT	CAGATGCGGA	TGATTTTCGTC	180
TACAATGAAA	TGACCGTTCA	CGTTCCCATG	GCTGTCCACC	CAAATCCAAA	GAAAGTATTG	240
GTTATTGGGG	GTGGTGACGG	CGGTGTTGCC	CAAGTATTAA	CACTCTATCC	TGAACTGGAA	300
CAAATCGATA	TCGTGGAACC	GGATGAGATG	TTGGTCGAAG	TCTGTCTGTA	GTATTTCCCA	360
GACTTTGCTG	CAGGGCTAGA	TGATCCTCGT	GTTACCATTT	ACTACCAAAA	TGGGCTACGC	420
TTTTTGCAG	ACTGCGAAGA	TGATTACGAT	ATTATCATCA	ACGATGCGAC	AGATCCATTT	480
GGCCATACGG	AAGGACTCTT	TACCAAGGAA	TTCTACGGCA	ATAGTTATCG	AGCTCTGAAG	540
GAAGACGGCA	TCATGATTTA	CCAGCATGGG	AGTCCCTTCT	TTGACGAGGA	TGAGTCGGCC	600
TGCCGAAGCA	TGCACCGCAA	GGTCAATCAA	GCCTTTCCAA	TCAGTCGGGT	TTATCAGGCC	660
CATATTCCAA	CTAGCCCAGC	TGGCTATTGG	TTGTTTGGAT	TTGCATCGAA	AAAATACCAC	720
CCTGTCAAAG	ATTTTGACAA	GGAAGGTTGG	AAAAAACGCC	AGCTTTTCAC	AGAATACTAC	780
ACTGCAAAC	TACACGTGGG	ATCCTTTATG	TTGCCCAAGT	ATGTTGAGGA	CATTTTAGAA	840
GAAGAGGAAG	GAAAAAATG	A				861

(2) INFORMATION FOR SEQ ID NO:1481:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...258
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1481:

TTTTGTTTAT	GTTTTCGCG	TTGCTGGACT	TATTGTGGGA	GGCTTAATAT	GGTTGAAATA	60
AAAAATTTAA	GTCTTGATTA	TGGTGAAGAG	CATATATTAG	ATGATATATC	ACTATCCATA	120
GCCGAGGGAG	AGTGCGTGCT	ATTACAGGA	AAAAGTGGAG	ATGGTAAGTC	ATCTTTAATA	180
AATTCAATCA	ATGGACTAGC	TGTAAGGTAT	GATAACGCAC	AGACAAAGGG	CGAAATAATT	240
ATGAAGGTTA	GAATATAA					258

(2) INFORMATION FOR SEQ ID NO:1482:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2826 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2826
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1482:

GGTCTCTTAT	GGAATAGAAG	AGGAGGACAT	GATTTGTCTA	AGAAAAGATT	GTACGAAATC	60
GCAAAAAGAAC	TTGGAAAAGA	AAGTAAAGAA	GTTGTAGCGC	GTGCAAAAAGA	GTTGGGCTTG	120
GATGTGAAAA	GCCACTCATC	AAGTGTGGAA	GAAGCTGTCTG	CTGCAAAAAT	TGCTGCCAGC	180
TTTAAGCCTG	CAGCTGCTCC	GAAAGTAGAA	GCAAAACCTG	CAGCACCAAA	AGTAAGTGCA	240
GAAAAGAAAAG	CCGAAAAATC	TGAGCCAGCT	AAACCAGCTG	TAGCTAAGGA	AGAGGCAAAA	300

CCGGCTGAGC	CAGTTGCTCC	GAAAAACAGAA	AAAGTAGCAG	CGAAACCGCA	AAGCCGTAAT	360
TTCAAGGCTG	AGCGTGAAGC	CCGTGCTAAA	GAGCAGGCAG	AACGACGTAA	GCAAAATAAG	420
GGCAATAACC	GTGACCAACA	ACAAAACGGA	AACCGTCAGA	AAAACGACGG	ACGTAATGGT	480
GGAAAAACAAG	GTCAAAGCAA	CCGCGACAAT	CGTCGCTTTA	ATGACCAAGC	TAAGAAGCAG	540
CAAGGTCAGC	AAAAACGTAG	AAATGAGCGC	CGTCAGCAAG	AGGACAAACG	TTCAAATCAA	600
GTGGCTCCAC	GTATTGACTT	TAAAGCCCGT	GCAGCAGCCC	TAAAAGCAGA	GCAAAATGCA	660
GAGTACGCTC	GTTCAAGTGA	GGAACGCTTC	AAGCAGTATC	AGGCTGCTAA	AGAAGCCTTG	720
GCTCAAGCTA	ACAAACGCAA	GGAACCAGAG	GAAATCTTTG	AAGAAGCGGC	TAAGTTAGCT	780
GAACAAGCAC	AGCAAGTTCA	AGCAGTGGTT	GAAATCGTCC	CTGAGAAAAA	AGAACCCTGCA	840
GTGGATACAC	GTCGTAAAAA	ACAAGCTCGA	CCAGACAAAA	ATCGTGACGA	TTATGATCAT	900
GAAGAAGATG	GTCCTAGAAA	ACAACAAAAG	AATCGAAGTA	GTCAAAATCA	AGTGAGAAAT	960
CAAAAAGAATA	GTAACCTGGAA	TAACAACAAA	AAGAACAAAA	AAGGCAATAA	CAAGAACAAC	1020
CGTAATCAGA	CTCCAAAACC	TGTTACGGAG	CGTAAATTCC	ATGAATTGCC	AACAGAATTT	1080
GAATATACAG	ATGGTATGAC	CGTTGCGGAA	ATCGCAAAAC	GTATCAAACG	TGAACCAGCT	1140
GAAATTGTTA	AGAAACTTTT	CATGATGGGT	GTCATGGCCA	CACAAAACCA	ATCCTTGGAT	1200
GGGGAAACAA	TTGAACTCCT	CATGGTGGAT	TACGGTATCG	AAGCCAAACA	AAAGGTTGAA	1260
GTGGATAATG	CTGACATCGA	ACGTTTCTTT	GTCGAAGATG	GTTATCTCAA	TGAAGATGAA	1320
TTGGTTGAGC	GTCCACCAGT	TGTTACTATC	ATGGGACACG	TTGACCACGG	TAAAACAACC	1380
CTTTTGGATA	CTCTTCGTAA	CTCACGTGTT	GCGACAGGTG	AAGCAGGTGG	TATTACTCAG	1440
CATATCGGTG	CCTACCAAAT	CGTGGAATAT	GGTAAGAAAG	TTACCTTCCT	TGATACACCA	1500
GGACACGCGG	CCTTTACATC	AATGCGTGCG	CGTGGTGCTT	CTGTTACCGA	TATTACGATC	1560
TTGGTCGTAG	CGGCAGATGA	CGGGGTTATG	CCTCAGACTA	TTGAAGCCAT	CAACCACTCA	1620
AAAGCAGCTA	ACGTTCCAAT	CATCGTAGCT	ATTAACAAGA	TTGATAAACC	AGGTGCTAAC	1680
CCAGAACGCG	TTATCGGTGA	ATTGGCAGAG	CATGGTGTGA	TGTCAACCGC	TTGGGGTGGA	1740
GATTCTGAAT	TTGTTGAAAT	CTCGGCTAAA	TTCAACCAAA	ATATCGAAGA	ATTGTTGGAA	1800
ACAGTCCTTC	TTGTGGCTGA	AATCCAAGAA	CTCAAAGCAG	ACCCAACAGT	TCGTGCGATC	1860
GGTACGGTTA	TCGAAGCGCG	CTTGGATAAA	GGAAAAGGTG	CGGTGCGAAC	CTTCTTGTA	1920
CAACAAGGTA	CCTTGAATGT	TCAAGACCCA	ATCGTTGTGCG	GAAATACCTT	CGGTGCTGTC	1980
CGTGCTATGA	CCAACGACCT	TGGTCGTCGT	GTTAAAAGTTG	CTGGACCATC	AACACCAGTC	2040
TCTATCACAG	GTTTGAACGA	AGCACCGATG	GCGGGTGACC	ACTTTGCCGT	TTACGAGGAT	2100
GAAAAATCTG	CGCGTGCAGC	AGGTGAAGAG	CGTGCCAAAC	GTGCCCTCAT	GAAACAACGT	2160
CAAGCTACCC	AACGTGTTAG	CCTTGAAAAC	CTCTTTGATA	CCCTTAAAGC	TGGGGAACCTC	2220
AAATCTGTTA	ATGTTATCAT	CAAGGCCGAT	GTACAAGGTT	CTGTTGAAGC	CTTTTCTGCC	2280
TCACTTCAA	AGATTGACGT	GGAAGGTGTC	AAAGTACTA	TCGTCCACTC	AGCGGTGCGT	2340
GCTATCAACG	AATCAGATGT	GACCCTTGCC	GAAGCTTCAA	ATGCCTTTAT	CGTTGGTTTC	2400
AACGTACGCC	CTACACCACA	AGCTCGTCAA	CAAGCAGAAG	CTGACGATGT	GGAAATCCGT	2460
CTTCACAGCA	TTATCTACAA	GGTTATCGAA	GAGATGGAAG	AAGCTATGAA	AGGGATGCTT	2520
GATCCAGAAT	TTGAAGAAAA	AGTTATTGGT	GAAGCGGTTA	TCCGTGAAAC	CTTCAAGGTG	2580
TCTAAAGTCG	GAACATACGG	TGGATTTATG	GTTATCAACG	GTAAGGTTGC	CCGTGACTCT	2640
AAAGTCCGTG	TTATCCGTGA	TGGTGTCGTT	ATCTATGATG	GTGAACTCGC	AAGCTTGAAA	2700
CACTATAAAG	ACGACGTGAA	AGAAGTGACA	AACGGTCGTG	AAGGTGGATT	GATGATCGAC	2760
GGCTACAATG	ATATTAAGAT	GGATGATGTG	ATTGAGGCGT	ATGTCATGGA	AGAAATCAAG	2820
AGATAA						2826

(2) INFORMATION FOR SEQ ID NO:1483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1483:

AAGCAGTTAT GTACTATTTT AGATTCACCTT TTCTATACTA AGATGAGTAG GGAGGAAAAG	60
GTAAAAGTTT ATGCCCAAAC TCTTCACATA AGAACTCTAG CTTACCCATT CTATGGAATC	120
TTGCATTATC CATTAAAACT TCCAGACTCA TACCCTTCTA AAATCTATTC AAACCACGTC	180
AGCTTCACAT TATATATGTT GGTTACCTCA CAAGTTTTAT CTGCAACCTC AAAGCTGTTC	240
TTTGAGCAGC CTACAGCTAG CTTCCTAGTT TAA	273

(2) INFORMATION FOR SEQ ID NO:1484:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1484:

CAGGTTCTAT GTTGTCTAAC AACGCTTCGC TATGAAATGA AAACAGCTAT TGGTCTCATG	60
GCACTGGATC AGAGCCGATA CTTTGATATG ACAGATTACG AATTGGAGCT TGAAGTGGAA	120
AATCATGAGC AAGGCAAACA GGATTTCGCA CAATTTTATAG AGAAAAATCA GATTTCCTAC	180
CAAAAAGCTC CTTCAAAATT GGTTTCGATT GTCAAAAAGTA TGAAAAATAG CTGA	234

(2) INFORMATION FOR SEQ ID NO:1485:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1227 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1485:

GCTTGTCTAT	GGATTAGAAC	ACTTATTATG	AGATTAACGC	AAATGCCTTC	TGAATTTTCAG	60
AAGGCTTTAC	CAGTATTAGA	AAAAATTAAA	GAAGCAGGCT	TTGAGGCTTA	TTTTGTTGGG	120
GGCTCTGTTT	GAGATGCCCT	TCTCCATAGC	CCTATCCACG	ATGTGGATAT	TGCGACGTCT	180
TCTTATCCAG	AAGAGACCAA	GCAGATTTTT	CCGCGAACAG	CCGATATCGG	AATCGAGCAT	240
GGAACCGTCT	TGGTCTTAGA	TGGGGATGAG	GAGTATGAGG	TAACAACCTT	TCGGACAGAG	300
GATGTCTATG	TGGACTATCG	CAGACCCAGT	GCGGTTTCCT	TTGTACGATC	GCTAGAAGAA	360
GACCTCAAAC	GCCGTGATTT	CACAGTCAAC	GCCTTTGCCT	TGGATGAGAC	AGGAGAAATC	420
GTTGACTTGT	TCCATGGTTT	AGAAGATTTG	GAAAAGCAAG	TCTTGCGAGC	AGTTGGAGTG	480
GCTAGTGAGC	GTTTCAACGA	AGATGCTTTA	CGGATTATGC	GTGGTTTCCG	TTTTCAGGCT	540
AGTCTTGGTT	TTGCACTTGA	GCCAGAAACA	TTTAAAGCTA	TGAAGACCTT	GACGCCGCTT	600
TTGGAGAAAA	TTTCTGTAGA	GCGTACCCTT	GTCGAGTTTG	ATAAACTCTT	GCTGGCTCCA	660
TTTTGGAGAA	GGGGCTTGGC	TTCCATGATT	GAGAGTCAAG	CTTATGACTA	TCTCCCTGAT	720
ATGGCATCTA	GCCAGGACAA	GCTCAACAGA	CTGTTTGATT	TGGAGACTGA	TTTTACTTTT	780
GAATCCTCTG	AACAAGCCTG	GGCGGCTTTA	CTATGGGCTT	TGGAGATTGA	AAATGCGCAG	840
TCATTTTTGA	AATCTTGGA	GACCTCACGC	CAGTTTGCCA	AGCAAGTTCA	GGATTTGCTG	900
ATTATTTTGG	CTCTGCCGTGA	AAATGGAGAA	TTGAGCAAGC	GAGATTGTTA	TCGCTTTGAC	960
ATAGATTTGC	TTTTACAGGC	TGAAAACTTT	CGTCAAGCTC	AAGGAAAAGA	AGTCAACCCA	1020
CAAGCCATCA	CAGAAAAATA	CCAAAGCTTG	ACTATCCATG	ACAAGAAAAGA	GATTCAGATT	1080
AATGGCGGTA	TTTTGATCAA	GGAATATGGC	TATCAGCCAG	GCCCAGACTT	GGGAGAGATT	1140
TTAACAGAGA	TTGAGTTTGC	CATTGTTCGAT	GGAGAAATGG	AGAATAATCG	TGAAGCCATC	1200
CATGCTTACC	TGAGGGAGAA	AAAATGA				1227

(2) INFORMATION FOR SEQ ID NO:1486:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1486:

AATAGTCTAT	GGAAAGAGGG	TGAGAGTATG	TCAAAGATGA	GTATGAGCAT	CCGTCTGGAT	60
AGTGAGGTTA	AGGAGCAGGC	CCAACAGGTG	TTTAGTAATC	TGGGAATGGA	TATGACAACA	120

GCTATTAATA TTTTCCTTCG TCAGGCAATT CAATATCAGG GATTACCTTT TGATGTTAGA	180
CTAGACGAAA ATCGGAAGTT GCTCCAAGTG TTAACGGATT TAGACCAAAA TCGTAATATG	240
AGCCAGTCTT TTGAATCAGT CTCAGATTTG ATGGAGGACT TACGTGCTTA A	291

(2) INFORMATION FOR SEQ ID NO:1487:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...309
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1487:

TTCTGCCTAT GCGATAGCAG TCCAAGGTTT AGGAGCAAGG CGACGCTAAG CTTGGTAAAC	60
TGCGAACCGC TAGAAGCTTA TCGTCAACTG GAAGAAGCTG AACTTGTTGG ATGTTGGGCA	120
CATGTGAGAA GGAAGTTTTT TGAAGCGACC CCAAGCAAG CAGATAAATC ATCCTTAGGA	180
GCTAAAGGTT TAGCTTATTG TGATCAGTTA TTTTCCCTGG AAAGAGACTG GGAGGCTTTG	240
CCAGCTGATG AACGACTACA GAAACGTCAA GAACATCTCC AGCCCTTAAT GGAAGACTTC	300
TTTGCTTAG	309

(2) INFORMATION FOR SEQ ID NO:1488:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1902 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1902
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1488:

AGCCATCCAT	GCTTACCTGA	GGGAGAAAAA	ATGAGTGATT	TTATCGTTGA	AAAAC TAAGT	60
AAATCCGTTG	GTGACAAGAC	CGTTTTTAGG	GATATTTCCCT	TTATTATCCA	TGACTTAGAC	120
AGAATTGGTT	TAATCGGTGT	CAATGGGACT	GGCAAGACCA	CCCTTTTGGA	CGTCCTTTCT	180
GGTGTTCCTG	GATTTGATGG	GGATGTCAGT	CCTTTTTT CAG	CTAAAAATGA	TTACCAGATT	240
GTTTACTTGA	CTCAGGATCC	TGATTTTGAT	GATAGAAAAG	CAGTTT TGGA	TACGGTTC TA	300
TCTAGTGAAC	TCAAGGAAAT	CCAGCTCATT	CGTGAGTATG	AATTGATTAT	GCTCGACTAT	360
AGTGAGGACA	AGCAGGCGCG	TTTGGAACGT	GTCATGGCAG	AGATGGACTC	TCTCCAAGCT	420
TGGGAAATCG	AAAGTCAGGT	CAAGACCGTT	CTTAGCAAAT	TGGGCATTCA	AGACTTATCT	480
ACTCCTGTTG	GGGAATTGTC	AGGTGGTCTG	AGAAGACGGG	TACAGTTGGC	ACAAGTCTTA	540
CTTGGCAACC	ACGACCTCTT	GCTTTTGGAT	GAGCCGACCA	ACCATCTGGA	TATTGCGATT	600
ATTGAGTGGC	TGACCTCTTT	TTTGAAAAAT	TCTAAGAAGA	CCGTCCTTTT	TATCACTCAC	660
GATCGTTATT	TCTTAGACGC	TTTGTCAACA	CGGATTTTCG	AGTTGGATCG	TGCAGGCTTG	720
ACCGAGTACC	AGGGAAATTA	CCAGGACTAT	GTTCGCCTAA	AGGCGGAACA	GGATGAGCGC	780
GACGCGGCTC	TTCTTCACAA	AAAAGAACAA	CTCTACAAAC	AAGAATTGGC	CTGGATGCGC	840
AGACAACCGC	AGGCGCGTGC	GACCAAGCAA	CAAGCTCGTA	TCAATCGTTT	CCATGATCTG	900
AAAAAGGAAG	TTTCAGGCAG	TAGTGCTGAG	ACAGACTTGA	CTATGAAC TT	TGAAACCAGT	960
CGGATTGGGA	AGAAAGTCAT	CGAGTTTCAG	GCTGTTTCCT	TTGCCATATGA	AAATAAGCCC	1020
ATTTTGCAAA	ATTTTAATCT	CTTAGTTCAG	GCTAAAGACC	GTATTGGAAT	TGTTGGGGAC	1080
AATGGTGTTG	GAAAATCAAC	CCTACTTAAC	CTGATTGCAG	GAAGTCTTGA	GCCGACAGCA	1140
GGACAAGTTG	TGATTGGGGA	AACTGTTTCGC	ATCGCCTATT	TCTCTCAACA	AATTGAGGGT	1200
TTGGATGAAA	GCAAGCGTGT	GATCAATTAC	CTGCAGGAAG	TGGCAGAGGA	GGTCAAGACC	1260
AGTGGTGGTT	CTACGACTTC	CATCGCTGAG	TTGCTGGAGC	AATTCCTCTT	CCCACGTTTCG	1320
ACGCATGGGA	CTTTGATTGA	GAAATGTCTA	GGGGGTGAGA	AAAAACGTCT	TTATCTCCTC	1380
AAACTGCTTT	TGGAAAAACC	AAATGTTCTT	CTTTTAGACG	AGCCAACCAA	TGACCTAGAT	1440
ATTGCAACTT	TGACAGTCTT	AGAGAATTTT	TTGCAAGGTT	TTGCAGGTCC	CGTTTTAACA	1500
GTCAGTCACG	ACCGCTATTT	CTTGATAAAG	GTAGCGACCA	AGATTCTCGC	TTTTGAGGAT	1560
GGCAAGATTG	GTCCTTTCTT	TGGTCATTAC	ACCGACTATC	TTGATGAAAA	AGCTTTTGAA	1620
ACAGATATGG	CCAATCAAGT	GCAAAAAGGCC	GAAAAGGAAA	AAGTGGTCAA	GGTTCGAGAA	1680
GACAAGAAAC	GCATGACCTA	CCAAGAAAAG	CAGGAGTGGG	CAAGTATTGA	AGGTGATATT	1740
GAAACCTTGG	AAAAACGTAT	CGCTGCTATT	GAAGAGGAAA	TGCAGGCTAA	CGGCTCTGAC	1800
TTTGGTAAAGC	TGGCTACTCT	CCAAAAAGAA	TTGGATGAGA	AAAATGAAGC	ACTCCTTGAA	1860
AAATACGAAC	GCTATGAGTA	TCTCAGTGAA	TTTGATAGTT	AA		1902

(2) INFORMATION FOR SEQ ID NO:1489:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 819 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...819
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1489:

AAATGTCCAT	GTGGTCAAAG	ACTTGGAAGA	AGTGGAATC	TAGCAGTCAC	AGAAAGGATA	60
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AGTATGCCTA	CTATTCTCAT	TACCGGAGCT	AGCGGTGGTC	TAGCTCAAGA	AATGGTCAAA	120
CTCCTGCCCC	ATGACCAACT	CATCTTGCTT	GGTAGAAATA	AGGAAAAATT	AGCCCAACTC	180
TACGGAAATT	ATTCCCATGC	AGAATTGATT	GAAATTGATA	TTACCGACGA	TTCAGCCCTA	240
GAAGCTCTGG	TAAC TGATCT	TTATCTCCGC	TATGGCAAGA	TTGATGTCTT	GATTAACAAC	300
GCTGGTTACG	GGATTTTGA	GGGATTTGAC	CAGATTGCTG	ATAAAGATAT	TCACCAGATG	360
TTTGAGGTCA	ATACCTTTGC	CCTGATGAAT	CTGTCTCGTC	ACCTTGCGGC	TCGTATGAAG	420
GAAAGCAGCA	AAGGGCATAT	CATCAACATC	GTCAGCATGG	CAGGTCTAAT	AGCTACTGGC	480
AAGTCTAGTC	TTTACTCAGC	GACCAAGTTT	GCGGCTATTG	GTTTTTCAAA	TGCTCTGCGA	540
CTCGAACTTA	TGCCCTATGG	AGTCTATGTG	ACAACAGTCA	ATCCAGGTCC	AATCCGAACA	600
GGATTTTFTT	ACCAAGCTGA	CCCAGATGGA	ACTTATCTTA	AATCGGTTGA	CCGCTTCCTC	660
TTAGAGGCAG	ATGCAGTGGC	TAAAAAGATT	GTCAAGATTA	TAGGCAAAAA	TAAACGAGAA	720
CTCAATCTCC	CGATTTTGTT	GAACCTAGCC	CATAAGTTTT	ATACTCTCTT	TCCCAAGCTA	780
GCTGATAAGT	TGGCAGGGGA	AACTTTTAAT	TATAAGTAA			819

(2) INFORMATION FOR SEQ ID NO:1490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1392

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1490:

AGAGGTAAAT	GTATGCTAAG	ATTTCCAAAAG	GTATTTGTCT	GGGGATCCTC	TACTTCTGGA	60
CCGCAACAG	AAGGACTTGT	AGCTGGTGAC	GGTAAGGGAG	ACAATCTCTG	GGATTACTGG	120
TTCCAAGTGG	AGCCAAATCG	TTACTATAAT	GGGATTGGTT	CAGATAAGAC	ATCGACTTTT	180
TATGAAAATT	GGGAGCGGGA	TATTGAGCTT	TTGTTAGAGA	CTGGTCACAC	AGCCTTTCGG	240
ACTTCTATT	AGTGGTCACG	GATTTTTC	CAAGGCTGTG	GAAAAGTCAA	CACTCAAGGT	300
GTGGATTTT	ATCGTAAGGT	CTTTGAGGCT	ATTAAGGCTA	AAGGAATTCT	TCTGTTAGTC	360
AATCTCTATC	ATTTTGATTT	ACCTTTTGCC	CTTCAAGAGG	ATGGTGATGG	TTGGGAAAAT	420
AAGGCGACAG	TCTCAGCCTA	TGAAGACTAT	GCTCGTTTTT	GTTTTGAGAC	TTATGGAGAT	480
TTAGTGATC	AATGGATTAC	CTTTAAAGAG	CCCATCGTTC	CTGTAGAATT	TGGTTATTTT	540
TATGATGCCC	ATTATCCACA	TAAGGTGGAT	GCAGAGCCAG	CTGTTAAGGT	AGCCTATCAT	600
ACACAATTGG	CCAGCAGCCG	GGCTGTTAAG	GCTTGCCATG	AACTTTTGCC	TGATTCCAAG	660
ATTGGGATTG	TCCTCAACTT	GACACCGGCT	TATCCACGTA	GCCAGCATCC	TGCTGATGTC	720
AAGGCAGCTC	GTATTGCGGC	CCTTTTTCAG	GCCCAATCTT	TCTTAGATCC	ATCTGTCTTG	780
GGGACTTATC	CACAGGAGTT	GGTAGAAATC	TTGCATGAAC	ACGGTCTTTT	ACCTGATGCT	840
ACAGAGGAAG	AGTTGGAAC	CATTTCGTGAT	AATACGGTGG	ACTTCCTTGG	TGTCAACTAC	900
TATCAACCTT	TGCGTGTTAT	GGCTCCTCGA	TTTGCTAAGC	ATCCAGAGAG	TCCACTCTTA	960
CCAGAACATT	TTTACGAGCC	TTATGTGATG	CCTGGACGTA	AAATCAATTC	TCACCGTGGT	1020
TGGGAGATTT	ATGAGCAAGG	GATTTATGAC	ATCGCCCAAA	ATATCAAGGA	AAATTATGGC	1080
AATATTGAGT	GGATGTTGAC	TGAGAATGGT	ATGGGTGTTG	AAGGGGAAGA	AAAATTCCGT	1140
CAAGATGGAA	TGATTCAAGA	TGATTACCGT	ATTGACTTTG	TAAAAGGTCA	TCTTCGTGAA	1200

CTTCACCGTG CCATTGAAGA TGGTGCCAAC TGTAAGGGCT ACTTGATTTG GACCTTTATT	1260
GACTGCTGGT CATGGCTCAA CAGCTATAAA AATCGCTATG GTTTGGTCGA ATTAGACTTG	1320
GAAACGCAAG AACGTCGTCT GAAGAAATCA GGCCACTGGT TCAAAGAATT AAGCGATAAT	1380
AATGGATTTT AA	1392

(2) INFORMATION FOR SEQ ID NO:1491:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 243 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...243
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1491:

TTGCCAAAAT GGAAAAAGGT GAAAGGAATA TCACGAATGG ATTTAAGTAA TAAAGCTTCA	60
AATCTTAGAA AAAAGTTGGG AGCTGATGGT GAATCGCCGA TAGATATTTT TAAATTGGTA	120
CAAAAGATAG AAAATTTGAC GCTGGTATTT TATGGACTCG GAAAGAATAT TAGCGGAGTC	180
TGTTATAAAG GAACTCAGTT CAGTCTCATT GCAGTCAATT CAGACATGCC ATTAGGAAGG	240
TAA	243

(2) INFORMATION FOR SEQ ID NO:1492:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 861 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...861
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1492:

GAGGAAAAAT	GGATGAAAAA	ATGGATGAAA	AAATGGATGC	TTGTATTAGT	CAGTCTGATG	60
ACTGCTTTGT	TCCTAGTAGC	TTGTGGGAAA	AATTCCTAGCG	AAACTAGTGG	AGATAATTGG	120
TCAAAGTACC	AGTCTAACAA	GTCATTACT	ATTGGATTG	ATAGTACTTT	TGTTCCAATG	180
GGATTTGCTC	AGAAAGATGG	TTCTTATGCA	GGATTTGATA	TTGATTTAGC	TACAGCTGTT	240
TTTGAAAAAT	ACGGAATCAC	GGTAAATTGG	CAACCGATTG	ATTGGGATT	GAAAGAAGCT	300
GAATTGACAA	AAGGAACGAT	TGATCTGATT	TGGAATGGCT	ATTCCGCTAC	AGACGAACGC	360
CGTGAAAAGG	TGGCTTTCAG	TAACTCATAT	ATGAAGAATG	AGCAGGTATT	GGTTACGAAG	420
AAATCATCTG	GTATCACGAC	TGCAAAGGAT	ATGACTGGAA	AGACATTAGG	AGCTCAAGCT	480
GGTTCATCTG	GTTATGCGGA	CTTTGAAGCA	AATCCAGAAA	TTTTGAAGAA	TATTGTCGCT	540
AATAAGGAAG	CGAATCAATA	CCAAACCTTT	AATGAAGCCT	TGATTGATTT	GAAAAACGAT	600
CGAATTGATG	GTCTATTGAT	TGACCGTGTC	TATGCAAAC	ATTATTTAGA	AGCAGAAGGT	660
GTTTTAAACG	ATTATAATGT	CTTTACAGTT	GGACTAGAAA	CAGAAGCTTT	TGCGGTTGGA	720
GCCCCGTAAG	AAGATACAAA	CTTGGTTAAG	AAGATAAATG	AAGCTTTTTTC	TAGTCTTTAC	780
AAGGACGGCA	AGTTCCAAGA	AATCAGCCAA	AAATGGTTTG	GAGAAGATGT	AGCAACCAAA	840
GAAGTAAAAG	AAGGACAGTA	A				861

(2) INFORMATION FOR SEQ ID NO:1493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1493:

TGTAGAAAAT	GCAGAAGCAC	GTTTGCGTGC	AGCTCTATAA	ACATCAAGGC	TGGGAGCACT	60
TCCCAGTCTT	ATTCTATTTT	AATTTCAAAA	AGAAAGAAGA	AAGAAATGAA	AAAAATAGTT	120
CTTGTTAGTC	TAGCTTTCCT	TTTTGTCCCT	GTTGGTTGCG	GACAGAAAAA	AGAAACTGGA	180
CCAGCTACAA	AAACAGAAAA	AGATACGCTT	CAGTCGGCAT	TGCCAGTTAT	TGAAAAATGCT	240
GAGAAGAATA	CAGTTGTAAC	TAAGACTTTG	GTCTTGCCCA	AGTCAGATGA	TGGTAGCCAG	300
CAGACACAAA	CAATTACTTA	CAAAGACAAG	ACTTTTTTTGA	GTCTAACTAT	CCAACAAAAA	360
CGTCCAGTCT	CTGATGAGTT	GAAGACTTAT	ATTGACCAAC	ATGGAGTGGA	GGAAACTCAA	420
AAAGCTCTTC	TTGAAGCGGA	GGAGAAGGAT	AAGTCTATCA	TTGAAGCTCG	TAAATTGGCA	480
GGTTTCAAAC	TTGAAACAAA	ACTATTGAGC	GCAACGGAAC	TTCAAACAAC	GACTAGTTTTT	540
GATTTTCAAG	TTCTGGATGT	CAAAGAAGGT	TCCCCAAGTG	GGAACATCTG	A	591

(2) INFORMATION FOR SEQ ID NO:1494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1005 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1494:

AAAGGAGAAT	GTTTAGAGAT	GGGAAAATCA	GTTGCAATTT	TAATGACCAC	TTATAATGGT	60
GAGAGATATT	TGTCACAACA	GATTGATAGT	ATTAGGTCTC	AAACATTTAC	CAATTGGACG	120
CTTTTTTATTA	GAGATGATGG	ATCAAAAAGAT	AAGACAGTAG	AAGTAATACA	GAGGTATTCT	180
AAGATAGATG	ATAGAAATTAG	ATTAGTTGAA	AATCCCCTCAA	AGTTTCATGG	AGCTTATTAT	240
AATTTTTTTTA	ATCTAATTGA	ATACGTTAAA	AACAATTATC	AATTTGATTA	TTACTTTTTTT	300
TGTGATCAAG	ATGATATTTG	GAAAGAGCAC	AAGCTAGAAA	TACAGCTGTT	AAGATTTTCT	360
AAGGATGAAA	TGCCAGAGAT	GGTTTACTCT	GATATGTCAA	CGATTGATGC	CAATAATAAG	420
TTGATAGATA	TTAGTATAAA	TAACATAATG	GGGATTGAAT	TACCGAACAT	AAATAATTTG	480
TATTTTATTC	ATGCCTATAT	CTGGGGGTGT	ACGGCAGGCT	TTAATCATGC	ATTGTTAGAG	540
ATGGTTCCTT	CAGTTGATAT	TGATAAAGAT	TATTTATATA	TAGAAAAACT	GTCTCATGAT	600
AAATTATTTTG	CAAAGTTTGC	ACTAGAGTAT	GGGAAGGTGT	TGTTCTGCCC	TGAGCAACTG	660
GTCTTGATATC	GAAGACACGG	ACATAATGTA	ACAACTAGTC	ATCATTTTAA	ATTATCTCCG	720
CTAAATATTC	TCAGAAAGGC	TATTTTGGGT	TTCAATGAAT	TGGCACTTAC	ACATGCTGGG	780
GTATATAATC	AAACTCTTTA	TATGCTAAAA	AAAGCTTCTG	AAAAAAGTCC	TTTAAGTGAT	840
AGACTGCTTG	AAATTCAGGA	AGTAATCAAA	ATTGGAGGAT	TAAAAGGTGT	GAGATATTTT	900
TGTCAGAATC	GAATTTCTCG	AAAGCAACTC	GTAAGAACCA	TCGGCTTATA	TACCATCATG	960
CTTTTGGCA	CCTATANAAA	ATATATTATG	AAAGAGCTCT	CATAA		1005

(2) INFORMATION FOR SEQ ID NO:1495:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2031 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2031
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1495:

AATAAGGAAT	GCACTATGAA	AAAATTATTT	ATACTCATAT	CCAACCTGCT	TGCTAGTTTG	60
TTCTTTGTTT	GGGTATTTAC	CATTTGGACT	GATACATATG	TCTCCATTAT	TTACTCCAAC	120
GTTGTTGTAC	ATGATTCTTC	CCCTGAAACA	ACTTTTCAGC	ATGTTGCTAC	ACGCTTGGA	180
AAACTAGCAG	AAGAAACAGA	TAGCTTTATT	GCGATTCAAC	ACCAAGATCC	TAACTCAGAA	240
GGTACTACAG	TTTTTTCTTA	TACGACCTTT	GGGGACGGAA	AGTTGCCTGA	TGGGCTTCAG	300
GAAAAAAAC	TAGAAGATGC	TCAAAGTAGT	AGTGTTGAAA	CAAACTATTT	TGTATTTCGAT	360
GGACACCTAG	ATATTCACTT	GCTAAGGGAG	GAGCTAAGTC	AACCTGGCTT	GACTAACATG	420
AACCTGACAA	TTCCATCTAA	ACTATCTACG	TTAATGGCTA	TCTTTAGTAA	CGGATTTTCAG	480
TTAATCAGTC	TATTGATTTT	CATCTTAACC	TTTGTAGCAC	TGACTTTAAT	TAGTCAAATT	540
AGCCAATTAC	GGTCGTCGGG	CATTCGCCCTC	ATTTTCAGGAG	AGAAACGGTG	GTCCATTTTTC	600
CTTAGACCAG	TTGGTGAGGA	TTTGAAAGGG	ATAGCTGTTG	GTTTCAGTTT	AGCTGGCGTG	660
CTCGCCATTC	TTATGCAAAA	AATTCTGTCTG	CTTCCAACGC	AATCCCTAAT	GACCATAGGA	720
GCAGGCTTGC	TCAGTTATAA	TCTCATCTTG	TTGTGCGATCT	CCCTGTTTTT	CGCTCAACTC	780
TTTCGAGTTG	GGATAAAAAA	GATACACCTG	ATGCAGATTA	TAAAAGGGCA	AGTGCCTGTC	840
AGAGGAATCA	TTAGTTTGAT	TTTAATCGGT	CAACTATTAG	CGATTATTAT	TGTAACGCTG	900
GGAATAGGGA	GTAGCTTAAA	GTATTCCCAA	GCCTGGCAAC	AGCATCGGAT	TGGACAAGAG	960
GCTTGGAGTC	AGGAAAGGCA	ACTGATTACC	CTATCAATCA	GCCGTGAAGG	AACGAGTCCT	1020
GGTTTTGATG	AACAAGCTCA	AAGGAAACTC	AGAACTTGGT	ATCAATTGAT	GGATCTGGCT	1080
GTTTCAGAAC	AAAAGGCTTT	CTTATCTAGA	CACCAGTTAA	TTGACCGTAC	TTTGCAAAAT	1140
GGCATGGCTT	CCTCCAAAAA	CTTGATAACC	TCTACAGAAT	GGCACGATTA	CAACCCGAAT	1200
GGCAATGTCC	TTATCGTCAC	ACCGCAATAC	TTGGAGCGTC	AAAACATTCC	TGTAGATACA	1260
ACTATTGAGC	AAAAGATGAA	TCACCTTGAT	GTAGGGGAGT	TTGTCTTATT	GCTGCCTGAA	1320
CACCTCCGTT	CAGAGGAAGA	ACATTATAAA	TCTGTTTTTG	AAGACGACTT	AACCAGTCGC	1380
ATGTCTAGTC	AAGATGAACG	ACAGCAAATG	ACTGCTACGG	TAGGTTATTT	AGAATCAGGT	1440
CAGGATCGTT	TTGTGTATAA	TACGACCCCT	ATTTCTTACC	AGCAGTTTTT	GAAAGATCCA	1500
ATCATCATTG	TTATAACACC	CCAATCAACT	GGTCCACAGT	CCATTTTGTT	TTGGATAGAC	1560
GCAGTACAGA	ACTACGTTCT	CTTTAATCAA	TTGTCTGATG	CCCAGGAGCT	TATCCAGAGA	1620
CAAGGCATTG	AAAATTGGGT	CTCAGAAATG	CAAAACAGTT	ACCACAACTA	CATCACATTA	1680
TTGGATAATA	TCCAGAGGGA	ACGTTGGGTA	ATGCTAGCAG	GAGCTGTGCT	TGGGATTGCA	1740
ACTTCAATCT	TGTTGTTTAA	CACTATGAAT	AGGCTCTACT	TTGAAGAATT	TAGACGTGCC	1800
ATTTTTATCA	AACGCATTGC	AGGTCTCAGG	TTCTTAGAAA	TCCATCGCAC	TTATCTCTTT	1860
GCTCAACTGG	GTGTGTTTTT	ACTGGGATTT	GTTGCGAGTG	TATTTCTTCA	GGTAGAGATA	1920
GGAGTTGCTT	TCTTAGTCTT	GTTACTCTTT	ACTGGTCTAT	CTCTTTTACA	GTTACATGTC	1980
CAAATGCAGA	AAGAAAACAA	GATGTCCATT	CTTGTTTTGA	AGGGAGGTTA	A	2031

(2) INFORMATION FOR SEQ ID NO:1496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1496:

TCTTTTAGAT	GTTTATCAAG	GCGGGTCGAA	TGTCTTGGTA	AGACAGGTCA	ACTCTTCAGT	60
TTCCATGACA	ATCCGAATCC	AAATTGCCCT	GTAGGAGCTC	ATATTCATGA	TGTTTTGGAT	120
CAAAAATTGG	AGAGAAATCA	GTTGACTATG	GAGGCAGAAC	TTGGTCAAAC	CAGTCTAGAA	180
AAAGTCGTGG	CCGATGCAGA	GAGTCAGATG	AAGGATTAA			219

(2) INFORMATION FOR SEQ ID NO:1497:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 885 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...885
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1497:

GAAACTAGAT	GTGGATCCAC	TGGATTTTAAC	GGCATTTTTAC	AAAGAAAGGA	GAGAGGGATG	60
CAAGCTAAAT	TAATCGGTTA	CCAGCATAGA	GATACTGTGA	TTCATCGCTT	GTCAGGAGCT	120
GGGAAACTTC	TCTTTTTTCAT	TCTGGTATCA	TTGGCGGCCA	TGATTAGCTA	TGATACCAGA	180
ATGCTCTTGC	TGATTGCCAT	CTTTTCAGTC	TTTCTCCTCT	ATTTATCAGA	AATTCGCTTT	240
AAAGATGTTT	CCTTTGTAGC	CGTTTTTGCG	ACGGTATTTG	CCGTTTTTAA	CGTTTTGATG	300
GTCTATCTCT	TTTCTCCCGA	GTATGGGGTT	GGACTTTATG	GAGAGAGAAG	TGTGATTTGG	360
CAGGGGAATCG	GTGTCTACAC	TCTAACCAGC	CAGGAGCTCT	TTTATCTGCT	AAATTTGGCC	420
ATTAAGTATC	TTTGCACCAT	TCCTCTGGCT	ATTATCTTTT	TGATGACAAAC	CCATCCTAGT	480
CAGTTTGCTT	CCAGTTTAAA	TCAAATTGGT	GTGCCCTATA	AGATTGCTTA	TTCTGTCAGC	540
CTGACCTTGC	GCTATATTCC	AGATTTGACG	GAAGAATTCT	TTACTATCAA	GATGTCTCAG	600
GAGGCGCGTG	GGATGGAATT	ATCCAAGAAA	GCTTCTCTTA	TGCAACGAAT	CAAAGGCAAT	660
CTGCTCATTA	TTACGCCCTT	GATTTTTTAGC	TCGCTAGAAC	GCATTGATAC	CATTGCGACT	720
GCCATGGAGC	TTCGCCGCTT	TGGGAAAGAG	AAAAAACGCA	CATGGTATAG	TTATCAGGCC	780
TTGAAAAAAG	GAGACTATAT	TACCTTGCTC	TTGGCAACCT	TGTTTTTAGT	AGTTAGTTTA	840
CTACTTATCT	TGCAGAAATCA	GGGACGATTT	TACAACCCTT	GGAAA		885

(2) INFORMATION FOR SEQ ID NO:1498:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 549 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1498:

ACTGGTGGAT	GTGAACAAAT	GACACTTAAT	TATATCGAAA	TTTAAATCAA	ACTGGTCTTG	60
ACTCTCAAAT	GGCTCAACAA	CAATGTTTAC	TTTGTGAAAC	GTTTGATTGA	TGGTAAGCCA	120
ACTCTCCTTA	TCAAAAATGG	GAATATTGAC	CCAGAAGCCT	GTCGTTTCA	TGGTTTGTCT	180
GCATCGGATG	TAGCCCTCAA	ACTTCGTAGC	CAAGGGATTT	TCCAGATGAA	GCAAGTCAAA	240
CGAGCTGTGC	AAGAGCAAAA	TGGGCAACTT	ATCGTTGTGC	AAATGGGAGA	TGAAAAATCCT	300
AAGTATCCAG	TTGTGACTGA	CGGTGTGATT	CAAGTAGATG	TCTTGGAATC	GATTGGTTCGT	360
AGCGAAGAGT	GGTTGCTTGA	TAACCTCAGT	AAACAAGGGC	ATGACAATGT	AGCCAATATC	420
TTTATTGCTG	AATATGACAA	GGGTGCTGTT	ACAGTCGTAA	CTTATGAAAA	AGAAAAACCT	480
GGGGTCTTGT	ACTCTTCGAA	AATCTCTTCA	AACCGCGTCA	ACGTCGCCTT	GCCGTATGTA	540
GGTACTGA						549

(2) INFORMATION FOR SEQ ID NO:1499:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1499:

TTGGAAGGAT	GTCTATCTGA	GCTCTTTAGC	AAGGAGGAAA	TCCTTGAAAG	TGATATGCCA	60
GTAGCTATCA	TGAGCGAGTT	GATTGAAGCC	AGAAATAAGC	AAGGAATCAG	TCAGAAAAAG	120
CTAGAGGAAG	TCAGTGAGT	GAGTCAGCCT	GTTATAGCTA	GGATGGAGAC	AGGTAAGACT	180
AGTCCACAGT	TGGACACAGT	CTTAAAAGTC	CTAGCTAGTC	TAGGAAAGAC	ACTAGCAGTC	240
GTTCCACTTG	AACAGGGAAA	AAGTTGA				267

(2) INFORMATION FOR SEQ ID NO:1500:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1731 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1731
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1500:

GAATTGGGAT	GTGGCATTTC	TTTATCAGTG	ATATGTTGGA	ACCTGTCTAT	GAAATCATCC	60
ATGAAAAATT	GGCGACAAAA	TAGAATGAAG	CAGTTTTGGC	TACATACGCT	TCTAAGAACC	120
TATAGTTCAG	TGATGATCAT	TATCATTGCG	AGTTTTGCAA	TCTTACTCTC	TTACGCTGAC	180
TGGGATTTCAC	GTGAAAAGGA	AGCCCAGAGA	GTAGCCCAGC	GTGTAAC'TGC	TAGAACAGTG	240
AGTGAAATTG	AATATTACCA	TAGAGAGTCA	ACCCAGATAG	CTCAGGCTTT	AGTTGAAAAT	300
CAAGCTCGTA	TTGAGGGAAT	CTATAAATAC	TTTAGCCTTA	GCATGCCAGA	CTATTTTTAC	360
TGGCAATTAG	AGCGGAAAGC	TTTCGCCTTAT	ATATCAGTCT	CTCTGTATGA	AAATGTTGAT	420
GACCTCTATG	TTTCGAAATGA	TTTTGTAACT	GGGGTGGCCA	TTGCTTTTCA	AGATTACAAG	480
GAAGTCTATG	TTTCTACTAA	AGACAAACGT	AGTGGAGAAA	AAATCAGGGC	TGAGGATTTT	540
AAACCAGCAG	GAAATAGTTT	TGCCATTCCG	GTGTCAGATC	CAGTGTGAGA	TCAAGATTTA	600
GGAGTGATTT	ACATCTCCTT	GGATCCTGCT	GTTTTATACC	ATGCCATTGA	TAATACTAGA	660
GGTCATACTC	CGATGGCAGT	AACAGTGACC	TCACCTTTTG	ATACGGAGAT	TTTTTCATATT	720
GGTGAGACAG	TTGATAGGGA	GAGTGAAAAT	TGGCTAGTTG	GCTTAACTTC	TCATGGATAT	780
CAGGTTTCAGG	TGGCAGTTCC	TAAAAACTTT	GTTTTACAAG	GAACAGTGAC	TAGCTCTGCT	840
TTGATTGTGG	GTTTGAGCCT	TCTCTTTATT	GTCATTCTTT	ATCTGACTTT	GAGGCAGACT	900
TTTGCTAATT	ACCAAAAGCA	GGTAGTGGAT	TTAGTAGAAT	CCATTCAAGT	CATTGCTCAA	960
GGCGAAGAGG	GGCGTCGGAT	TGACATTTCC	GAGAAAGATC	AGGAATTACT	CCTAATCGCG	1020
GAGACGACCA	ATGATATGTT	GGATCGATTG	GAAAAGAATA	TCCATGATAT	TTACCAGTTA	1080
GAGCTTAGTC	AAAAAGATGC	CAATATGCGA	GCCTTGCAGG	CGCAAATCAA	TCCTCATTTT	1140
ATGTATAATA	CGCTGGAGTT	CTTGCGCATG	TATGCAGTTA	TGCAGAGTCA	AGATGAGTTG	1200
GCAGATATCA	TTTATGAATT	CAGTAGTCTC	TTGCGTAACA	ATATTTCCGA	CGAAAGAGAG	1260
ACCTCCTCA	AACAGGAATT	AGAATTTTGC	CGTAAATACA	GCTATCTCTG	CATGGTTCGC	1320
TATCCCAAGT	CCATTGCCTA	TGGTTTCAAG	ATAGATCCAG	AGTTAGAGAA	TATGAAGATT	1380
CCCAAGTTTA	CCTTGCAACC	GCTGGTAGAA	AACTATTTTCG	CGCATGGTGT	TGACCACAGG	1440
CGGACAGATA	ATGTGATTAG	CATCAAGGCT	CTTAAACAGG	ATGGTTTTGT	GGAAATTTTG	1500
GTGGTCGATA	ATGGTAGAGG	AATGTCGGCT	GAAAAGTTGG	CAAATATCCG	AGAAAAATTA	1560
AGTCAGAGAT	ATTTTGAACA	CCAAGCCAGC	TACAGTGATC	AAAGGCAGTC	TATCGGGATT	1620
GTCAATGTAC	ACGAGCGTTT	TGTGCTCTAT	TTTGGAGACC	GCTATGCCAT	TACTATAGAG	1680
TCTGCAGAGC	AAGCCGGTGT	TCAGTATCGT	ATTACAATTC	AAGATGAGTA	G	1731

(2) INFORMATION FOR SEQ ID NO:1501:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 489 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1501:

CTGTTTTTGT	GTCGTTTAAG	GGAAAGGACA	AGAATGACTC	AACAAGACTT	TCGGACAAAA	60
GTAGACAATA	CGGTTTTTGG	TGTTTCGGGCG	ACAGCTTTGA	TTCTTCAAAA	TCGCAAGCTT	120
CTAGTCACCA	AAGACAAGGG	CAAGTATTAC	ATTATCGGCG	GTGCGATTCA	AGTTAACGAA	180
AAAACGGAAAG	ACGCGGTAGT	CCGTGAAGTG	AAGGAAGAAC	TGGGTGTTAA	ATCTCAAGCT	240
GGGCAGCTAG	CTTTTGTGGT	TGAAAATCGT	TTTGAAGTGG	ACGGCGTTTC	CTATCACAAT	300
ATCGAGTTTC	ATTATCTGGT	GGATTTGCTT	GAAGATGCCC	CGTTGACCAT	GCAGGAAGAT	360
GAGAAAAGGC	AGCCCTGTGA	GTGGATTGAC	TTGGATAAGC	TCCAGAATAT	CCAGCTAGTT	420
CCAGCCTTTT	TAAAAACAGC	CCTACCAGAT	TGGGAAGGCC	AACTAAGACA	CATTCATCTT	480
GAGGAATAG						489

(2) INFORMATION FOR SEQ ID NO:1502:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1257 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1502:

CTGGTATTGT	GGAGCTACAA	AATGCTTAAA	CGCTTATGGA	TGATCTTCGG	ACCGGTCTTG	60
ATCGCTGGTT	TGTTGGTTTT	TCTGCTCATT	TTCTTTTATC	CTACTGAGAT	GCATCATAAT	120
CTAGGAGCTG	AAAAGCGTTC	AGCAGTGGCT	ACTACTATCG	ATAGTTTTTA	GGAGCGAAGT	180
CAAAAAGTCA	GAGCACTATC	TGATCCAAAT	GTGCGTTTTG	TTCCCTTCTT	TGGCTCTAGT	240
GAATGGCTTC	GTTTTGACGG	TGCTCATCCT	GCGGTATTAG	CTGAGAAATA	CAATCGTTCC	300
TACCGTCCTT	ATCTTTTAGG	ACAGGGGGGA	GCTGCATCGC	TTAACCAATA	TTTTGGAATG	360
CAACAGATGT	TACCACAGCT	GGAGAATAAA	CAAGTTGTGT	ATGTTATCTC	ACCTCAGTGG	420
TTCACTAAAA	ATGGCTATGA	TCCAGCAGCC	TTCCAGCAGT	ATTTTAATGG	AGACCAGTTG	480
ACTAGTTTTT	TGAAACATCA	ATCTGGAGAT	CAGGCTAGTC	AATATGCAGC	GACTCGCTTA	540

CTGCAACAGT	TCCCAAACGT	AGCTATGAAG	GATCTGGTTC	AGAAGTTGGC	AAGTAAAGAA	600
GAATTGTCGA	CAGCAGACAA	TGAAATGATT	GAATTATTGG	CTCGTTTTAA	TGAACGCCAA	660
GCCTCCTTTT	TTGGTCAGTT	TTCGGTTAGA	GGCTATGTTA	ACTACGATAA	GCATGTAGCT	720
AAGTATTTAA	AAATCTTGCC	AGACCAGTTT	TCTTATCAAG	CAATAGAAGA	TGTTGTCAAA	780
GCAGATGCTG	AAAAAAATAC	TTCCAATAAT	GAGATGGGAA	TGGAAAATTA	TTTCTATAAT	840
GAGCAGATCA	AGAAGGATTT	GAAGAAATTA	AAGGATTCTC	AGAAAAGCTT	TACCTATCTC	900
AAGTCGCCAG	AGTATAATGA	CTTGCACTTG	GTTTTAACAC	AGTTTTCTAA	ATTTAAGGTA	960
AACCCGATTT	TTATCATTCC	ACCTGTTAAT	AAAAAATGGA	TGGACTATGC	TGGTTTACGA	1020
GAGGATATGT	ACCAACAAAC	GGTGCAGAAG	ATTCGCTACC	AGTTAGAAAAG	TCAAGGTTTT	1080
ACCAATATAG	CAGATTTTTT	TAAGGACGGC	GGGGAGCCTT	TCTTTATGAA	GGACACCATT	1140
CACCTTGGTT	GGTTGGGTTG	GTTGGCTTTT	GACAAGGCAG	TTGATCCTTT	CCTATCCAAT	1200
CCCACACCAG	CTCCGACTTA	CCATCTGAAT	GAGTTTTTTT	CAGCGACCTT	GGGGCCT	1257

(2) INFORMATION FOR SEQ ID NO:1503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1503:

AACCTTCTGT	GTTATACTAG	AGATATGTTA	GATTTGAAAG	AATACGGTAT	CGTCATGTGG	60
CCGGAGGAGA	AAGTCATTTT	TTTCCGTGAG	AAACTTCTCG	CTTGGGTATGA	TGAAAACAAA	120
AGAGATTTGC	CTTGAGGAG	AAGTAAAAAT	CCTTATCACA	TCTGGGTATC	TGAAATCATG	180
CTTCAGCAGA	CCAGGGTGGA	TACAGTTATC	CCTTACTACG	AAAGATTCCCT	GGACTGGTTT	240
CCAACTGTCG	AAAGTCTGGC	AACTGCGCCT	GAGGAGAGTT	TACTGAAAGC	TTGGGAGGGC	300
TTGGGCTATT	ATTCTCGAGT	TCGCAATATG	CAGGCTGCAG	CCCAGCAGAT	TATGACTGAC	360
TTTGGTGGCC	AATTTCCAAA	TACCTATGAA	GGAAATTTCCA	GCTTGAAAGG	GATTGGACCT	420
TACACAGCAG	GAGCCATTTT	CAGTATTGCT	TTTAACTTGC	CTGAGCCAGC	TGTAGATGGT	480
AATGTCATGC	GGGTCTTGGC	GCGTCTGTTT	GAAGTCAACC	ACGATATTGG	GATTCCAAGT	540
AATCGAAAAA	TTTTTCAGGC	AATGATGGAG	ATCTTGATTA	ATCCGGATCG	TCCGGGTGAT	600
TTTAATCAAG	CCTTGATGGA	CTTAGGGTCT	GATATTGAGT	CTCCTGTAAA	TCCCAGACCT	660
GAAGAAAAGCC	CAGTCAAGGA	CTTTAGTGCG	GCATATCAGA	ATGGAACCAT	GGACCGTTAT	720
CCAATTAAAT	CTCCTAAGAA	AAAGCCGGTT	CCTATTTATC	TTAAAGCCTT	AGTTGTGAAA	780
AATTCTCAAG	GACAATTTTT	ACTTGAAAAA	AATGAAAGCG	AAAAGCTCTT	GGCAGTTTTT	840
TGGCATTTCC	CCTTTATAGA	AGTTGATAAC	TTTTTCGCAAG	AAGAGCAGTT	TGACCTCTTT	900
CATCAGGTTG	CGGAAGAAAG	TGTGAACTTT	GGCCCCAGTC	CAGAAGAGAG	TTTCCAGCAG	960
GACTATGACC	TAGATGTTGA	TTGGCTTGAT	GTTTGTTTTG	ATACAGTCCA	GCATGTTTTT	1020
AGTCATCGAA	AATGGCATGT	ACAGATTGTA	GCAGGTCAGG	TGAGTGACTT	CCATGATTTT	1080
TCAGATAGGG	AAGTTCGTTG	GCTTTCACCA	GAAGAATTCA	AGAATTACCC	ACTTGCCAAA	1140
CCCCAACAAA	AAATTTGGCA	GGCTTATGCA	CAAGCCAACT	TAGACAGTAG	CCAAGACTAG	1200

(2) INFORMATION FOR SEQ ID NO:1504:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1104 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1104
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1504:

ATAATCATGT	GGCTACAACA	TCTATCTCTC	AAGACTTTTC	GTAATTACAA	AGAAACGAAA	60
ATAGACTTTA	ATCCTAAATT	GAATGTCTTT	TTGGGACGTA	ATGCACAAGG	AAAAACAAAC	120
ATGTTAGAGG	CTATCTATTT	TTTAGCCTTA	ACGCGTAGTC	ATCGAACTCG	AACAGATAAA	180
AATCTCATTC	ATTTTGATGA	GGAACAACTT	CATCTTTCAG	GTCTCGTTCA	GAAAAAAACT	240
GGATCCATTC	CCCTAGAAAT	CGAACTAACA	CAAAAAAGGCC	GTGTAACAAA	AGTTAATCAC	300
TTAAAAACAGG	CACGCCTTTC	AGATTATGTA	GGACACATGA	ATGTTGTCTT	ATTTGCTCCT	360
GAAGATTTAC	AACTAATTAA	AGGAGCACCT	TCGATTCGAC	GAAAATTCAT	TGATATGGAA	420
CTTGGGCAAA	TTAAGCCAAT	CTATTTATCT	GACTTAACCA	ATTATAACCA	CATCCTAAAG	480
CAAAGAAACA	CTTACCTAAA	ATCAGCTCAA	AAAATAGATG	AAACATTCCT	TTCTGTGTTA	540
GATGATCAGC	TAGTTGATTA	TGGATGTCGT	GTAATGAATC	ACCGCTTAGA	TTTCATAAAA	600
AAACTAGAAT	CATTTGGGCG	TAAGAAACAT	TTTGAACCTC	CTAATCAGAT	CGAAGAGTTG	660
TCAATATCCT	ATCAATCTTC	TGTCAATATA	ACTGACAAAC	AAAACTTATC	CGAATCTTTC	720
AAAATTGCTT	TAGAAAAAAG	TAGATCCAGA	GATTTATTTA	AAAAGAATAC	TGGTGTCGGT	780
CCTCATCGAG	ATGACATTTT	TTTTTATATA	AATGGGATGG	ATGCTAGTTT	CGGAAGCCAA	840
GGTCAACATC	GTAGTCTCGT	CCTCTCGATA	AAATTAGCAG	AAATCGAATT	AATGGAAAGC	900
ATTACCACAG	AATCTCCGAT	ATTACTGCTT	GACGATGTGA	TGAGTGAAC	TGACAACACT	960
AGACAGTTAA	AATTATTAGA	AACGATTTCT	CAATCAATCC	AAACCTTTAT	CACAACAACA	1020
AGCTTAGACC	ATCTTCAAAA	TCTGCCAGAA	AATCTAAGTA	TCTTCACTAT	TCAGGATGGT	1080
AAAGCTGCTG	TAAATGGAAA	TTGA				1104

(2) INFORMATION FOR SEQ ID NO:1505:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1505:

TACACAATGT	GGTATAATCT	TCTTATGGCA	TATTCAATAG	ATTTTCGTAA	AAAAGTTCTC	60
TCTTATTGTG	AGCGAACAGG	TAGTATAACA	GAAGCATCAC	ACGTTTTCCTA	AATCTCACGT	120
AATACCATTT	ATGGCTGGTT	AAAGCTAAAA	AAGAAAACAG	GAGAGCTAAA	CCACCAAGTA	180
AAAGGAACAA	AACCAAGAAA	AGTTGATAGA	GATAGACTTA	AAAACATCT	TACTGACAAT	240
CCAGACGCTT	ATTTGACTGA	AATAGCTTCT	GAATTTGGCT	GTCATCCAAC	TACCATCCAC	300
TATGCGCTCA	AAGCTATGGG	CTACACTCGA	AAAAAAGAAC	CACACCTACT	ATGA	354

(2) INFORMATION FOR SEQ ID NO:1506:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1506:

TACACAATGT	GGTATAATCT	TCTTATGGCA	TATTCAATAG	ATTTTCGTAA	AAAAGTTCTC	60
TCTTATTGTG	AGCGAACAGG	TAGTATAACA	GAAGCATCAC	ACGTTTTCCTA	AATCTCACGT	120
AATACCATTT	ATGGCTGGTT	AAAGCTAAAA	GAGAAAACAG	GAGAGCTAAA	CCACCAAGTA	180
AAAGGAACAA	AACCAAGAAA	GGTTGATAGA	GATAGACTTA	AAAACATCT	TACTGACAAT	240
CCAGACGCTT	ATTTGACTGA	AATAGCTTCT	GAATTTGGCT	GTCATCCAAC	TACCATCCAC	300
TATGCGCTCA	AAGCTATGGG	CTACACTCGA	AAAAAAGAAC	CACACCTACT	ATGA	354

(2) INFORMATION FOR SEQ ID NO:1507:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1507:

TACACAATGT	GGTATAATCT	TTTTATGGCA	TATTCAATAG	ATTTTCGTAA	AAAAGTTCTC	60
TCTTATTGTG	AGCGAACAGG	TAGTATAACA	GAAGCATCAC	ACGTTTTCCTA	AATCTCACGT	120
AATACCATTT	ATGGCTGGTT	AAAGCTAAAA	GAGAAAACAG	GAGAGCTAAA	CCACCAAGTA	180
AAAGGAACAA	AACCAAGAAA	AGTTGATAGA	GATAGACTTA	AAAACATATCT	TACTGACAAT	240
CCAGACGCTT	ATTTGACTGA	AATAGCTTCT	GAATTTGGCT	GTCATCCAAC	TACCATCCAC	300
TATGCGCTCA	AAGCTATGGG	CTACACTCGA	AAAAAAGAAC	CACAGCTACT	ATGA	354

(2) INFORMATION FOR SEQ ID NO:1508:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 897 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1508:

AAGCGGATGT	GGATTAGGAG	TAGAGAGACT	ATGAAAAAAG	TATTACAAAA	ATATTGGGCA	60
TGGGCTTTTG	TGGTCATCCC	CCTCTTGTTA	CAAGCAATTT	TCTTCTATGT	GCCGATGTTT	120
CAAGGAGCCT	TTTACAGTTT	TACCAACTGG	ACAGGATTGA	CTTACAACCTA	CAAATTTGTC	180
GGCTTAAACA	ACTTTAAGCT	CCTCTTCATG	GATCCAAAAT	TCATGAATGC	GATTGGCTTT	240
ACCGCAATCA	TTACGATTGC	CATGGTGGTT	GGTGAGATTG	CACCTCGGGAT	CTTCATTGCG	300
CGTGTCTTGA	ACTCTAAAAT	CAAAGGCCAA	ACCTTCTTCC	GTGCTTGGTT	CTTCTTCCCA	360
GCTGTTTTAT	CTGGTTTGAC	AGTGGCTTTG	ATCTTCAAGC	AAGTCTTCAA	CTACGGTCTT	420
CCAGCGATTG	GGAATGCCCT	TCATATTGAA	TTTCTCCAAA	CCAGTCTTTT	AGGGACTAAG	480
TGGGGAGCAA	TCCTTGCGGC	TGTCTTTGTC	CTTCTTTGGC	AAGGGGTGGC	TATGCCCATC	540
ATCATCTTCC	TAGCTGGTTT	GCAATCTATT	CCAACCTGAGA	TTACAGAGGC	AGCAAGGATT	600
GATGGTGCGA	CTAGCAAGCA	AGTTTCTCTG	AACATTGAAT	TGCCCTTACTT	GCTACCAAGT	660
GTCTCTATAG	TCCTTATCCT	AGCCCTAAAA	GGTGGGCTGA	CTGCCTTTGA	CCAAGTCTTT	720
GCCATGACCG	GTGGTGGTCC	AAACAATGCC	ACAACCTCAC	TTGGGCTCTT	GGTTTATAAC	780

TATGCCTTTA AAAACAACCA ATTCGGTTAT GCCAATGCCA TTGCCGTAAT CTTGTTCTTC	840
TTAATTGTAG TGATTTTCGAT CATCCAATTG AGAGTATCTA AGAAATTTGA AATTTAA	897

(2) INFORMATION FOR SEQ ID NO:1509:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1509:

TTGCTGCAGT GCGCAAATGG CTCTCTTAAT TTAGAAAAAC TAGAAGCTAT GACGGCTATC	60
TGTTCTGTTG GATTGGATAT GATTGCCATC CCAGAAGATA CGCCTGCTGA AACTATTGCG	120
GCTATGATTG CGGATGAAGC AGCAATCGGT GTTATCAACA TGAAAACAAC AGCTGTTCGT	180
ATCATTCCCA AAGGAAGAGA AGGCGATATG ATTGAGTTTG GTGGTCTATT AGGAACTGCA	240
CCCGTTATGA AGGTTAATGG GGCTTCGTCT GTCGACTTCA TCTCTCGCGG TGGACAAATC	300
CCAGACCAA TTCATAGTTT TAAAAATTAA	330

(2) INFORMATION FOR SEQ ID NO:1510:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 678 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1510:

GAGGTAAAGT	GTATGAATCA	AGATAGGAAT	AAACTGCTTT	CTAAAAATTGC	TTATCTGTAT	60
TATATTGAAA	ACTTAAATCA	GTCACAAATA	GCAGCAAAAT	TAGGAATTTA	TAGAACCCTCT	120
ATTAGTAGAA	TGTTAACAGA	AGCAAGGAAT	GTAGGAATTG	TTAAAAATTGA	AATAGAGAAT	180
TTTGATACAA	ATATGTTTAA	GTTGGAAAAT	TATGTAAAAG	AAAAATACAG	TTTGGAAAGT	240
TTAGAAAATTA	TTCCAAATGA	ATTTGATGAT	ACTCCAACAA	TTTTATCTGA	AAGAATTTCT	300
CAAGTTGCAG	CAGGCGTCCT	TAGGAATCTA	ATTGATGATA	ATATGAAAAT	TGGCTTTTCT	360
TGGGGGAAAA	GTTTAAGTAA	TTTAGTAGAT	TTAATTCACA	GTAAAAGTGT	CCGAAATGTT	420
CACTTCTATC	CTCTAGCAGG	TGGTCCTAGT	CACATACACG	CTAAATACCA	TGTGAATACA	480
CTGATTTATG	AAATATCTAG	AAAATTTTCAT	GGAGAGTGTA	CATTTATGAA	TGCAACGATT	540
GTGCAAGAAA	ATAAATTGTT	AGCAGATGGT	ATTTTGTCAAT	CAAGATATTT	TGAAAAATTTG	600
AAAAATAGTT	GGAAAGATTT	AGATATAGCT	GTAGTCGGAA	TTGGTGATTT	TAGCAATAAA	660
GGAAAACATC	AATGGTAG					678

(2) INFORMATION FOR SEQ ID NO:1511:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 816 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...816
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1511:

GATTGCAAGT	GGATTATCAG	AAGGATCTGT	GAAGTAGACG	AAAGAAGGAA	AAAAATGAAT	60
AAAAGAGGTC	TTTATTCAAA	ACTAGGAATT	TCTGTTGTAG	GCATTAGTCT	TTTAATGGGA	120
GTCCCACTT	TGATTTCATGC	GAATGAATTA	AACTATGGTC	AACTGTCCAT	ATCTCCTATT	180
TTTCAAGGAG	GTTTCATATCA	ACTGAACAAT	AAGAGTATAG	ATATCAGCCC	TTTGTTATTA	240
GATAAATTGT	CTGGAGAGAG	TCAGACAGTA	GTAATGAAAT	TTAAAGCAGA	TAAACCAAAC	300
TCTCTTCAAG	CTTTGTTTGG	CCTATCTAAT	AGTAAAGCAG	GCTTTAAAAA	TAATTACTTT	360
TCAATTTTCA	TGAGAGATTC	TGGTGAGATA	GGTGTAAGAA	TAAGAGACGC	CCAAAAGGGA	420
ATAAATTATT	TATTTTCTAG	ACCAGCTTCA	TTATGGGGAA	AGCATAAAGG	ACAGGCAGTT	480
GAAAATACAC	TAGTATTTGT	ATCTGATTCT	AAAGATAAAA	CATACACAAT	GTATGTTAAT	540
GGAATAGAAG	TGTTCTCTGA	AACAGTTGAT	ACATTTTTCG	CAATTTCAAA	TATAAATGGT	600
ATAGATAAGG	CAACACTAGG	AGCTGTTAAT	CGTGAAGGTA	AGGAACATTA	CCTCGCAAAA	660
GGAAGTATTG	GTGAAATCAG	TCTATTTAAC	AAAGCAATTA	GTGATCAGGA	AGTTTCAAAAT	720
ATTCCCTTGT	CAAAATCCATT	TCAGTTAATT	TTCCAATCAG	GAGATTCTAC	TCAAGCTAAC	780
TATTTTAGAA	TACCGACACT	ATTGAAAGTT	CTATAA			816

(2) INFORMATION FOR SEQ ID NO:1512:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 936 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1512:

GATATGAAGT	GGACAAAAAG	AGTAATCCGT	TATGCGACCA	AAAATCGGAA	ATCGCCGGCT	60
GAAAAACAGAC	GCAGAGTTGG	AAAAAGTCTG	AGTTTTATAT	CTGTCTTGGT	TTTTGCCATT	120
TTTTTTAGTCA	ATTTTGCGGT	CATTATTGGG	ACAGGCACCTC	GCTTTGGAAC	AGATTTAGCG	180
AAGGAAGCTA	AGAAGGTTCA	TCAAACCAACC	CGTACAGTTC	CTGCCAAACG	TGGGACTATT	240
TATGACCGAA	ATGGAGTCCC	GATTGCTGAG	GATGCAACCT	CCTATAATGT	CTATGCGGTC	300
ATTGATGAGA	ACTATAAGTC	AGCAACGGGT	AAGATTCTTT	ACGTAGAAAA	AACACAATTT	360
AACAAGGTTG	CAGAGGTCTT	TCATAAGTAT	CTGGACATGG	AAGAATCCTA	TGTAAGAGAG	420
CAACTCTCGC	AACCTAATCT	CAAGCAAGTT	TCCTTTGGAG	CAAAGGGAAA	TGGGATTACC	480
TATGCCAATA	TGATGTCTAT	CAAAAAAGAA	TTGGAAGCTG	CAGAGGTCAA	GGGGATTGAT	540
TTTACAACCA	GTCCCAATCG	TAGTTACCCA	AACGGACAAT	TTGCTTCTAG	TTTTATCGGC	600
CTAGCTCAGC	TCCATGAAAA	TGAAGATGGA	AGCAAGAGCT	TGCTGGGAAC	CTCTGGAATG	660
GAGAGTTCCT	TGAACAGTAT	TCTTGCAGGG	ACAGACGGCA	TTATTACCTA	TGAAAAGGAT	720
CGTCTGGGTA	ATATTGTACC	CGGAACAGAA	CAAGTTTCCC	AACGAACGAT	GGACGGTAAG	780
GATGTTTATA	CAACCATTTC	CAGCCCCCTC	CAGTCCTTTA	TGGAAACCCA	AATGGATGCT	840
TTTCAAGAGA	AGGTAAAAGG	AAAGTACATG	ACAGCGACTT	TGGTCAGTGC	TAAACAGGG	900
GAAATTCTGG	CAACAACGCA	ACGACCCGAC	CTTTGA			936

(2) INFORMATION FOR SEQ ID NO:1513:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1038 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1038
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1513:

AATAAGGAGT	GGAATATGAC	AGTAACGATT	GATTGGGAAA	ACCTCGGTTT	TTCCTATATG	60
AAATTACCTT	ATCGCTATCT	TGCTCATTTT	AAAAATGGAC	AATGGGATCA	AGGAGAGCTT	120
ACAGAGGATG	CAACTTTGCA	TATTTTCAGAG	TCTTCTCCAA	GTCTTCACTA	TGGACAACAA	180
GCATTTGAAG	GTTTGAAAGC	TTATCGTACT	AAGGATGGCA	GTGTTCAACT	GTTCCGTCCT	240
GATGAAAATG	CTAAACGTCT	GCAACGTACA	TGTGACCGTC	TCTTGATGCC	ACAAGTTCCG	300
ACAGACATGT	TTGTAGAAGC	TTGTAAAGCA	GTTGTCCGTG	CGAATGAAGA	ATACGTACCA	360
CCATACGGAA	CAGGTGGAAC	CTTATATCTT	CGCCCTCTTT	TGATTGGTGT	CGGAGATATT	420
ATCGGGGTAA	AACCGGCAGA	AGAGTACATT	TTCACCATCT	TTGCTATGCC	AGTTGGAAAT	480
TACTTTAAAG	GCGGTTTGGT	CCCAACCAAC	TTCTTGATTG	AGGATGAGTA	CGACCGTGCA	540
GCACCAAATG	GTACAGGTGC	GGCTAAGGTT	GGTGGAAACT	ATGCTGCAAG	TCTCTTACCA	600
GGAAAAATGG	CCAAGTCACG	TCATTTCTCA	GATGTTATCT	ATCTGGACCC	ATCAACTCAT	660
ACAAAGATTG	AAGAAGTCGG	ATCAGCTAAC	TTCTTTGGAA	TTACAGCTGA	TAATGAATTT	720
GTAACACCAT	TGAGTCCATC	TATCTTGCCA	TCTATTACCA	AGTATTCCTT	GCTTTATTTG	780
GCAGAACATC	GCTTGGGATT	AACTCCTATT	GAGGGTGATG	TTCCAATTGA	TAATCTTGAC	840
CGTTTTGTAG	AGGCAGGTGC	CTGTGGTACA	GCAGCGGTTA	TTTCTCCAAT	TGGAGGTATT	900
CAACATGGTG	ATGATTTCCT	TGTATTCTAT	AGTGAAACAG	AAGTAGGTCC	TGTGACGCGT	960
AAATTATATA	ATGAATTGAC	GGGTATTGAG	TTTGCGGATA	TTGAAGCGCC	AGAAGGTTGG	1020
ATTGTAAAAG	TAGATTAA					1038

(2) INFORMATION FOR SEQ ID NO:1514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1514:

GAAAGTTGGT	GTTTGATGAA	AATTTTAGCT	ATTGATCCAA	GTAGTAATAA	AATTGAAACC	60
AGCACAACAG	GAGTTGTCTT	GTTGGATAAT	GCAAGATTAG	TTGATAGCTG	GGTTGTCTCT	120
TATGGTATGA	GAGGTTTCGC	TGATTGGTTT	CACGAAATCG	GAACAAATCT	TGAATTTCGAT	180
GTAGTTATTG	TTGAAGAATT	TAAGGCGAGG	GATAACGACA	AGTCGAAAGA	TAATAGCGTG	240
GCAGAAACCA	TCGCCTATAT	CCAACTTTGC	TATCCAGGTG	CCATTCTTCA	ATTCAATGCA	300
GGTTACAAGT	CGGATATTCC	AAACGATCTT	TTGAAAATCT	TAGACCTTTG	GAAATTTGAA	360
AAAAGTCATC	ATCAAGATAT	TCGAGCAGCA	GCAAGACTTG	GATTATTTTG	GGCAATGAGA	420
AATGATATTG	AAGAAGTGGT	TCATGATATC	GGAAAGGTGG	TGAGTGAGTA	TCACAATAAC	480
GCTAAGAAAG	TGGCAAGCTG	A				501

(2) INFORMATION FOR SEQ ID NO:1515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...363
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1515:

GGGGGCCCGT GTGGGCTGGT GCGGAGTGG GGGGGGTGTG CGGGGGCGGG GTGGGGCGGT	60
GAGGCCCGTG CCGTGTGGGC CCGGGGTGGG GCGGCCGATT CCTGCGGGGG GGGGCGTGGG	120
GGGGTTGGCG TCGGCGGGC GGTGGTGGGG GTGGGGGGGG GGAGTTGCTC GCGCGCGGTG	180
GGGATTGGC CGCGTGAGG GGGCGGCAT GCGGGGGAAC GGGGGGTGGA GGGAAAGTGGG	240
GTGGCCGGGG TTGAGGCGGG GCGGTCCGG GGACGGGTGG AGTGGGGTGA GTGGGGGGCA	300
GTTGGTGTGA GGAGGGCCGT GTCGGCAGGG AGATATGGGC TGCACGGATG TGTGCCGTGG	360
TGA	363

(2) INFORMATION FOR SEQ ID NO:1516:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...330
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1516:

AAGTCTAGGT GGGCCGACA AGCTCTGCTA GTTGGTTCTC AACCGGTTGC TGCCAATGAA	60
CACCATGCTA TTCTTGCTTT TGAGTCTAAC TTCAATGCTG GTCAAACAT GAAACGAGAC	120
AATCTCAATA CCATGTTTGG TAATATCCTC AGTCAGGCGG CAGGTTTTTC ACCTGAGATT	180
TTAGCTATTT CCATGGAGGA ATGGAAAGAA GTTCGCGCAG CCTTTTCAGC CAAAGCCAAA	240
TCTTCTCAA CTGAAAAAGA AGTAGAAGAA AGCCTGATTC CAGAAGGATT TGAATTTTGG	300
GCTGATAAAG TGAAGGTAGA GGAAGACTAA	330

(2) INFORMATION FOR SEQ ID NO:1517:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 864 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...864
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1517:

GAAAAGAGGT	GTCCTATGAT	TAAAAAAATT	TACCCCATTT	TTACCATTTT	ACTAGGTGCT	60
GCTATTTATG	CTTTTGGA	GACTTATTTT	GTAAGTCCCC	ATCATCTCTT	TGAAGGAGGG	120
GCGACAGGTA	TTACCCTCAT	CACATTTTAT	CTTTTAAAA	TCCCTGTTTC	CCTCATGAAC	180
CTGCTGATTA	ATATTCCCTT	TTTCATCCTA	GCTTGGAAGA	TCTTTGGAGC	CAAATCCCTC	240
TATTCTAGTT	TACTAGGAAC	CTTAGCTTTG	TCCGGCTGGT	TAGCTTTTTT	TGAGCATATT	300
CCCCTTCATA	TTGATCTTCA	AGGTGATTTA	CTAATCACAG	CCCTTATAGC	GGGAATCCTA	360
TTGGGAATTG	GCCTTGGAAT	TATTTTAAAT	GCTGGAGGTA	CAACTGGCGG	AACTGATATT	420
CTAGCTCGTA	TTCTCAACAA	ATACACTCAT	ATATCCATAG	GAAAACTGCT	CTTTATCTTA	480
GATTTTGTGA	TTCTCATGTT	GATTCTCCTA	ATCTTCAAGG	ATTTGAGATT	GGTTTCCTAC	540
ACGCTTTTGT	TTGATTTTAT	TGTTTCTCGT	GTTATTGATT	TGATTGGTGA	AGGAGGATAT	600
GCCGGCAAAG	GCTTTATGAT	TATCACAAAA	CGTCCTGACC	AACTTGCTAA	GGCGATTAAAT	660
GATGACCTCG	GAAGAGGTGT	TACTTTTATT	TCTGGTCAAG	GCTACTATAG	TAAAGAAAAT	720
TTGAAAATCA	TCTACTGTAT	TGTCGGAAGA	AATGAAATTG	TGAAAACGAA	GGAAATGATT	780
CATCGAATCG	ATCCTCAAGC	CTTTATAACT	ATTACAGAAG	CCCATGAAAT	CCTAGGAGAA	840
GGCTTCACCT	TTGAAAAAGA	ATAA				864

(2) INFORMATION FOR SEQ ID NO:1518:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1128 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...1128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1518:

CCTAGGAGGT	GTCTTATGAA	TGATAAGTTA	AAAATCTTCT	TGTTGCTAGG	AGTATTTTTT	60
CTAGCCATAA	CCGGTTTCTA	TGTTCTATTG	ATACGAAATG	CAGGGCAGAC	AGATGCCTCG	120
CAAATTGAAA	AGGCGGCAGT	TAGCCAAGGA	GGAAAAGCAG	TGAAAAAAC	AGAAATTAGT	180
AAAGACGCAG	ACTTGCACGA	AATTTATCTA	GCTGGAGGTT	GTTTCTGGGG	AGTGGAGGAA	240
TATTTCTCAC	GCGTTCCCGG	GGTGACGGAT	GCCGTTTCAG	GCTATGCAAA	TGGTAGAGGA	300
GAAACAACCA	AGTACGAATT	GATTAACCAA	ACAGGTCATG	CAGAAACCGT	CCATGTCACC	360
TATGATGCCA	AGCAAAATTC	TCTCAAGGAA	ATCCTGCTTC	ACTATTTCCG	CATTATCAAT	420
CCAACCAGCA	AAAAATAACA	AGGAAATGAT	GTGGGGACCC	AGTACCGTAC	TGGTGTTTAT	480
TACACAGATG	ACAAGGATTT	GGAAGTGATT	AACCAAGTCT	TTGATGAGGT	GGCTAAGAAA	540
TACGATCAAC	CTCTAGCAGT	TGAAAAGGAA	AACCTGAAGA	ATTTTGTGGT	GGCTGAGGAT	600
TACCATCAAG	ACTATCTCAA	GAAAAATCCA	AATGGCTACT	GCCATATCAA	TGTTAATCAG	660
GCGGCCTATC	CTGTCAATGA	TGCCAGCAAA	TATCCAAAAC	CAAGTGATGA	GGAATTGAAA	720
AAGACCTGT	CACCTGAGGA	GTATGCAGTT	ACCCAGGAAA	ATCAAACAGA	ACGAGCTTTC	780
TCAAACCGTT	ACTGGGATAA	ATTTGAATCC	GGTATCTATG	TGGATATAGC	AACTGGGGAA	840
CCTCTCTTTT	CATCAAAAAG	CAAATTTGAG	TCTGGTTGTG	GCTGGCCTAG	TTTTACCCAA	900
CCCATCAGTC	CAGATGTTGT	CACCTACAAG	GAAGATAAGT	CCTACAATAT	GACGCGTATG	960
GAAGTGCGGA	GCCGAGTAGG	AGATTCTCAC	CTTGGGCATG	TCTTTACGGA	TGGTCCACAG	1020
GACAAGGGCG	GCTTACGTTA	CTGTATCAAT	AGCCTCTCTA	TCCGCTTTAT	TCCCAAAGAC	1080
CAAATGGAAG	AAAAAGGCTA	CGCTTATTTA	CTAGATTATG	TTGATTAA		1128

(2) INFORMATION FOR SEQ ID NO:1519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1519:

AATTCTGGGT	GCCTATCCTA	TTTATCCAAT	ATCAGACCAT	GGAAAGGAGA	GAAGATGAGT	60
AAAGAAAATC	CCTTAAGTCA	TCATGAGCAG	TTGCGTTATG	ATTATTTGCT	AAAAAATATT	120
CACTATCTCA	ATGAGAGAGA	AAAAAATGAG	TTTGCTTATT	TGCAAGAAAA	GCTAACTCTT	180
GCTAGGGGAA	ATAGTAGCTC	TAGCTTGGA	CAAGAAAGAG	AAGAGCAGGT	TGACTTACCA	240
AGCTATGCGA	ACCGAGTCG	CTCACAATCC	AAATCACAAG	CACTCTCTTT	CCCTCCAAAA	300
AAGAAAAGAC	GGAAGCTCCG	TCTTAAACGA	ATTTTATG	TGATTTTTTC	ACTTTTGGTC	360
TGTGTGGCTT	TGGCCATGGT	ATTCATGTTT	TTGCGTGGTT	ACCAAGATGC	TAGCGCAAAG	420
AAAAC TGCTG	ATGCCCCGGC	AGCTCAAGTA	GAAGTCTTTA	ATGGTCAGGA	CACTAGAGAT	480
GGAGTTAATA	TTTTAATCAT	GGGTACTGAT	GGTCGAATCG	GCCAGAACAG	TGTTGAGACA	540
CGAACTGACT	CTATTATGGT	ATTAAATGTC	GGGGGCTCAG	ATAAGAAAA	GAAGCTAGTC	600

AGTTTCATGC	GTGATAATTT	GGTCTATATA	GATGGTTATA	GTCAAGTGAT	TAATGGTAGA	660
AAACAGACAG	ATAACAAGTT	AAACGTAGCC	TACGAGTTAG	GAGAACAAAG	GGGCAAAAAG	720
GGGCAGAAAT	GTTTCGCCAA	GTCTTGA				747

(2) INFORMATION FOR SEQ ID NO:1520:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 804 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...804
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1520:

GGGAGGTTTC	GGATGTCAGC	ATATCAATTA	CCGACCGTAT	GGCAGGATGA	AGCTAGTAAT	60
CAAGGAGCTT	TTACGGGGCT	AAACAGACCA	ACAGTAGGTG	CCCGTTTCGA	ACAAAACCTG	120
CCAAAAGGAG	AACAAGCTTT	TCAGCTTTAT	TCACTGGGAA	CACCAAATGG	TGTGAAGGTT	180
ACTATCTTAT	TGGAAGAAAT	ACTAGAAGCT	GGTTTTAAGG	AAGCGGCTTA	CGACTTGTAT	240
AAGATTGCTA	TCATGGATGG	GGATCAATTC	GGATCAGACT	TTGTGAAGCT	CAATCCAAAT	300
TCCAAGATTC	CAGCCTTATT	GGACCAGTCA	GGTACTGAAG	ATGTAAGAGT	CTTTGAGTCT	360
GCTCATATTC	TTCTTTACCT	TGCTGAGAAA	TTTGGAGCCT	TTTTACCAAG	TAATCCTGTG	420
GAAAAGGTAG	AAGTTTTGAA	TTGGCTATTC	TGGCAAGCAG	GTGCAGCACC	TTTTCTAGGT	480
GGGGGATTTG	GACATTTCTT	CAATTATGCT	CCTGAAAAAT	TGGAATATCC	TATTAACCGT	540
TTTACAATGG	AAGTGAAAACG	CCAGTTGGAT	TTATTGGATA	AGGAATTGGC	TCAGAAACCT	600
TATATTGCAG	GCAATGACTA	TACGATTGCA	GATATTGCTA	TCTGGTCTTG	GTATGGACAG	660
TTAGTTCAAG	GAAATCTTTA	CCAAGGTTCT	GCAAAATTCT	TGGATGCCTC	AAGTTATCAA	720
AATCTAGTAA	AATGGGCAGA	AAAAATTGCC	AATCGTCCAG	CTGTTAAGCG	TGGCTTGGA	780
GTAACCTATA	CAGAAATTAT	ATAG				804

(2) INFORMATION FOR SEQ ID NO:1521:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1521:

GATTTTATTT	TCGTGTACAA	TTTCAGCTAT	TCTTGTGTATA	ATCAGCCTAT	AGGAATCAAG	60
GAGGTGACTC	TTATGGCTGT	TTTTGTGTCT	TTGGATGGAA	TTGTGGTAGA	AGTACTTGAT	120
GTCTTTTCTT	CTTTTAATGG	GGATAGTGAG	TTTTTCTTGT	GTAAACGTCT	TAAAGACAAG	180
AGTCAGTTTG	TTATGGAACG	CTCTCAGTTC	GAGGAGATGT	TCCAACCTCA	AAGTAGTCGC	240
TTGACGACGC	AAGAAAAATT	ACAATTGTTT	ACCTCTGTGT	TTGCTGGCCG	TTATGATGTT	300
TATGCTAAGA	GTTTTATCAA	TGATCAAGGG	AAAATTCAGT	ATTTTCCTTC	CTATGATTGT	360
GGTTGGAAGC	AGTTGCTACC	TGAAAAACGG	AGTTTCCAGA	CATTGACGGA	TTCCGTTTTG	420
AAATCTCATT	TTCGTGGGGA	GACAGCTATC	GGTATCTTTC	CTATGCACTT	AGATGATAGC	480
TGTCATTTTT	TGGTACTGGA	TTTTGATGAA	GGAGATTGGA	AAGAAGCTGG	TTTAACCATT	540
CGAAGAATAG	CCAGGGAACG	CCAGATGGAA	GCCCATTTAG	AGATTTCTCG	TTCGGGTCAC	600
GGACTCCATA	TTTGGTTCTT	CTTTGAGGAA	GCGATTCCGA	GTCGAGAGGC	TCGCTTGTTT	660
GGAAAGAAAC	TGATAGAACT	GGCAATGCAG	GAAAGTATGC	AACGTCTCCT	TGATTCTTTT	720
GATCGCATGT	TTCCAAATCA	GGATGTCCTT	CCTAAGGGGG	GATTTGGAAA	TTTGATTGCC	780
TTGCCTTTTC	AAGGAGAAGC	TTACCATCAA	GTGCGAACGG	TCTTTGTGGA	TGAACATTTT	840
CAACCTTATG	GAGACCAATG	GAGGTATCTG	CAAGGAATTC	AGAAGATTTT	AACTGCTAAA	900
GTGGCACTGT	TAATCCAAGA	GGAGTTAGGC	AAGCAAGAAT	TGGATAAGGA	GTTGAAGGTC	960
GTTTTATCCA	ATATGATCCA	ACTTAAAAAA	TCGTCTGTGA	CACCCAAGAC	ACTGTTTTTC	1020
TTGAAAAATA	TGGCTTCATT	TTCTAATCCC	GAATTTTATT	TAAAGCAGGC	TATGCGACAG	1080
CCAACCTATC	AAATTCCTGA	GCGAATGTAT	TTATTTGGAG	AATCCGATTA	TTATTTATGG	1140
CTGCCAAGAG	GCTTGTTATA	TCCATTGCAA	GATAAATTTA	AGCAGGTAGT	TGTGGAGGAT	1200
AGGAGAAAGG	TACAAAGGTC	TATTAGAGTA	GCATTTAAGG	GAGAGCTTAC	TTTGGAGCAA	1260
GAATTAGCCC	TGTCAGATAT	GAATTCTAAA	GAAAATGGTT	TACTTCATGC	GGGACAGGTT	1320
TTGGAAAGAG	CGTTTTAG					1338

(2) INFORMATION FOR SEQ ID NO:1522:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1522:

TGTGCGCTTC	GAANCAAAGG	ATCCGTCATG	GCGAAAACAT	TTTTTATTCC	AAATAAACAG	60
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AGCATTTTAG	GAGAACAAGA	GATTTTGAAT	GCCAAGTCGA	TCTTGGCCTT	GCTAGACGGT	120
TTGGAGTCAC	ATAGCTATGA	TGTAGTCTAT	CTCCGTCAGC	CTCTTAATCG	TCTCGAATAT	180
ATCGAGTGTG	CGATAGTGGG	GCAATCACAA	TTTCTCTTTA	AGGTCAGTTA	TGCTGATGGT	240
CAAAAGGCTT	ACCGTGTCGA	TCTTCCTGAC	CTACTAACAA	AGACAGACTG	GCAGATTATC	300
AAGTCATTTT	TAGATGCTTT	GCTTGCTTAT	ACAGGGACTG	ATATTGAAGG	GCTAGATGGT	360
TTTGATTTTG	AAGCTTATTT	CCAAGCAAGT	ATTCAAGCCT	ATCTAGCAGA	CGCTGTAGCT	420
CGTTTTACGA	TTTGCCAAGG	AATTTTTTAAT	CCTATTTTCT	TTAGTCGTGA	GAAC TTGAAA	480
AGCTTTTTAG	AGGCAGATGG	CTTGGCTCAG	TTTGAAGCGC	GTGTGCGTGC	GGTTCAAGAG	540
ACAGATGCCT	ATTTTGCAAG	AGTTTCCTTC	TATCAGGATG	GAGAAGGAAA	AGTGCATGGC	600
GTTTACCATT	TAGCTCAAGG	AGTCAAGACA	GTTTTACCGA	GAGAACCGTT	TGTTCCCTGCA	660
GCCTATATTG	AGCAATTGGT	GGATAAGGAA	GTCCAGTGGG	AGATTGACTT	GGTTCAAATC	720
ACAGGAGACG	GCTCTAAACC	AGAAGACTAT	GAATCCATAG	CTCGCTTGGA	CTATGCAAAA	780
TTCTTAGAGG	TATTACCCCC	ATCTTTTTTAC	CACCAGCTAG	ACGCCAATCA	AATAGAAATA	840
CACCCCATCT	TAGGACAAGA	TTTTAAAACA	TTAGCACAAAG	AAAAGTAA		888

(2) INFORMATION FOR SEQ ID NO:1523:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...321
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1523:

GGAAACTTGC	TCATGTGTGA	AAAAATCCGT	ATTTCGCAGGG	TATCTGATTA	TCCTAGTGCC	60
AGAGGTGGTT	TAGAAGATAT	CCTCATCATG	GAAAATATGA	CCAATCATCT	CCTTTTGGTT	120
CAAATCCGAG	TGCATGGCTA	TTTGCTTGAT	TTTGCTAGTA	TTGAAGGGCA	AAGGCAAAAG	180
CATTATCGTT	TGAAAAATTT	ACCTCAGACG	GTTGAACTGA	CAGTGGATGA	TGTGGAGGAG	240
GATGTGGATT	TGACCCTACC	CGAAAATCGA	AGTTATCAAG	AAGCTGATTT	TTTTGAACGC	300
ATGTTTCGAG	AGAACTGTTA	A				321

(2) INFORMATION FOR SEQ ID NO:1524:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 888 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1524:

CAGCTTGTTTC	GAAAGGTGTC	AGAAGGGGCA	GACCTTATCA	GCATGAAAGG	GGATGTCATC	60
ACAGAACATC	AATTTTATGA	GCAAGTGAAA	AACAACCCCT	CAGCCCAACA	AGTCTTGTTA	120
AATATGACCA	TCCAAAAAGT	TTTTGAAAAA	CAATATGGCT	CAGAGCTTGA	TGATAAAGAG	180
GTTGATGATA	CTATTGCCGA	AGAAAAAATA	CAATATGGCG	AAAACCTACCA	ACGTGTCTTG	240
TCACAAGCAG	GTATGACTCT	TGAAACACGT	AAAGCTCAA	TTCGTACAAG	TAAATTAGTT	300
GAGTTGGCAG	TTAAGAAGGT	AGCAGAAGCT	GAATTGACAG	ATGAAGCCTA	TAAGAAAGCC	360
TTTGATGAGT	ACACTCCAGA	TGTAACGGCT	CAATCATCC	GTCTTAATAA	TGAAGATAAG	420
GCCAAAGAA	TTCTCGAAAA	AGCCAAGGCA	GAAGGTGCTG	ATTTTGCTCA	ATTAGCCAAA	480
GATAATTCAA	CTGATGAAAA	AACAAAAGAA	AATGGTGAG	AAATTACCTT	TGATTCTGCT	540
TCAACAGAA	TACCTGAGCA	AGTCAAAAAA	GCCGCTTTCG	CTTTAGATGT	GGATGGTGTT	600
TCTGATGTGA	TTACAGCAAC	TGGCACACAA	GCCTACAGTA	GCCAATATTA	CATTGTAAAA	660
CTCACTAAGA	AAACAGAAAA	ATCATCTAAT	ATTGATGACT	ACAAAGAAAA	ATTAAAAACT	720
GTTATCTTGA	CTCAAAAACA	AAATGATTCA	ACATTGTTC	AAAGCATTAT	CGGAAAAGAA	780
TTGCAAGCAG	CCAATATCAA	GGTTAAGGAC	CAAGCCTTCC	AAAATATCTT	TACCCAATAT	840
ATCGGTGGTG	GAGATTCAAG	CTCAAGCAGT	AGTACATCAA	ACGAATAG		888

(2) INFORMATION FOR SEQ ID NO:1525:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1525:

TGGCGGTCTC	GCTCCCTTGG	TTATCTTTGG	AGTAGCAGTA	TCTTGGAAGG	CTATTGCAGG	60
TGGAACAGCA	CTTATAGGTT	CTGGTTTGGC	AGCTGGTTAT	TTTTTAGGAG	GAGATTAACT	120
ATGATGAAAG	ATTTGAACAA	CTATCGTGAA	ATTTCTAATA	AGGAATTGCA	AGAAATCAAG	180
GGTGGCTTTG	GTGTAGGTGT	TGGTATCGCT	TTATTTATGG	CAGGTTATAC	CATTGGAAAA	240
GACCTTCGTA	AAAAAGTTTG	TAAGTCATGC	TAG			273

(2) INFORMATION FOR SEQ ID NO:1526:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 255 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...255
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1526:

AGATCAACTC	GTGGTGAAGA	ACACCTAAGA	TATTTTGCTT	TTTATCTTGA	TTATTACCTA	60
AGAACTGGGG	TAGCTGGATT	CGAACCAACG	CATGAGGGAG	TCAAAGTCCC	TTGCCTTACC	120
GCTTGGCTAT	ACCCCATTA	TGAAATGGAG	AGAGAGGGAT	TCGAACCCCC	GAACCCGAAG	180
GAGCGGATTT	ACAGTCCGCC	GCGTTTAGCC	TCTTCGCTAT	CTCTCCTACA	ATCAACATGG	240
ACTATTATAT	CATGA					255

(2) INFORMATION FOR SEQ ID NO:1527:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 518 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...518
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1527:

AACAGGCTCG	TATCGCAGAA	GCTGCTGGTG	CGGCAGCTGT	GATGGCCTTG	GAACGAATTC	60
CGGCTGATAT	TCGTGCAGCT	GGAGGAGTTT	CCCGCATGAG	CGACCCAAAG	ATGATTAAGG	120
AAATCCAAGA	AGCGGTTAGT	ATTCCAGTAA	TGGCTAAGGT	CAGAATCGGG	CATTTTGTTG	180
AAGCTCAGAT	TTTAGAGGCT	ATTGAAATTG	ATTATATCGA	CGAGAGTGAA	GTTCTATCTC	240
CAGCTGATGA	CCGTTTCCAT	GTGGATAAGA	AAGAATTCCA	AGTTCCTTTT	GTCTGTGGTG	300
CTAAGGATTT	AGGTGAAGCC	TTGCGTCGTA	TCGCTGAAGG	TGCTTCCATG	ATTTCGTACCA	360

AAGGAGAACC AGGGACAGGG GATATCGTCC AAGCTGTTTCG TCATATGCGT ATGATGAATC	420
AGGAAATTCG CCGCATTCAA AACTTACGTG AGGACGAGCT TTATGTTGCT GCCAAGGATT	480
TTGCAAGTCC CTGTAGAATT GGTCCAATAT GTTCATGA	518

(2) INFORMATION FOR SEQ ID NO:1528:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 567 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...567
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1528:

TCAGTATATC GATCAGCTAG GAGAAGCTTA ATGGACAAGA AAACAGTAAA GGTAATTGAA	60
AAATACAGCA TGCCTTTTGT CCAATTGGTA CTTGAAAAAG GAGAAGAAGA CCGTATCTTT	120
TCAGACTTGA CTCAAATCAA GCAAGTTGTT GAAAAAACAG GTCTGCCTTC TTTTTTAAAA	180
CAAGTGGCAG TAGACGAGTC GGATAAGGAA AAAACAATTG CTTTTTTCCA AGATTCTGTG	240
TCACCTTTAT TACAAAATT TATCCAGGTT CTGGCCTACA ATCACAGAGC AAATCTTTTT	300
TATGATGTGC TTGTAGATTG CTTGAACCGA CTTGAAAAAG AAACAAATCG ATTTGAAGTG	360
ACGATTACGT CTGCTCATCC TCTAACTGAT GAACAGAAGA CTCGTTTGCT CCCTTTGATT	420
GAGAAAAAAA TGTCTCTGAA AGTAAGGAGT GTAAAAGAAC AAATCGATGA AAGTCTCATT	480
GGTGGTTTTG TCATTTTTGC CAATCACAAAG ACAATTGATG TGAGTATTAA ACAACAACCTT	540
AAAGTTGTTA AAGAAAATTT GAAATAG	567

(2) INFORMATION FOR SEQ ID NO:1529:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1350 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1529:

TCCCAACATC	GTGGTGAAGA	CTCTGCTAGT	CAATTAGAAA	AAGTTTTTAAA	CATCGTCAAA	60
AGCGATTGAG	AGCGTCGTTT	TGTAGTCGTT	TCTGCGCCTG	GTAAACGCAA	TGCTGAAGAT	120
ACTAAGGTTA	CGGATGCCCT	GATTAAATAC	TACCGCGACT	ATGTTGCGGG	TAACGATATT	180
AGCAAGAGCC	AAAGCTGGAT	TATCGACCGC	TATGCTGCTA	TGGTTAGTGA	ATTGGGACTA	240
AAACCAGCTG	TGCTAGAAAA	AATTTCTAAA	AGCATTACAC	CCTTGGCCAC	TCTTCCTATT	300
GAAGAAAATG	AATTTCTCTA	CGATACTTTC	CTAGCAGCCG	GTGAAAATAA	CAATGCCAAA	360
TTGATTGCTG	CCTACTTTAA	CCAAAATGGT	ATCGATGCAC	GCTATATGCA	CCCTAGAGAA	420
GCTGGGATTG	TGGTCACAAG	TGAACCTGGT	CACGCTCGCA	TCATTCCATC	AAGTTATGAC	480
AAGATTGAAG	AATTGACAAA	CACCAATGAA	GTCTTGTCA	TTCTGGTTT	CTTTGGTGTC	540
ACTAAGGAAA	ATCAAATCTG	TACTTTCTCA	CGTGGAGGAT	CTGATATTAC	AGGTTCTATC	600
ATTGCTGCTG	GTGTCAAAGC	TGACCTCTAT	GAAAACCTTTA	CGGACGTTGA	TGGTATCTTT	660
GCAGCCCACC	CTGGTATTAT	CCACCAACCA	CACTCGATTG	CTGAGTTGAC	CTACCGTGAA	720
ATGCGCGAGT	TGGCCTATGC	AGGCTTCTCA	GTCTTTCATG	ACGAGGCTCT	TCTTCCTGCC	780
TACCGTGGAA	AAATTCCTCT	GGTTATCAAG	AATACCAACA	ACCCTGACCA	TCCAGGTACT	840
CGTATCGTTC	TAAAACACAG	TAATGATGAA	TTTCCAGTTG	TGGGAATTGC	TGGTGACTCA	900
GGCTTTGTCA	GCATTAATAT	GTGAAATAC	CTCATGAACC	GTGAGATTGG	ATTTGGCCGC	960
AAGGTTCTGC	AAATCCTGGA	AGAACTTAAC	ATCGGTTGGG	AACATATGCC	AACAGGTATC	1020
GACGATCTTT	CTATCATCTT	CCGTTCTCGC	CAACTAACTC	CCATCAAGGA	AGAAGAAATC	1080
CTGCGTCAGT	TGGTTCAAAA	GGCTAAAGTA	GATCATGCAG	AAATCGAACA	CGACCTTTCT	1140
ATCATTATGA	TTGTTGGTGA	AAAAATGAAG	AGCCACATCG	GAGTGACTGC	TACTGCGACA	1200
CGCGCTCTAT	CTGAAAACAA	AATCAACATC	CAGATGATGT	CTCAAGGTTT	TAGTGAAGTT	1260
TCTATTATGT	TTGTTGTCAA	TAAAGACCAA	GAGAAAGCAG	CAATTAAAGC	CCTCTACAAT	1320
GCCTTTTTTG	GAGAAAGTAA	GGAAGACTAA				1350

(2) INFORMATION FOR SEQ ID NO:1530:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1041 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1530:

TCTGAGAATC	GAGGAAAAAA	GATGCAAGAA	AAGATTTTGG	TAAGTGGTGG	TGCCGGTTTT	60
ATTGGAACCC	ACACTGTTAT	TGAATTGATC	CAAGCAGGCC	ATCAAGTTGT	TGTGGTGGAT	120
AATCTTGTC	ATAGCAATCG	TAAGAGTTTA	GAAGTTGTTG	AAAGAATCAC	AGGAGTTGAG	180
ATTCCTTTCT	ATGAGGCAGA	TATTCGTGAC	ACAGATACCC	TCAGAGATAT	TTTCAAGCAG	240
GAAGAACCGA	CTGGTGTGCT	TCACTTTGCT	GGTTTGAAGG	CTGTTGGCGA	ATCAACACGT	300

ATCCCTCTTG	CCTACTATGA	CAACAATATC	GCTGGAAC TG	TCAGCCTTTT	GAAAGCCATG	360
GAAGAAAACA	ACTGTAAAAA	CATCATCTTC	AGTTC'TTCTG	CGACAGTTTA	CGGGGATCCG	420
CACACAGTGC	CCATCTTGGA	AGATTTC'CCA	CTTTCAGTGA	CCAACCCATA	CGGTCGTACT	480
AAGCTCATGC	TAGAGGAAAT	TTTGACTGAT	ATTTACAAAG	CAGACTCAGA	ATGGAATGTT	540
GTCTTGCTTC	GTTACTTTAA	CCCAATCGGA	GCCCATGAGA	GTGGTGATTT	GGGAGAAAAT	600
CCAAACGGTA	TTCCAAACAA	TCTCTTGCCA	TATGTGACTC	AAGTAGCCGT	TGGAAAATTA	660
GAGCAAGTGC	AAGTGT'TTGG	AGACGATTAC	GATACGGAAG	ATGGAACAGG	TGTTTCGTGAC	720
TATATCCACG	TTGTTCGATTT	GGCTAAGGGT	CACGTTGCAG	CTTTGAAAAA	AATCCAAAAA	780
GGTTCAGGAC	TAAACGTTTA	TAACCTTGGA	ACTGGTAAAG	GTTACTCAGT	TCTTGAAATT	840
ATCCAAAACA	TGGAAAAAGC	GGTGGGACGT	CCTATTCC'TT	ACCGCATCGT	AGAACGTCGC	900
CCAGGTGATA	TCGCTGCCTG	CTACTCAGAC	CCAGCAAAAG	CTAAAGCAGA	ACTCGGTTGG	960
GAAGCAGAAC	TCGACATCAC	C'CAAATGTGT	GAAGACGCAT	GGCGTTGGCA	AAGCAAGCAT	1020
CCAAATGGAT	TTGAAGACTA	A				1041

(2) INFORMATION FOR SEQ ID NO:1531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1531:

ATGGAGAATC	GTCACATGAA	ACATTTT'TTT	GCAGGAATTG	GTGAGATAAA	ACTTGTTGGC	60
TACTTATTGT	ATATATGTGT	AGGACTAGCC	CCTCTTTTTC	ATATATATGT	CATAGGTTTCG	120
GAAGTGAGTT	TTGTGAAAAT	AGTGT'TATCT	ATTTTGGGAG	TTATATTTGT	AAGTATGTTA	180
ACTATTGCTC	GAATTTATCG	GACTTTTCTA	TAA			213

(2) INFORMATION FOR SEQ ID NO:1532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1532:

AGACTTTGTC	GCCTAGACCC	TATATTTCAA	GAATTAAGTG	ACCTTGATGA	TCTAAATGTA	60
TTGTGGTATA	CTATTTTTGT	CATCGGTTAC	CGATTACGTT	CCTATGGGTT	CGTGAGAGGA	120
GGTGAAACTA	ATGAGCCTTA	TCATAGAGCT	CGCTCTTACT	ATTATAGCGG	ATGTTATAGC	180
TGGAATTATC	TTGTATTTTC	TCTGCAGATG	GCTAGATAG			219

(2) INFORMATION FOR SEQ ID NO:1533:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1107 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1533:

CCTGTGCGTC	GATCCGGCTG	GTGGGCACCT	TTCATCACGA	CTTTGGTGGC	CGATGGTTTT	60
AATAACGTAT	CGGACATCAT	TGGAAATGTG	GCCCTCTTAA	TCGGGATTCG	GATGGCGCGC	120
CAGCCTGCAG	ACCGTGACCA	CCGTTTTGGT	CATTGGAAGA	TTGAAGATTT	GGCAAGCTTG	180
ATCACTTCTA	TCATCATGTT	CTATGTCGGT	TTCGATGTTT	TAAGAGATAC	CATTCAAAAG	240
ATTCTCAGTC	GGGAAGAAAC	GGTCATTGAT	CCTCTTGGTG	CAACTCTAGG	AATCATTTCT	300
GCAGCGATTA	TGTTTGTGGT	CTATCTCTAC	AATACTCGCC	TCAGTAAGAA	ATCCAACCTC	360
AAGGCGCTGA	AGGCAGCTGC	TAAGGACAAT	CTTTCTGACG	CTGTTACCTC	ACTTGGAACC	420
GCCATTGCCA	TCCTAGCTAG	TAGTTTCAAT	TATCCGATTG	TGGATAAACT	GGTTGCTATC	480
ATCATCACTT	TCTTTATCTT	GAAGACTGCC	TATGATATCT	TCATCGAGTC	TTCCTTTAGT	540
CTTTCAGATG	GCTTTGACGA	CCGCCTGCTC	GAGGACTACC	AAAAGGCTAT	CATGGAAATT	600
CCCAAAATCA	GCAAGGTCAA	ATCGCAAAGA	GGTCGCACCT	ACGGTAGCAA	CATCTACCTG	660
GATATTACAC	TAGAGATGAA	TCCTGACTTG	TCTGTTTTTG	AAAGCCATGA	AATCGCGGAT	720
CAGGTCGAGT	CTATGCTGGA	GGAGCGTTTT	GGCGTCTTTG	ATACCGATGT	CCATATCGAA	780
CCAGCACCTA	TCCCTGAGGA	TGAAATTTTA	GACAATGTCT	ATAAAAAATT	GCTTATGCGT	840
GAACAATTGA	TTGACCAAGG	AAACCAACTA	GAAGAACTCT	TGACTGATGA	TTTTGTCTAT	900
ATTCGCCAAG	ATGGAGAGCA	GATGGATAAA	GAGGCTTATA	AGACCAAAAA	AGAGTTAAAT	960
TCTGCTATCA	AGGACATTCA	AATTACTTCC	ATCAGTCAAA	AAACCAAACT	CATCTGCTAT	1020
GAGTTAGATG	GTATCATCCA	TACCAGTATC	TGGCGTCGCC	ACGAAACCTG	GCAAAATATC	1080
TTTCATCAAG	AAACCAAAAA	AGAATAG				1107

(2) INFORMATION FOR SEQ ID NO:1534:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...282
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1534:

ACACAGCTGC TACAACTCTT AATGGAGGAG CTACTGCAGG GGCTTTTTC	60
GGTGTTCCTT GTACTCTTGA ATGCCTTGAA GATTGAAAAT CTTGTTCTTG	120
GTATCATTGC TATTGTTTAC TATAAAGGAG ATAAGCGTGT	180
AGGTGCAGCT CCGTCTGTAC TAATGATTGT TTCTGGTGGA	240
GTTAGTCTCA TTCCATTCTT AGGATGGGTT GGGGGGATTC TTGCTATTAT	282
CGGAGGATCT CTATTCCTTG CAACATTGAA GAAATTCAA TCAGAAGAAT AA	

(2) INFORMATION FOR SEQ ID NO:1535:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...192
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1535:

GCCATTATGC TAGTGTGCGA AATACAGCAA GTACCTACTC CGTATCTTCT	60
GGAAGTGGAA GTTCTGGCGG TGGCTTCTCT GGAGGCGGAG GTGGCGGCAG	120
TATCGGAGCC TTTTAAAGAG AGCTACCATA GACTGAAAAA	180
GTATGATATA ATGGAAGATA GAAGAAAGAC AAACCTATAAG	192
AAAAGTCAAT AG	

(2) INFORMATION FOR SEQ ID NO:1536:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1356 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1356
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1536:

GAAATAATGC	TTGATTTACT	GAAACAAACC	ATTTTTACCA	GAGATTTTAT	CTTTATCCTG	60
ATTTTGTTAG	GTTTCATCCT	TGTTGTGACC	CTCTTATTAC	TGGAAAATAG	ACGTGATAAT	120
ATTCAGTTGA	AGCAAATCAA	TCAAAAGGTT	AAAGATTTGA	TTGCAGGAGA	TTATTCCAAG	180
GTTCTTGATA	TGCAAGGTGG	GTCTGAAATC	ACCAATATTA	CCAATAATTT	GAATGACTTG	240
TCGGAGGTTA	TTCGTCTCAC	TCAGGAAAAT	CTAGAACAAG	AGAGTAAGAG	GCTAAAATAGT	300
ATTCTGTTTT	ATATGACAGA	TGGGGTTCTT	GCGACCAACC	GTCGGGGTCA	GATTATCATG	360
ATTAACGATA	CAGCCAAGAA	GCAACTGGGG	TTGGTTAAGG	AAGATGTTCT	GAATAGAAGC	420
ATTTTGGAAT	TGCTCAAGAT	AGAAGAAAAC	TATGAATTGC	GTGATTTGAT	TACCCAAAGT	480
CCAGAATTGT	TGCTAGATTC	CCAAGATATC	AATGGTGAAT	ATTTGAACCT	TCGAGTTCGC	540
TTTGCCTTGA	TACGTCGAGA	GTCTGGCTTT	ATTTCAAGTT	TGGTGGCTGT	TTTGCATGAT	600
ACGACGGAGC	AGGAGAAGGA	AGAACGCGAA	CGAAGACTCT	TTGTTTCCAA	TGTTAGCCAT	660
GAGTTACGGA	CTCCTCTGAC	TAGCGTAAAA	TCCTATCTTG	AAGCCTTGGA	TGAGGGGGCT	720
TTGTGTGAAA	CTGTAGCACC	AGACTTTATC	AAGGTTTCTC	TTGATGAGAC	CAACCGTATG	780
ATGCGCATGG	TGACGGATCT	CCTCCATCTT	TCACGTATTG	ATAATGCTAC	CAGTCACCTA	840
GATGTGGAAC	TGATTAACTT	CACTGCTTTT	ATTACCTTTA	TCCTCAATCG	TTTTGACAAG	900
ATGAAAGGAC	AGGAAAAGGA	GAAAAAATAT	GAGTTGGTGA	GAGATTATCC	CATCAATTCT	960
ATCTGGATGG	AAATTGATAC	AGATAAGATG	ACGCAGGTTG	TCGACAAATAT	TTTAAATAAT	1020
GCTATTAAAGT	ATTCGCCAGA	TGGGGGTAAA	ATCACTGTCA	GAATGAAGAC	AACTGAAGAC	1080
CAGATGATTT	TATCCATTTT	TGACCACGGT	TTGGGGATTG	CTAAGCAGGA	TTTACCACGT	1140
ATCTTTGACC	GTTTCTATCG	TGTGGATCGT	GCTAGAAGTC	GTGCACAAGG	TGGTACAGGT	1200
CTAGGACTGT	CTATCGCTAA	AGAAATTATC	AAACAACATA	AGGGCTTTAT	TTGGGCCAAG	1260
AGTGAATACG	GCAAGGGTTC	AACCTTTACC	ATTGTGCTCC	CTTATGATAA	GGATGCAGTG	1320
AAAGAAGAAG	TATGGGAGGA	TGAAGTAGAA	GACTAG			1356

(2) INFORMATION FOR SEQ ID NO:1537:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1537:

CCATCATTCC	GTCTGGTGA	CACTGTTTCGT	GTACATGCCA	AAGTTGTCGA	AGGTAACCGT	60
GAACGTATCC	AGATTTTGA	AGGTGTTGTT	ATCGCACGTA	AAGGTGCTGG	AATCTCAGAA	120
AACTACACAG	TTCGTAAAAT	CTCTAACGGT	GTAGGTGTTG	AGCGTATCTT	CCCAATCCAC	180
ACTCCACGTG	TTGAAAAAAT	CGAAGTTGTT	CGTTACGGTA	AAGTACGTCG	TGCGAAATTG	240
TACTACTTGC	GTGCTCTTCA	AGGTAAAGCA	GCTCGTATCA	AAGAAATCCG	TCGTTAA	297

(2) INFORMATION FOR SEQ ID NO:1538:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 729 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1538:

TTGCCTCTCC	GCTTGGGAAT	GGCGAAACAG	CACAAGCCGT	GGAACTTTTTC	TATCCCTTGT	60
GCATTTTTGA	CCTATATTTT	CATCGTTTTT	GGGGAATTAT	ATCCTAAGAG	AATCGCTCTT	120
AATCTAAAGG	ATGCCTTGCG	AATTCGTACA	GCGCCGGTTA	TCATTGGGAT	CGGAAAACATA	180
GTCAGTCCTT	TTGTTTGGCT	TTTAGCTGCT	TCGACCAATT	TCTTGAGCCA	TTTGACTCCT	240
ATGTCATTCT	ATGATGCGGA	TGAAAAGATG	ACCCGTGATG	AAATTGCCTA	TATGCTGACA	300
AATAGTGAAG	AAACATTGGA	TGCTGATGAG	ATTGAGATGC	TACAAGGTGT	CTTTTCGCTC	360
GATGAACTGA	TGGCACGAGA	GGTTATGGTT	CCTCGAACGG	ATGCCTTTAT	GGTGGATATT	420
CAGGATGATA	GTCAAGCCAT	TATCCAAAGT	ATTTTAAAC	AAAATTATTC	TCGTATCCCG	480
GTTTATGATG	GGGATAAGGA	CAATGTAATT	GGAATCATTC	ACACCAAGAG	TCTCCTTAAG	540
GCAGGCTTTG	TGGACGGTTT	TGACAATATT	GTTTGAAGA	GAATTTTGCA	AGATCCACTT	600
TTTGTACCTG	AAACTATTTT	TGTGGATGAC	TTGCTANAAG	AACTGCGAAA	TACCCAAAGA	660
CAAATGGCGA	TCTTGCTGGA	TGAATACAGT	GGTATGGCTG	GGTTGGTGAC	TTTGGGAAAA	720
CTCTTATAA						729

(2) INFORMATION FOR SEQ ID NO:1539:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1734 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1734
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1539:

CAAGTTATTT	TTAAGAGAAC	AGAGCGGGGA	ACAATGGAGA	AAATCAGTTT	AGAATCTGCT	60
AAGAGGGGGT	CGGACCTAGT	TTTGGACACA	CTTCGTGATT	TAGGAGTGGA	TACCATCTTT	120
GGTTATCCTG	GTGGTGCGGT	TTTGCCTTTT	TATGATGCGA	TATATAATTT	TAAAGGCATT	180
CGCCACATTC	TAGGGCGCCA	TGAGCAAGGT	TGTTTGCATG	AAGCTGAAGG	TTATGCCAAA	240
TCAACTGGAA	AGTTGGGTGT	TGCCGTCGTC	ACTAGTGGAC	CAGGAGCAAC	AAATGCCATT	300
ACAGGGATTG	CGGATGCTAT	GAGCGATAGC	GTTCCCTTTT	TGGTCTTTAC	AGGTCAGGTG	360
GCGCGCAGGG	GATTGGGGAA	GGATGCCCTT	CAGGAGGCAG	ACATCGTAGG	AATTACCATG	420
CCAATCACTA	AGTACAATTA	CCAAGTTCGT	GAGACAGCTG	ATATTCCGCG	TATCATTACG	480
GAAGCTGTCC	ATATCGCAAC	TACAGGCCGT	CCAGGGCCAG	TTGTAATTGA	CCTACCAAAA	540
GACATATCTG	CTTTAGAAAC	AGACTTCATT	TATTCACCAG	AAGTGAATTT	ACCAAGTTAT	600
CAGCCGACTC	TTGAGCCGAA	TGATATGCAA	ATCAAGAAAA	TCTTGAAGCA	ATTGTCCAAG	660
GCTAAAAAGC	CAGTCTTGTT	AGCTGGTGGT	GGAATTAGTT	ATGCTGAGGC	TGCTACGGAA	720
CTAAATGAAT	TTGCAGAACG	CTATCAAATT	CCAGTGGTAA	CCAGTCTTTT	GGGACAAGGA	780
ACGATTGCAA	CGAGTCACCC	ACTCTTCTTT	GGAATGGGAG	GCATGCACGG	GTCAATTCGCA	840
GCAAATATTG	CCATGACGGA	AGCGGACTTT	ATGATTAGTA	TTGGTTCTCG	TTTCGATGAC	900
CGTTTGACGG	GGAATCCTAA	GACTTTCGCT	AAGAATGCTA	AGGTTGCCCA	CATTGATATT	960
GACCCAGCTG	AGATTGGCAA	GATTATCAGT	GCAGACATTC	CTGTAGTTGG	AGATGCTAAG	1020
AAGGCCTTGC	AAATGTTGCT	AGCAGAACCA	ACAGTTCACA	ACAATACTGA	AAAGTGGATT	1080
GAGAAAGTCA	CTAAAGACAA	GAATCGTGTT	CGTTCCTATG	ACAAGAAAGA	GCGTGTGGTT	1140
CAACCGCAAG	CAGTTATTGA	ACGAATTGGT	GAATTGACGA	ATGGAGATGC	CATTGTGGTA	1200
ACAGACGTTG	GTCAACACCA	AATGTGGACA	GCTCAGTATT	ATCCCTACCA	AAATGAACGT	1260
CAGTTAGTGA	CTTCAGGTGG	TTTGGGAACA	ATGGGCTTTG	GAATTCCAGC	AGCAATCGGT	1320
GCTAAAATTG	CTAACCCAGA	TAAGGAAGTA	GTCCTGTTTT	TTGGGGATGG	TGGTTTCCAA	1380
ATGACCAACC	AGGAGTTGGC	TATTTTGAAT	ATTTACAAGG	TGCCAATCAA	GGTGGTTATG	1440
CTGAACAATC	ATTCACTCGG	AATGGTTCGC	CAGTGGCAGG	AATCCTTCTA	TGAAGGCAGA	1500
ACATCAGAGT	CGGTCTTTGA	TACCTTCCCT	GATTTCCAAT	TGATGGCGCA	GGCTTATGGT	1560
ATTAAAAACT	ATAAGTTTGA	CAATCCTGAG	ACCTTGGCTC	AAGACCTTGA	AGTCATCACT	1620
GAGGATGTTT	CTATGCTAAT	TGAGGTAGAT	ATTTCTCGTA	AGGAACAGGT	GTTACCAATG	1680
GTACCGGCTG	GTAAGAGTAA	TCATGAGATG	TTGGGGGTGC	AGTTCCATGC	G TAG	1734

(2) INFORMATION FOR SEQ ID NO:1540:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 975 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1540:

GGGACCTCCC	GGCTCGTGGT	GAAGACGACC	TGCAACTGGC	CATGGCCATG	CAGGACCTGC	60
ACCTCCACGG	CGCCGAGCTG	GGGCAGTCGC	ACCTGCAGGC	GCGCCGCATG	GCTTTCGGCT	120
GCGCTGGCGA	CCTGGATGCG	CCCCTGCACG	GCATCTAGCA	GGCGCGCGAG	ATCGGCCAGC	180
GGCAGTGGCC	GGCTCCCGCT	CGATGCCAGC	AGGCGTGCCA	GCAGGCGGTC	GCCGGGGGTT	240
TGCATGGCAG	GCAATGGCAC	AGGCGCTTGG	TCGTCGGGGG	GCAGTGCGGA	TGGATCGGTT	300
TCTCCGGGTT	GCCGACGCTC	CTCTCCGCGG	CCTTCGCCGC	CCGCTGTCGG	CGCGGGCGGC	360
GAGACCTGGA	CACTGGCCTG	CGCCGTGGAC	GCGACCTCGG	CTGCGGTTTT	CGCCGGGAAG	420
CCGGGGCCGG	GCTGTGGCCG	CTCATGCGTC	CGACCTGCGA	TTTGCGGGTG	GGAGGACACC	480
GGCACCAGCG	GCGGTTTCGT	GACCGGAGGC	GCCGAAACGC	TGGCCGGCTC	CCGGGCTTGC	540
GTGGACGCCG	CGACGCGCGC	GGAAACCGCC	GGCGCTTGCC	GTGCTACCGA	TCCGGACGGC	600
AACACTGTTC	GCGTTGGCGT	TGGCGTTGGC	GTTGGCGTTG	GCGTTGGCGT	TGGCGTTGGC	660
GTTGCTTCCG	CGGCAACTGG	CACGGGGGCT	TGCCNATTGG	TCGGCGGCCG	GTCGGCGGCA	720
GGCGCCGCGG	GCTGGTCCGC	GAGAGGCGTC	GAGGTCGGCG	CGTCGCTGTT	CGCGGCGGGC	780
TCTTCGGCCT	CTGTCGTTTC	GTCGCCCTTG	TCGAACGGTG	GCCTGGGCGC	CGGCGGTCGG	840
TGCGCGGGCA	GGGCCTGTTC	GAAGGCGATC	TGCTGCGCGC	GCAGCGGCGG	AAGGGGGGCA	900
GGGGTGTCGG	ACGACACGAG	CGGAGCCGTA	TCCACGGCGT	TCAGCTTGAG	CATGGCCAGG	960
TCTCGTGGCG	GGTGA					975

(2) INFORMATION FOR SEQ ID NO:1541:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1541:

TGCCTCCCCC	GTCAGTTTTT	AGGTATTTTG	GCAGTTGCAG	AAAGCTATCC	AGATCTGAAA	60
GCTAGTGCTA	ACTTTGTTAA	ATTGCAAGAG	GAGTTGACAA	ACACAGAAAA	TAAAATTTCT	120
TACTCTCGTC	AACTCTATAA	CAGTGTGTC	AGCAACTACA	ATGTAAAATT	AGAAACTTTC	180
CCGAGCAATA	TTATCGCTGG	AATGTTTGGA	TTTAAAGCGG	CAGATTCCT	TCAAACACCT	240
GAAGAGGAAA	AGTCGGTTCC	TAAAGTTGAT	TTTAGCGGTT	TAGGTGACTA	A	291

(2) INFORMATION FOR SEQ ID NO:1542:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 252 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...252
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1542:

GCAAGCCCCC	GTGCCAGTTG	CCGCGGAAGC	AACGCCAACG	CCAACGCCAA	CGCCAACGCC	60
AACGCCAACG	CCAACGCCAA	CGCCAACAGT	GTTGCCGTCC	GGATCGGTAG	CACGGCAAGC	120
GCCGGCGGTT	TCCGCGCGCG	TCGCGGCGTC	CACGCAAGCC	CGGGAGCCGG	CCAGCGTTTC	180
GGCGCTCCG	GTCGACGAAC	CGCCGCTGGT	GCCGGTGTCC	TCCCACCCGC	AAATCGCAGG	240
TCGGACGCAT	GA					252

(2) INFORMATION FOR SEQ ID NO:1543:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 183 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1543:

```
TTGCCACCCC GTGGTGAAGA AGCCGCAGGC TACTCAAAGT ATAGCTTTGA GGTGCAAAT      60
AAACTGACG  AAGTCAGCTC AAAACACTGT TTTGAGATTG TGGATAGAAC TGACGAAGTC      120
AGTAACCATA CGCACGGTAA GGCACGTTG  ACGTGGTTTG AAGAGATTTT CGAAGAGTAT      180

TAA                                                                    183
```

(2) INFORMATION FOR SEQ ID NO:1544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1544:

```
ACGGACTACC GCCTTTATAT CGAACTCTTA CGCAATCTAG CAGATGAAGC AGGTTTGCCG      60
AAAACGCTTG ATACAGGGAG TTTAGCTGGA ATTTAAACGC ACGAGTATTG CACGAATAAC      120
CAACCAAACA ACCACTCAGA CCATGTGGAT CCATACCCTT ACTTGGCAAA ATGGGGCATT      180
AGCGCTGAGC AGTTTAAGTA TGATATTGAG AACGGCTTGA CGATTGAAAC AGGCTGGCAG      240
AAGAATGACA CTGGCTACTG GTACGTACAT TCAGACGGCT CTTATCCAAA AGACAAGTTT      300
GAGAAAATCA ATGGCACTTG GTACTACTTT GACAGTTCAG GCTATATGCT TGCAGACCGC      360
TGGAGGAAGC ACACAGACGG CAACTGGTAC TGGTTCGACA ACTCAGGCGA AATGGCTACA      420
GGCTGGAAGA AAATCGCTGA TAAGTGGTAC TATTTCAACG AAGAAGGTGC CATGAAGACA      480
GGCTGGGTCA AGTACAAGGA CACTTGGTAC TACTTAGACG CTAAAGAAGG CGCCATGGTA      540
TCAAATGCCT TTATCCAGTC AGCGGACGGA ACAGGCTGGT ACTACCTCAA ACCAGACGGA      600
ACACTGGCAG ACAAGCCAGA ATTCACAGTA GAGCCAGATG GCTTGATTAC AGTAAAATAA      660
```

(2) INFORMATION FOR SEQ ID NO:1545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1545:

TTCTTGTTACC	GAAAATTGCC	TCAAAGGTAT	GCAAGATACA	GAAGGTGCTN	GAAC TTATCC	60
CAAACTCAAT	TCCAAGAAAG	TAAAACAGCT	GCTATCATCG	ACGGACCTTG	GAAAGCTCAA	120
GCCTTTAAAG	ATGCTAAAGT	AAACTACGGA	GTTGCAACTA	TCCCAATTCT	TCCAAATGGA	180
AAAGAATATG	CTGCATTTCG	TGGTGGTAAA	GCTTGGTTCA	TTCTTCAAGC	CGTTAAGAAC	240
CTTGAAGCTT	CTCAAAAATT	TGTAGACTTC	CTTGTTGCAA	CTGAACAACA	AAAAGTATTA	300
TATGATAAGA	CTAACGAAAT	CCCAGCTAAT	ACTGAGGCTC	GTTCATAACG	TGAAGGTAAA	360
AACGATGAGT	TGACAACAGC	TGTTATCAAA	CAGTTCAAGA	ACACTCAACC	ACTGCCAAAC	420
ATCTCTCAA	TGTCTGCAGT	TTGGGATCCA	GCGAAAAATA	TGCTCTTTGA	TGCTGTAAAGT	480
GGTCAAAAAG	ATGCTAAAAC	AGCTGCTAAC	GATGCTGTAA	CATTGATCAA	AGAAACAATC	540
AAACAAAAAT	TTGGTGAATA	A				561

(2) INFORMATION FOR SEQ ID NO:1546:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1224 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1546:

GAAATGTACC	GTTATCAAAT	TGGCATTCCC	ACATTAGAAT	ATGATCAGTT	TGTCAAAGAA	60
CATGAATTAG	CCAATGTATT	ACAAAGTAGT	GCTTGGGAGG	AAGTTAAGTC	TAATTGGCAA	120
CATGAGAAGT	TTGGTGTTTA	CAGGGAAGAA	AAATTACTGG	CGACAGCTAG	TATTTTGATT	180
AGAACTCTTC	CGCTAGGCTA	TAAAATGTTT	TACATCCCAA	GAGGACCTAT	ATTGGATTAT	240
GGGGATAAAG	AACTCTTGAA	TTTTGCCATT	CAGTCTATTA	AGTCCTATGC	TCGCAGTAAG	300
AGAGCGGTTT	TTGTGACTTT	TGACCCAAGT	ATTTGCCTAT	CTCAAAGTTT	AATCAATCAG	360
GAAAAGACAG	AATTTCTTGA	AAATCTGGCT	ATTATTGATA	GTTTGCAACA	AATGGGAGTA	420
AGGTGGTCAG	GAAAAACGGA	GGAAATGGGA	GACACCATTC	AACCTCGTAT	TCAGGCGAAA	480
ATATACAAGG	AAAATTTTGA	AGAAGATAAA	CTTTCCAAGT	CAACAAAACA	GGCTATTCCA	540
ACAGCACGAA	ACAAAGGGCT	TGAGATTCAA	TATGGTGGAC	TGGAAC TATT	AGATTCA TTT	600
TCGGAGTTGA	TGAAAAAAAC	TGAGAAGCGA	AAAGAGATTC	ATTTGAGGAA	TGAAGCCTAT	660
TATAAAAAAT	TGTTAGATAA	TTTTAAGGAC	AAGGCCTATA	TCACCTTGGC	CACCTTG GAT	720
GTTTCTAAAC	GTTTCGAAGA	ATTAGAAGAA	CAGTTAGCGA	AAAATAGAGC	CTTGGAAGAG	780

ACCTTTACTG	AGTCGACTCG	AAC TTCAAAA	G TAGAAGCGC	AGAAGAAGGA	AAAAGAACGT	840
TTGTTTAGAGG	AATTGACCTT	CTTGCAGGAA	TATATAGATG	TAGGTCAAGC	GAGAGTTCCT	900
TTAGCGGCTA	CTTTGAGTTT	GGAATTTGGT	ACTACCTCTG	TCAATATATA	TGCTGGTATG	960
GATGATGATT	TTAAACGTTA	CAATGCACCA	ATTTTAACAT	GGTATGAAAC	GGCTCGCTAT	1020
GCCTTTGAGC	GAGGTATGGT	CTGGCAAAAT	TTAGGTGGTG	TTGAAAAC TC	TCTCAATGGT	1080
GGACTTTTATC	ATTTTAAGGA	AAAATTTAAT	CCAACGATTG	AAGAATACTT	GGGTGAATTT	1140
ACAATGCCCA	CTCATCCTCT	CTATCCTCTG	TTAAGACTTG	CTCTTGATTT	CCGTAAAACA	1200
TTAAGAAAAA	AACATAGAAA	GTAA				1224

(2) INFORMATION FOR SEQ ID NO:1547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 864 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1547:

GGTGAAACC	GCGTTTCTGA	CGCCCCTAGG	TTAAATCAAC	CTAGGATTGT	CGGACGCGGT	60
TCTTTTGCTT	ATTTAGTCTA	TTGTGTGAAA	GAAAGGAGAG	CCGTGGACAA	CCTTTATCTT	120
GTAAGACG	ATAGTCAACT	AGCTGCATTT	CGTGATTTTG	TAGTAAGAAA	TACTGAAAAG	180
TTGAAAGATT	ATCAATCTTT	TTTAAAGAAT	GAAC TTGCAG	TCTGTGATTT	ACCGCAAGCC	240
GTTATTTGGT	CAAGTTTTAA	TGCTGCTACA	CAGATTATTA	GGGAAAGCGC	TGTTCCAGCC	300
TATACAAATA	ATAGACGAAT	GGTTATGACG	CCTGATTTAG	CTGTATGGAA	AGAGTTGTAT	360
TTGTATCAGT	TGATGGACTA	CGAGTGTTC	CAGCAAATC	AAGCAATAGA	AAGCCATTAT	420
CATTCTTTAT	CTGAAAATTT	CCTCTTACAG	ATTGTAGGAC	ATGAGTTAGC	TCATTGGTTCG	480
GAGTATTTTT	TAGATGATTT	TGATGGTTAC	GACTCTTACA	TCTGGTTTGA	AGAGGGGATG	540
GTTGAATATA	TTAGTCGCAA	GTATTTCTTG	ACAGAAGAGG	AATTTCAAGC	GGAAAAAATT	600
TGTAATCAGT	CTCTTGTAGA	ACTTTTTCAG	AAGAAGTATG	GTTGGCATT	ATTGAATGAT	660
TTTGGTTCTT	CGACTTATGA	TAAGAATTAT	GCAAGTATTT	TTTACGAATA	CTGGCGTAGT	720
TTTTTGACAA	TAGATAAGTT	GGTAGAAAAT	CTAGGTAGTG	TACAAGCGGT	CTTCGATTCT	780
TATCATTTAT	GGGCAAATAC	AGATAAACT	CTTCCCTTGT	TAAATTGGTT	TGTTTCAGCAG	840
AAATTAATTG	AAAAAGAGAT	ATAA				864

(2) INFORMATION FOR SEQ ID NO:1548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1548:

AAAGGAAACC	GTATGACAGA	TGCGATTTTA	CAGGTATCAG	ACCTGTCCGT	TTATTATAAT	60
AAAAAGAAGG	CTTTGAATAG	TGTTTCCCTA	TCTTTCCAAC	CTAAGGAAAT	TACAGCCTTG	120
ATTGGTCCAT	CTGGATCAGG	GAAGTCAACC	CTCCTCAAGT	CTCTCAACCG	CATGGGAGAT	180
CTCAATCCAG	AGGTGACCAC	AAC TGGATCC	GTGGTGTACA	ATGGCCACAA	CATCTACAGT	240
CCGCGTACAG	ATACGTTTGA	ATTACGTAAG	GAAATCGGAA	TGGTTTTCCA	ACAACCTAAT	300
CCTTTCCCTA	TGACTATCTA	TGAGAATGTT	GTCTACGGGC	TTCGTATCAA	TGGAATTAAG	360
GATAAGCAGG	TTCTGGATGA	AGCCGTAGAA	AAAGCCTTGC	AAGGTGCCTC	TATCTGGGAT	420
GAGGTCAAGG	ATCGTCTATA	TGATTTCAGCT	ATTGGATTGT	CAGGTGGTCA	ACAGCAGCGT	480
GTCTGCGTGG	CCCGTGTCTT	GGCAACTAGT	CCTAAAATCA	TCCTCTTGGA	TGAGCCAACT	540
TCGGCTTTGG	ATCCGATTTC	AGCTGGTAAA	ATTGAGGAAA	CCTTGATATG	TCTAAAAGAC	600
AAGTACACCA	TGCTTCTGGT	AACCCGTTCC	ATGCAGCAAG	CTTCACGTAT	CTCTGATAAG	660
ACAGGATTTT	TCCTAGATGG	AGATTTGATT	GAATTTAATG	ATACCAAGCA	GATGTTCCCTT	720
GATCCCCAAC	ACAAGGAAAC	GGAAGACTAT	ATTACAGGAA	AATTTGGATA	A	771

(2) INFORMATION FOR SEQ ID NO:1549:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 498 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1549:

TTCTCTATTT	TTCTTGTTTC	AATAGCTGAG	AATGATTTTT	ACATTGGATT	TTACCATTCC	60
TTTCAACACT	CCATTATATC	GGATTTTAGC	ATTTTTTTTCA	ATTTCTATTT	CTTTTCACTT	120
CCCCCTCCCT	TATTTATAGG	AAAATATGGT	AAAATAGAAC	AGACTAAAAA	TCATCATTTTC	180
ACGAAAGGAT	GCAAGATGAA	AATTACGCAA	GAAGAGGTAA	CACACGTTGC	CAATCTTTCA	240
AAATTAAGAT	TCTCTGAAGA	AGAACTGCT	GCCTTTGCCA	CCACCTTGTC	TAAGATTGTT	300
GACATGGTTG	AATTGCTGGG	CGAAGTTGAC	ACAACTGGTG	TCGCACCTAC	TACGACTATG	360

GCTGACCGCA AGACTGTACT CCGCCCTGAT GTGGCCGAAG AAGGAACAAA CCGTGATCGC	420
TTGTTTAAAA ACGTACCTGA AAAAGACAAC TACTATATCA AGGTGCCAGC TATCCTAGAC	480
GATGGAGGAG ATGCCTAA	498

(2) INFORMATION FOR SEQ ID NO:1550:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...195
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1550:

GAAGTTAGCC GCAGGTTGCT CAAAGCAGTG TTTGAGGTTG TCGATAAAAC TGACGAAGTC	60
AGCTTAAAAAC ACTGTTTTGA GGTTCGAGAT AGAACTGACG AAGTCAGTAA CCATACCTAC	120
GACAAGGTGA AGCTGACGTG GTTTGAAGAG ATTTTCGAAG AGTATCATAC GAAAAAGCCC	180
TGTTCTCTCAA GATGA	195

(2) INFORMATION FOR SEQ ID NO:1551:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...198
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1551:

CAAGGTAGCC GTATCGGAAG GTGCGGCTGG ATCACCTCCT TTCTAAGGAT AAGGAACTGC	60
GCATTGGTCT TGTTTAGTCT TGAGAGGTCT TGTGGGGCCT TAGCTCAGCT GGGAGAGCGC	120

CTGCTTTGCA	CGCAGGAGGT	CAGCGGTTCTG	ATCCCCGTAG	GCTCCATTGG	TGAGAGATCA	180
TCAAGTAATG	CACATTGA					198

(2) INFORMATION FOR SEQ ID NO:1552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4962 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...4962

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1552:

AAGGTCTTAC	GTATTCGTAA	GTTATCAGTA	GGAGCCTGCT	CGCTGATGAT	TGGTGCTGTT	60
TTATTTGCTG	GTCCAGCCTT	GGCTGAAGAA	ACTGCAGTTC	CTGAAAATAG	CGGAGCTAAT	120
ACAGAGCTTG	TTTCAGGAGA	GAGTGAGCAT	TCGACCAATG	AAGCTGATAA	GCAGAATGAA	180
GGGGAACATA	CTAGAGAAAA	CAAGCTAGAA	AAGGCAGAAG	GAGTAGCGAC	AGCATCTGAA	240
ACTGCAGAAG	CAGCTAGCGC	AGCTAAACCA	GAGGAAAAAG	CAAGTGAGGT	GGTTGCAGAA	300
ACACCATCTG	CAGAAGCAAA	ACCTAAGTCT	GACAAGGAAA	CAGAAGCAAA	GCCCCAAGCA	360
ACTAACCAAG	GGGATGAGTC	TAAGCCAGCA	GCCGAAGCTA	ATAAGACTGA	AAAAGAAGTC	420
CAGCCAGATG	TCCCTAAAAA	TACAGAAAAA	ACATTAAAAAC	CAAAGGAAAT	CAAATTTAAT	480
TCTTGGGAAG	AATTGTTAAA	ATGGGAACCA	GGTGCTCGTG	AAGATGATGC	TATTAACCGC	540
GGATCTGTTG	TCCTCGCTTC	ACGTCCGACA	GGTCATTTAG	TCAATGAAAA	AGCTAGCAAG	600
GAAGCAAAAG	TTCAAGCCTT	ATCAAACACC	AATTCTAAAG	CAAAAAGACCA	TGCTTTTGTT	660
GGTGGAAGAAG	AGTTCAAGGC	CTATGCTTTT	GACTATTGGC	AATATCTAGA	TTCAATGGTC	720
TTCTGGGAAG	GTCTCGTACC	AACTCCTGAC	GTTATTGATG	CAGGTCACCG	TAACGGGGTT	780
CCTGTATACG	GTACACTTTT	CTTCAACTGG	TCTAATAGTA	TTGCAGATCA	AGAAAGATTT	840
GCTGAAGCTT	TGAAGCAAGA	CGCAGATGGT	AGCTTCCCAA	TTGCCCGTAA	ATTGGTAGAC	900
ATGGCCAAGT	ATTATGGCTA	TGATGGCTAT	TTCATCAACC	AAGAAACAAC	TGGAGATTTG	960
GTTAAACCTC	TTGGAGAAAA	GATGCGCCAG	TTTATGCTCT	ATAGCAAGGA	ATATGCTGCT	1020
AAGGTAAACC	ATCCAATCAA	GTATTCTTGG	TACGATGCCA	TGACCTATAA	CTATGGACGT	1080
TACCATCAAG	ATGGTTTGGG	AGAATACAAC	TACCAATTCA	TGCAACCAGA	AGGAGATAAG	1140
GTTCCGGCAG	ATAACTTCTT	TGCTAACTTT	AACTGGGATA	AGGCTAAAAA	TGATTTACACT	1200
ATTGCAACTG	CCAACCTGGAT	TGGTCGTAAT	CCTTATGATG	TATTTGCAGG	TTTGGAATTG	1260
CAACAGGGTG	GTTCCCTACAA	GACAAAGGTT	AAGTGGAATG	ACATTTTAGA	CGAAAATGGG	1320
AAATTGCGCC	TTTCTCTTGG	TTTATTTGCC	CCAGATACCA	TTACAAGTTT	AGGAAAAACT	1380
GGTGAAGATT	ATCATAAAAA	TGAAGATATC	TTCTTTTACAG	GTTATCAAGG	AGACCCCTACT	1440
GGCCAAAAAC	CAGGTGACAA	AGATTGGTAT	GGTATTGCTA	ACCTAGTTGC	GGACCGTACG	1500
CCAGCGGTAG	GTAATACTTT	TACTACTTCT	TTTAATACAG	GTCATGGTAA	AAAATGGTTC	1560
GTAGATGGTA	AGGTTTCTAA	GGATTCTGAG	TGGAATTATC	GTTCAGTATC	AGGTGTTCTT	1620
CCAACATGGC	GCTGGTGGCA	GACTTCAACA	GGGGAAAAAC	TTCGTGCAGA	ATATGATTTT	1680
ACAGATGCCT	ATAATGGCGG	AAATTCCCTT	AAATTCTCTG	GTGATGTAGC	CGGTAAGACA	1740
GATCAGGATG	TGAGACTTTA	TTCTACTAAG	TTAGAAGTAA	CTGAGAAGAC	CAAAC'TTCGT	1800
GTTGCCACCA	AGGGAGGAAA	AGGTTCTAAA	GTTTATATGG	CATTCTCTAC	AACTTCAGAC	1860

TACAAATTCG	ATGATGCAGA	TGCATGGAAA	GAGCTAACCC	TTTCTGACAA	CTGGACAAAT	1920
GAAGAATTTG	ATCTCAGCTC	ACTAGCAGGT	AAAACCATCT	ATGCAGTCAA	ACTATTTTTC	1980
GAGCATGAAG	GTGCTGTAAG	AGATTATCAG	TTCAACCTAG	GACAAATTAAC	TATCTCGGAC	2040
AATCACCAAG	AGCCACAATC	GCCGACAAGC	TTTTCTGTAG	TGAAACAATC	TCCTTAAAAAT	2100
GCCCAAGAA	CGGAAGCAGT	TGTGCAATTT	AAAGGCAACA	AGGATGCAGA	TTTCTATGAA	2160
GTTTATGAAA	AAGATGGAGA	CAGCTGGAAA	TTACTAACTG	GCTCATCTTC	TACAACATTT	2220
TATCTACCAA	AAGTTAGCCG	CTCAGCAAGT	GCTCAGGGTA	CAACTCAAGA	ACTGAAGGTT	2280
GTAGCAGTCG	GTAAAAATGG	AGTTTCGTTCA	GAAGCTGCAA	CCACAACCTT	TGATTGGGGT	2340
ATGACTGTAA	AAGATACCAG	CCTACCAAAA	CCACTAGCTG	AAAAATATCGT	TCCAGGTGCA	2400
ACAGTTATTT	ATAGTACTTT	CCCTAAGACT	GAAGGTGGAG	AAGGTATTGA	AGGTATGTTG	2460
AACGGTACCA	TTACTAGCTT	GTCAGATAAA	TGGTCTTCAG	CTCAGTTGAG	TGGTAGTGTG	2520
GATATTCGTT	TGACCAAGCC	ACGTACCGTT	GTTAGATGGG	TCATGGATCA	TGCAGGGGCT	2580
GGTGGTGAGT	CTGTTAACGA	TGGCTTGATG	AACACCAAAG	ACTTTGACCT	TTATTATAAA	2640
GATGCAGATG	GTGAGTGGA	GCTAGCTAAG	GAAGTCCGTG	GCAACAAAGC	ACACGTGACA	2700
GATATCACTC	TTGATAAACC	AATCACTGCT	CAAGACTGGC	GCTTGAATGT	TGTCACCTCT	2760
GACAAATGGA	CTCCATGGAA	GGCTATTTCG	ATCTATAACT	GGAAAATGTA	TGAAAAGCTT	2820
GATACTGAGA	GTGTCAATAT	TCCGATGGCC	AAGGCTGCAG	CCCGTTCTCT	AGGCAATAAC	2880
AAGGTACAAG	TTGGCTTTGC	AGATGTACAG	GCTGGAGCAA	CTATTACCGT	TTATGATAAT	2940
CCAAATTCCT	AAACTCCGCT	CGCAACCTTG	AAGAGCGAAG	TTGGAGGAGA	CCTAGCAAGT	3000
GCACCATTTG	ATTTGACAAA	TCAATCTGGT	CTTCTTTATT	ATCGTACCCA	GTTGCCAGGC	3060
AAGGAAATTA	GTAATGTCC	AGCAGTTTCC	GTTCCAAAAG	ATGACAGAAG	AATCAAGTCA	3120
GTCAGCCTAG	AAACAGGACC	TAAGAAAACA	AGCTACGCCG	AAGGGGAGGA	TTTGGACCTT	3180
AGAGGTGGTG	TTCTTCGAGT	TCAGTATGAA	GGAGGAACTG	AGGACGAAC	CATTCGCCTA	3240
ACTCACGCAG	GTGTATCAGT	ATCAGGTTTT	GATACGCATC	ATAAGGGAGA	ACAGAATCTT	3300
ACTCTCCAAT	ATTTGGGACA	ACCGGTAAAT	GCTAATTTGT	CAGTGACTGT	CACCTGGCCAA	3360
GACGAAGCAA	GTCCGAAAA	TATTTTGGGA	ATTGAAGTAA	GTCAGGAACC	GAAAAAAGAT	3420
TACCTAGTTG	GTGATAGCTT	AGACTTGTCT	GAAGGACGCT	TTGCAGTGGC	TTATAGCAAT	3480
GACACCATGG	AAGAACATTC	CTTTACTGAT	GAGGGAGTTG	AAATTTCTTG	TTACGATGCT	3540
CAAAAGACTG	GTCTGCAAA	CTTGACGCTT	CGTTACCAAG	GTCATGAATT	CAATTTTGAT	3600
GTTTTGGTAT	CTCCAAAAGC	AGCATTTGAAC	GATGAGTACC	TCAAACAAAA	ATTAGCAGAA	3660
GTTGAAGCTG	CTAAGAACAA	GGTGGTCTAT	AACTTTGCTT	CACCAGAAGT	AAAAGCAGCT	3720
TTCTTGAAAG	CAATTGAAGC	GGCCGAACAA	GTGTTGAAAG	ACCATGAAAC	TAGCACCCAA	3780
GATCAAGTCA	ATGACCGACT	TAATAAATTG	ACAGAAGCTC	ATAAAGCTCT	GAATGGTCAA	3840
GAGAAATTTA	AGGAAGAAAA	GACAGAACTT	GATCGCTTAA	CAGGTGAGGT	TCAAGAAGCT	3900
TTGGCTGCCA	AACCAAACCA	TCCTTCAGGT	TCTGCCCTAG	CTCCGCTTCT	TGAGAAAAAC	3960
AAGGCCTTGG	TTGAAAAAGT	AGATTTGAGT	CCAGAAGAGC	TTGCAACAGC	GAAACAGAGT	4020
CTAAAAGATC	TGGTTGCTTT	ATTGAAAAGAA	GACAAGCCAG	CAGTCTTTTC	TGATAGTAAA	4080
ACAGGTGTTG	AAGTACACTT	CTCAAAATAAA	GAGAAGACTG	TCATCAAGGG	TTTGAAAGTA	4140
GAGCGTGTTT	AAGCAAGTGC	TGAAGAGAA	AAATACTTTG	CTGGAGAAGA	TGCTCATGTC	4200
TTTGAAAATAG	AAGGTTTGGA	TGAAAAAGGT	CAAGATGTTG	ATCTCTCTTA	CGCTTCTATT	4260
GTGAAAATCC	CAATTGAAAA	AGATAAGAAA	GTTAAGAAAG	TATTTTCTTT	ACCTGAAGGC	4320
AAAGAGGCAG	TAGAATTGGC	TTTTGAACAA	ACGGATAGTC	ATGTTATCTT	TACAGCAGCA	4380
CACTTTACTC	ATTATGCCTT	TGTTTATGAA	TCTGCTGAAA	AACCACAACC	TGCTAAACCA	4440
GCACCACAAA	ACAAAGTCCT	TCCAAAACCT	ACTTATCAAC	CGGCTTCTGA	TCAACAAAAG	4500
GCTCCTAAAT	TGGAAGTTCA	AGAGGAAAAAG	GTTGCCTTTC	ATCGTCAAGA	GCATGAAAAT	4560
ACTGAGATGC	TAGTTGGGGA	ACAACGAGTC	ATCATACAGG	GACGAGATGG	ACTGTTAAGA	4620
CATGTCTTTG	AAGTTGATGA	AAACGGTCAG	CGTCGTCTTC	GTTCAACAGA	AGTCATCCAA	4680
GAAGCGATTG	CAGAAATTGT	TGAAATTGGA	ACAAAAGTAA	AAACAGTACC	AGCAGTAGTA	4740
GCTACACAGG	AAAAACCAGC	TCAAAATACA	GCAGTTAAAT	CAGAAGAAGC	AAGCAAACAA	4800
TTGCCAAATA	CAGGAACAGC	TGATGCTAAT	GAAGCCCTAA	TAGCAGGCTT	AGCCAGCCTT	4860
GGTCTTGCTA	GTTTAGCCTT	GACCTTGAGA	CGGAAAAGAG	AAGATCAAAG	ATTAAATATC	4920
GAAAAATCTT	GTGAAATCTT	TCCTTATATT	TCCAAAGTGT	GA		4962

(2) INFORMATION FOR SEQ ID NO:1553:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 678 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1553:

AAGGAATTAC	GA	CTAAGTTC	TATGAAGGAG	ATGTTGTTTG	TATCATCGGT	CCTTCAGGTT	60
CTGGTAATGT	ACAACANACT	CCGTAGCCTC	AATCTTTTAG	AAGAAGTCAC	TAGCGGTCAC		120
ATCACTGTGA	ACGGCTATGA	TTTAACTGAA	AAAACAACCA	ATGTTGACCA	CGTCCGTGAA		180
AATATCGGCA	TGGTATTCCA	ACACTTCAAC	CTCTTCCCTC	ATATGTCTGT	ATTGGACAAC		240
ATCACCTTTG	CTCCTATTGT	GCACAAGTTG	ATGACTAAGG	AAGAAGCTGA	GAAATTGGGA		300
ATGGAGTTGC	TTGAAAAGGT	TGGACTAGCA	GATAAAGCTA	ATGCCAATCC	AGATAGCCTA		360
TCAGGTGGTC	AAAAACAACG	TGTGGCCATA	GCTCGTGGCC	TAGCAATGAA	TCCAGACATC		420
ATGCTCTTCG	ATGAACCAAC	TTCTGCCCTT	GACCCTGAGA	TGGTTGGAGA	CGTACTTAAC		480
GTATGAAGG	AATTGGCTGA	GCAAGGCATG	ACCATGATTA	TCGTAACCCA	TGAGATGGGA		540
TTTGCTCGTC	AGGTTGCCAA	CCGCGTTATC	TTTACTGCAG	ATGGCGAGTT	CCTTGAAGAC		600
GGAACACCTG	ACCAAATCTT	TGATAACCCA	CAACACCCCTC	GTCTGAAAGA	GTTCTTAGAT		660
AAGGTCTTAA	ACGTCTAA						678

(2) INFORMATION FOR SEQ ID NO:1554:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 657 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
 (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae
 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1554:

AAGATGTTAC	GATCTCAATT	TGAAGAAGAT	TTAGAGAAAT	TACATAACCA	GTTCTACGCT	60
ATGGGACAAAG	AAGTGCTCTC	ACAAATCAAT	CGTACGGTAC	GTGCTTTTGT	CACGCATGAC	120

CGTGACCTGG	CAAAAGAGGT	CATCGAAGAT	GATGCAGAAG	TAAATGAATA	CGAAGTGAAA	180
CTGGAAAAGA	AATCATTTGA	AATGATCGCA	CTCCAACAAC	CAGTCTCTCA	AGATTTGCGT	240
ACAGTCTTGA	CTGTCCTTAA	GGCTGTATCA	GATGTGGAGC	GTATGGGGGA	TCACGCTGTA	300
GCCATTGCCC	AGGCAACCAT	CCGTATGAAG	GGGGAAGAAC	GCATCCCAGC	TGTAGAGGAA	360
GAAATTAAAA	AAATGGGACG	TGAAGTTAAA	AGCGTTGTTG	AAGCAGCACT	TGATCTTTAT	420
CTTAATGGTT	CTGTTGACGA	CGCATACCGG	GTGGCCTCCA	TGGATGAGCA	AATTAACCAC	480
TATTTTGAAA	CTATCCGTGA	CCTTGCGACT	GAAGAGATTA	AGAAAAATCC	AGAAGCCATT	540
GTTACGGGTC	GTGATTATTT	CCAAGTTATT	TCCTACTTGG	AGCGTATCGG	TGACTATGCT	600
AAAAATATCT	GTGAATGGGT	TGTCTACTTT	GAAACAGGTA	AGATTGTCTGA	ACTATAA	657

(2) INFORMATION FOR SEQ ID NO:1555:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...213
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1555:

AAGTTTATAC	GACCATTGTT	AGGGATTTTA	TCATGTGCAT	CCCAAGCTAC	AGCAATATTG	60
TTGGCAAAAT	TACCATATAC	ATCAGCTGCG	AGCACAGCTA	TTCGTAAAAT	CCATCCAAAA	120
ATCTTAGTCA	ATAATCCTAC	TCTTGCTGCC	GCAGTTGCAG	CTGCCCTATT	TAAGATAGAA	180
CGCGCCATAC	TAATACCATA	CTTAGCCGCA	TAA			213

(2) INFORMATION FOR SEQ ID NO:1556:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 867 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1556:

ATCATGGTAC	GTCCAATTGG	AATTTATGAA	AAGGCAACCC	CAACACACTT	TACTTGGCTA	60
GAACGTTTAA	ATTTTGCCAA	GGAGTTAGGC	TTTGATTTTG	TCGAGATGTC	TATTGACGAA	120
CGTGACGAGC	GTTTAGCAAG	ACTTGACTGG	AGTAAGGAAG	AACGCTTGGA	AGTTGTCAAA	180
GCAATCTATG	AAACTGGTGT	TCGTATTCCT	TCTATCTGTT	TTTCAGGCCA	TCGTCGCTAC	240
CCATTGGGTT	CAAAAGATCC	AGTTCCTAGAG	GAAAAATCTC	TAGAACTCAT	GAAAAAATGT	300
ATCGAATTAG	CTCAAGACTT	GGGAGTTCGT	ACGATTCAAT	TAGCTGGTTA	CGATGTTTAC	360
TATGAGGAAA	AGTCACCCCA	GACACGCCAA	CGTTTTATCA	AAAATTTGAG	AAAAGCCTGT	420
GACTGGGCTG	AAGAAGCTCA	GGTGGTACTT	GCTATTGAAA	TTATGGATGA	TCCTTTCATC	480
AGTAGCATCG	AAAAATATTT	GGCTATAGAA	AAAGAGATTG	ACTCTCCCTT	CCTCTTTGTA	540
TATCCAGATA	TTGGTAATGT	GTCTGCATGG	CATAATGATA	TCTATAGTGA	GTTTTATCTT	600
GGTCATCATG	CCATCGCAGC	TCTCCATCTC	AAGGATACTT	ATGCAGTGAC	AGAAAGTTCA	660
AAGGGCCAGT	TCCGAGATGT	ACCTTTCGGG	CAAGGTTGTG	TCAAATGGGA	AGAAGCTTTC	720
GATATTTTAA	AGGAAACCAA	TTATAATGGA	CCTTTCCTAA	TCGAAATGTG	GTCTGAAAAT	780
TGTGAAACAG	TAGAAGAAAC	ACGCGCAGCC	ATTCAAGAGG	CGCAAGCTTT	TCTCTATCCA	840
CTCATTAAGA	AAGCAGGTTT	GATGTAA				867

(2) INFORMATION FOR SEQ ID NO:1557:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1557:

CTCGTATCGC	TAGCGCCCTT	CAACAAGAAA	AGGAAAATGC	TGAGCAAGAT	TCTCAGACAC	60
TTGTACTCTA	TCAAAAACTC	TACGATATTC	TCATGTCGCT	TAGAAAGTAA	TAATGGATCT	120
GATGCGGACT	TTGATAAGGT	GGATGCATTA	TTAGATCAAC	TTTCTGCTAA	TAGTAAAGAC	180
AAAACAGCTT	TACTTGAATC	GACAAAAGCT	ATTCTAGTTT	TGAATCATCA	AATCCAGTCA	240
AAAGCTAGCG	CAAGTGAAGA	AACAAGTCCA	GCAAGAAATG	CTGAAGCAAA	TGGTGATAAC	300
ACCAAGTCTG	AGAACCAACC	AAACGCAACT	GCAGAATCTA	ACATTGAAAC	TGCTAGCGAC	360
GAAAACAAAC	CAAGCAATAC	AAGAGATTCT	AAACCTGCTG	AATCAACTTC	AGAAAATAAA	420
ACAACAGAAAT	CTTCTACAAC	TACTGGAAAT	CAAGAAAAAC	CAGTAGAATA	A	471

(2) INFORMATION FOR SEQ ID NO:1558:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 783 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...783
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1558:

TGGCAATCGC	TGATGCAGGT	TGAGAATCGT	TTGGACCTCC	TTCATACTAT	TACTCGTAAG	60
TATGGTGGGA	CTGTTGATGA	TGTTTTGCTT	TATTTTGCCA	AGATTACGGA	AGAATACAAT	120
CTCTTGACAG	GCAATAATCT	TTCGTCTGAG	GACATGGAAG	CAGAGCTTAA	GAAGTTGGAA	180
GTCAATCTTG	TCAATTTGGC	AGGTCAACTT	GCTTCTGCTC	GTCAATAATT	GGCTCAGCAA	240
CTCGAAGCTG	AGATTAAACA	AGAACTGCAA	GATCTTTATA	TGGAAAAAGC	CCAGTTTCAG	300
GTTCGTTTTA	GTAAGGGAAA	ATTCAGTCGT	GAGGGAAATG	AAATGGTTGA	GTTTTATATT	360
TCAACCAACC	CTGGAGAAGA	CTTTAAACCC	TTGGTTAAGG	TTGCTTCTGG	AGGGGAATTA	420
TCTCGTCTCA	TGTTAGCCAT	TAAGTCTGCC	TTTTCACGTA	AAGAAGGCAA	GACTAGCATT	480
GTCTTTGATG	AGGTGGATAC	GGGAGTTTCA	GGTCGTGTTG	CTCAAGCTAT	TGCTCAGAAA	540
ATTCATAAAA	TTGGTCAGTA	TGGTCAGGTT	TTGGCTATCT	CCCATTTGCC	ACAAGTAATT	600
GCGATTGCAG	ATTATCAATT	CTTTATTGAG	AAGATTAGTA	ATGACCATTG	AACGGTTTCG	660
ACTGTTCTGC	TCTTGACAGT	CGAAGAGCGA	GTGGAGGAAG	TTGCCAAGAT	GTTGGCAGGT	720
GATGATGTGA	CAGAAGCAGC	CCTGACGCAA	GCCAGAGAAT	TGTTGAGAAA	CAGGGAGAAA	780
TAA						783

(2) INFORMATION FOR SEQ ID NO:1559:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 189 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...189
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1559:

TCACTTGCAC	GAGCAGCCTG	CTGCATATTA	TGCGTTACAA	TGATGATGGT	AAAGTTTTTC	60
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TTGAGCTCAA ACATGGTCTC TTCTAGTTGC ATGGTCGCAA TCGGATCCAA GGCTGAGGCT	120
GGCTCATCCA TTAAGAGGAT ATCTGGCTTA ACAGAGATGG CACGAGCGAT ACAGAGACGT	180
TGTTGCTGA	189

(2) INFORMATION FOR SEQ ID NO:1560:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...483
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1560:

AGAACTCAAC GCCCAAAAAG CCCGCTTGAA ACTCCTCATC GCCCTCAATG CCGGACTAAC	60
AGGACAGGCT TTGAAAGACT ATATGGAAGG CTAATACTCT TCGAAAATCT CTGCAAACCA	120
CGTCACGTCG CCTTACCGTA TGTATGGTTA CTGACTTCGT CAGTTTCATC CACAACCTCA	180
AAAACATGTT TTGAGCTGAC TTCGTCAGTT TCATCCACAA CCTCAAAAAC ATGTTTTGAG	240
CTGACTTCGT CAGTTTCATC CACAACCTCA AAAACATGTT TTGAGCTGAC TTCGTCAGTT	300
TCATCTGCAA CCTCAAAGCA GTGCTTTGAG CTGACTTCGT CAGTTCTATC TACAACCTCA	360
AAGCAGTGCT TTGAGCTGAC TTCGTCAGTT CTATCTGCAA CCTCAAAACA GTGTGTTGCA	420
CAGCCTTTAA CCAGCCGCCT AGTCCGCTCT ATGGTATTCA TTAAGTCAAC ATCTCTTGT	480
TAA	483

(2) INFORMATION FOR SEQ ID NO:1561:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...3210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1561:

CTTTGTCCGC	TTGACGCCCT	TAATATCTTA	TATATGCCTA	AACGTACTGA	TATTCAAAAA	60
ATTATGGTGA	TTGGTTCTGG	TCCGATTATT	ATTGGTCAGG	CTGCTGAGTT	TGATTACGCT	120
GGGACCCAGG	CTTGCTTGTC	GTTGAAAGAG	GAAGGTTATG	AGGTTGTTTT	GGTTAACTCA	180
AATCCTGCAA	CCATCATGAC	GGACAAGGAA	ATTGCTGACA	AGGTTTACAT	TGAACCGATT	240
ACACTTGAGT	TTGTGACACG	TATTCTTCGT	AAGGAACGTC	CAGATGCCTT	GCTACCAACA	300
CTCGGTGGTC	AGACAGGTCT	CAACATGGCC	ATGGAATTGT	CTAAAAATGG	TATCTTAGAT	360
GAGCTTGGCG	TTGAACTTCT	GGGTACTAAA	TTGTCTGCCA	TTGACCAAGC	GGAGGACCGT	420
GACCTCTTTA	AACAATTGAT	GGAAGAGCTT	GAGCAACCCA	TTCAGAATC	TGAAATTGTT	480
AACACAGTAG	AAGAAGCAAT	TGCCCTTTGCA	GCGACAATTG	GCTACCCAGT	CATCGTTCGT	540
CCAGCCTTTA	CCCTTGGTGG	TACTGGTGGT	GGTATGTGTG	CCAACGAGAA	AGAATTGCGT	600
GAAATCACTG	AAAATGGTTT	GAAATTGTCA	CCTGTTACCC	AATGTTTGAT	TGAGCGTTTCG	660
ATTGCCGGTT	TCAAGGAAAT	TGAATACGAA	GTGATGCGTG	ACTCAGCTGA	CAATGCCTTG	720
GTTGTTTGTA	ACATGGAAAA	CTTTGACCCA	GTTGGGATTTC	ACACAGGGGA	TTCCATTGTA	780
TTTGCCCTTG	CGCAAACCAT	GTCAGACTAT	GAAAACCAAA	TGCTTCGTGA	TGCGAGCTTG	840
AGCATTATTTC	GTGCCCTCAA	GATTGAAGGT	GGATGTAATG	TTCAGCTAGC	TCTTGATCCT	900
AACAGCTTCA	AGTATTATGT	TATCGAAGTA	AACCCCTCGTG	TATCACGTTT	GTCAGCCCTT	960
GCTTCTAAAG	CGACAGGATA	TCCGATTGCT	AAGTTGGCTG	CCAAGATTGC	AGTAGGTTTG	1020
ACCTTGGATG	AGGTTATAAA	CCCAGTTACA	GGTTCAACCT	ATGCCATGTT	TGAACCAGCC	1080
CTTGACTACG	TAGTTGCTAA	GATTCACAGT	TTCCCATTTG	ACAAGTTTGA	AAAGGGTGAA	1140
CGCCGTCTCG	GTACACAAAT	GAAGGCGACT	GGAGAAGTCA	TGGCAATCGG	TCGTAACATC	1200
GAGGAATCTC	TTCTCAAGGC	CTGCCGCTCC	CTTGAAATTG	GGGTGCACCA	CAATGAAATA	1260
CCTGAACTTG	CAGCAGTTTC	TGATGATGCC	TTGATTGAAA	AGGTTGTCAA	AGCCCAAGAT	1320
GACCGTCTCT	TCTATGTGTC	AGAAGCCATT	CGCCGTGGTT	ACACACCTGA	AGAAATTGCA	1380
GAGCTTACAA	AAATTGATAT	CTTCTATCTT	GATAAACTCT	TGCATATCTT	TGAAATTGAG	1440
CAAGAATTGG	GTGCTCATCC	ACAAGATCTA	GAAGTTTTGA	AAACAGCCAA	ACTTAATGGT	1500
TTTTCAGACC	GTAAGATTGC	TGAACTCTGG	GGAACGACTG	ATGATCAAGT	TCGCCAACTT	1560
CGTTTGGAAA	ACAAGATTAT	CCCAGTTTAT	AAGATGGTAG	ACACTTGTGC	GGCAGAGTTC	1620
GACTCTGAAA	CGCCATATTT	CTATTCAACC	TATGGTTGGG	AAAATGAATC	TATCAGATCT	1680
GATAAAGAAT	CTGTACTTGT	CCTAGGTTCA	GGTCCAATCC	GTATCGGTCA	AGGGGTTGAG	1740
TTTGACTACG	CAACCGTTCA	CTCTGTTAAG	GCTATCCAGG	CAGCTGGTTA	TGAAGCTATT	1800
ATCATGAACT	CAAACCCAGA	GACCGTTTCA	ACAGACTTCT	CTGTATCAGA	TAAGCTTTAC	1860
TTTGAGCCAT	TGACATTCTGA	AGATGTTATG	AACGTCATTG	ACTTGGAACA	ACCAAAGGGA	1920
GTTATCGTTC	AGTTCCGGTG	TCAAACAGCC	ATCAACCTTG	CGGAGCCATT	GGCAAAAGCA	1980
GGTGTGACCA	TCCTTGGTAC	ACAGGTTGCT	GACCTAGACC	GTGCCGAAGA	CCGTGACCTC	2040
TTCGAGCAAG	CTCTCAAAGA	ATTGGATATT	CCACAGCCAC	CAGGACAAAC	GGCTACCAAT	2100
GAAGAAGAAG	CAGCTCTTGC	AGCTCGTAAG	ATTGGCTTCC	CAGTTCCTGT	CCGCCCATCT	2160
TATGTACTTG	GTGGACGTGC	CATGGAAATC	GTTGAAAACG	AAGAAGACCT	TCGTTCTTAC	2220
ATGCGAACTG	CTGTTAAGGC	TAGTCCAGAC	CACCCAGTTC	TTGTCTGACT	TTACATCGTT	2280
GGGCAAGAGT	GCGAAGTTGA	TGCCATTTCA	GATGGTAAAA	ATGTACTCAT	TCCTGGTATT	2340
ATGGAGCATA	TCGAACGTGC	TGGTGTCCAC	TCAGGTGACT	CAATGGCTGT	TTACCCACCA	2400
CAAACCTTGT	CGCAAAAGGT	TCAGGAGACC	ATCGCAGACT	ACACCAAACG	CTTAGCAATC	2460
GGTCTTCACT	GCCTTGGAAT	GATGAACATC	CAGTTTTGTTA	TCAAGGATGA	AAAAGTCTAC	2520
GTTATTGAGG	TCAATCCACG	TGCCAGCCGT	ACAGTTCCAT	TCCTATCTAA	GGTAACCAAT	2580
ATTTCTATGG	CTCAAGTAGC	GACCAAGCTC	ATTCTTGGTC	AAAGTTTATC	AGAACTTGGC	2640
TACCAAAATG	GACTTTACCC	TGAAAGCACC	CGTGTTTATA	TCAAGGCACC	TGTCTTCTCC	2700
TTTACCAAAC	TAGCTAAGGT	AGACAGCTTG	CTCGGTCCTG	AAATGAAGTC	AACAGGTGAA	2760
GTTATGGGTT	CTGATGCTAC	TTTGGAAAAA	GCTCTCTATA	AAGCCTTTGA	AGCTTCTTAT	2820
CTACACTTGC	CAACTTTTGG	TAATGTCGTC	TTTACCATCG	CTGATGATGC	CAAAGAAGAA	2880
GCCTTGAACT	TGGCTCGTCG	TTTCCAAAAC	ATTGGTTATG	GAATCCTTGC	GACAGAAGGG	2940
ACAGCAGCCT	TCTTTGCTAG	TCATGGCTTG	CAAGCCCAAC	CTGTTGGTAA	GATTGGTGAT	3000
GATGATAAGG	ATATCCCAAG	TTTTGTACGC	AAAGGAAGAA	TTCAAGCTAT	CATTAACACA	3060
GTAGGAACAA	AACGAACTGC	TGACGAAGAT	GGTGAGCAAA	TTCGTCGTTT	AGCCATTGAA	3120
CACGGGGTGC	CCCTCTTCAC	AGCGCTAGAT	ACAGCTAATG	CCATGCTTAA	GGTACTTGAA	3180
AGTCGTAGCT	TTGTTACAGA	AGCGATTTAA				3210

(2) INFORMATION FOR SEQ ID NO:1562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1562:

ATGCAACAAC	GGTTCCTGAT	TATCCTTGAT	AATCAAGGTG	ATTTACAGAA	TATTGGTGGC	60
TTGTCTTACT	TGGTTGAGAT	TGTTAATTCT	GTGCCAACTT	CTGCTAATGC	GGAGTATTAT	120
GCTAAGATTG	TTGCAGAAAA	AGCAATGCTA	CGTCGTTTAA	TTGCCAAGTT	GACAGAGTCT	180
GTCAACCAAG	CTTACGAAAG	GTCACAACCA	GCTGATGAAA	TTATTGCTCA	GGCAGAAAAA	240
GGGTTGATTG	ATGTCAGTGA	AAATGCAAAT	CGAAGCGGGT	TTAAGAACAT	TCGAGATGTG	300
TTGAATCTCA	ACTTTGAAAA	TCTGGAAGCT	CGCTCGCAAC	AAACGACCGA	TATTACAGGT	360
ATTGCGACAG	GTTATCGTGA	TTTGGATCAT	ATGACAACAG	GACTTCATGA	GGAGGAGTTG	420
ATTATCTTAG	CAGCTCGTCC	AGCAGTTGGT	AAGACAGCAT	TTGCCCTTGAA	TATCGCTCAG	480
AACATTGGGA	CTAAGTTGGA	CAAAACGGTT	GCTATTTTTT	CACTCGAAAT	GGGTGCGGAA	540
AGCTTGGTAG	ATCGTATGTT	AGCTGCAGAA	GGCTTGGTGG	AGTCACATTC	TATCCGTACA	600
GGGCAATTGA	CAGATGAGGA	GTGGCAAAAA	TATACTATTG	CTCAGGGTAA	TCTAGCTAAC	660
GCCAGTATCT	ATATCGATGA	TACGCCAGGT	ATTCCGATTA	CAGAGATTCT	TTCTCGTTCT	720
CGTAAATTGG	CTCAAGAAAC	TGGAAATCTT	GGTTTGATTG	TGATAGACTA	TTTGCAACTT	780
ATCACGGGAA	CTGGTCGAGA	AAATCGTCAA	CAAGAAGTTT	CTGAAATTTT	TCGTCAGTTG	840
AAAATACTAG	CCAAGGAATT	GAAGGTTCCA	GTAATCGCTC	TGAGTCAGCT	TTCTCGTGGT	900
GTAGAACAAC	GTCAGGACAA	GAGACCGGTC	TTGTCTGATA	TTCGTGAATC	TGGGTCTATT	960
GAGCAGGACG	CTGATATCGT	AGCTTTTCTC	TATCGCGATG	ACTACTATGA	ACGTGGTGGT	1020
GAAGAAGAGG	AGGGTATCCC	AAATAATAAG	GTGGAAGTTA	TTATCGAGAA	AAACCGTAGT	1080
GGAGCTCGTG	GAACAGTGGA	ATTGATTTTC	CAAAAAGAAT	ACAATAAATT	TTCAAGTATC	1140
TCAAAGAGGG	AGGCATAA					1158

(2) INFORMATION FOR SEQ ID NO:1563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...858

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1563:

ATTACCAAC	GGAAGGAAAC	CACAATGAAC	CATAAAATCG	CAATTTTATC	AGATGTTTCAT	60
GGCAATGCGA	CGGCGCTAGA	AGCAGTGATT	GCAGATGCTA	AAAATCAAGG	GGCCAGTGAA	120
TATTGGCTTC	TGGGAGATAT	TTTTCTTCCT	GGTCCAGGCG	CAAATGACTT	AGTCGCCCTG	180
CTAAAGGACC	TTCTATCAC	AGCAAGTGTT	CGAGGCAATT	GGGATGATCG	TGTCCTTGAG	240
GTCTTGATG	GCGAATATGG	TTTGGAATAT	CCGAAAGAAA	TCCAGTCAAT	GCGCATGACC	300
CAGTTTTTGA	TGGAGCGAAT	GGATCCTGCA	ACGATTGTCT	GGCTACGAAG	CTTGCCTTTG	360
CTGGAAAAGA	AAGAAATTGA	CGGATTGCGC	TTTTCTATCT	CTCATAATTT	ACCTGACAAA	420
AACTATGGTG	GTGACTTGCT	AGTTGAGAAT	GATACAGAGA	AATTTGACCA	ACTGCTAGAT	480
GCGGAAACGG	ACGTGGCAGT	TTATGGTCAT	GTTCAACAAGC	AGTTGCTTCG	TTATGGAAGT	540
CAAGGGCAAC	AAATCATCAA	TCCAGGGTCG	ATTGGCATGC	CCTATTTTAA	TTGGGAGGCG	600
TTAAAAAATC	ACCGTGCCCA	GTATGCCGTG	ATAGAGGTTG	AAGATGGGGA	ATTGGTAAAT	660
ATCCTATTTT	GTAAAGTCGC	TTATGATTAC	GAGGCTGAGT	TAGAATTTGC	CAAATCCAAG	720
AGGCTTCCCT	TTATCGAAAT	GTATGAAGAA	CTGCGTCGTG	AAGATAACTA	TCAGAGGCAC	780
AATCTGGAAC	TATTAGCAAG	CTTAATAGAA	AAGCATAGGT	ATGTAGAGGA	TGTGAAGAAT	840
TTTTTTGATT	TTTTGTAA					858

(2) INFORMATION FOR SEQ ID NO:1564:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 291 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1564:

TTGATACCGC	TGGAACGATT	TGTCATGCGG	CAGATGCTCT	TGCGGAAGCT	GGTGCTGTTG	60
AAGTCTATGC	AAGCTGTACG	CACCCAGTTC	TTTCTGGTCC	TGCTACGGAC	AATATCCAAA	120
AATCAGCTAT	TAAGAAAGTG	GTTGTTTTTG	ATACCATCTA	TCTGCCAGAA	GAGCGCTCTG	180
ATTGATAAGA	TTGAGCAGAT	CTCAATCGCT	CATCTCCTAG	GGGATGCTAT	CGTACGTATT	240
CATGAAAAAC	GACCACTTTC	TCCACTTTTC	GATATTGAGA	AAAAAATTTA	A	291

(2) INFORMATION FOR SEQ ID NO:1565:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...450
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1565:

CGAATACGAC	GATGTTTTCA	AAGCTTTGGT	GGAAAAATGA	CAATCTATCT	GACAGAAAAG	60
CAAATTGAAA	AAATAAATGC	TTTAGCAATT	CAACGGTATT	CTCCAAATGA	GAAAATTCAA	120
ACAGTTAGTT	CTTCTGCCTT	AAATATGATT	GTGAACCTAC	CAGAACAATT	TGTCCTTGGG	180
AAGTCTCTTT	ATCCAACAAT	TTTTGATAAA	GCAACGATAC	TATTTGTCCA	ATTGATAAAG	240
AAGCATGTTT	TTGCTAATGC	TAATAAAAGA	ACTGCTTTCT	TCGTTTTGGT	CAAATTTTTA	300
CAATTAAACG	GCTATCGTTT	TTCTGTAACG	GTAGAAGAAG	CAGTAAAAAT	GTGTGTAACC	360
ATCGCAGTAG	AAGCTTTAAC	TGATGAAAAA	ATGACAAGCT	ATTCCAAATG	GGTTTCTGAA	420
CATTCTGTTA	GAGAAAAGGT	CAAAAAGTAA				450

(2) INFORMATION FOR SEQ ID NO:1566:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1221 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1221
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1566:

TTGAAAACGC	TTAAAAAGGG	GTATCATGTT	ATGACAAAAA	CAATTGCAAT	CAATGCAGGA	60
AGTTCAGTT	TGAAATGGCA	ATTATACTTA	ATGCCAGAAG	AAAAAGTATT	GGCGAAAGGT	120
TTGATTGAAC	GTATCGGTTT	GAAAGATTCA	ATTTCAACTG	TAAAATTTGA	CGGCCGTTCT	180

GAACAACAAA	TTTTGGATAT	TGAAAATCAT	ACACAAGCCG	TTAAAATTTT	ATTGGATGAC	240
TTGATTCGTT	TCGATATTAT	CAAGGCTTAT	GACGAGATTA	CAGGTGTTGG	ACATCGTGTT	300
GTTGCTGGTG	GAGAATATTT	CAAACAATCA	ACAGTTGTTG	AGGGAGATGT	TTTAGAAAAA	360
GTTGAAGAGT	TGAGTTTGTC	GGCTCCTCTA	CACAACCCGG	CCAATGCAGC	AGGTGTTTCGT	420
GCCTTCAAGG	AATTGTTGCC	AGACATTACC	AGTGTAGTTG	TTTTTGATAC	TTCCTTCCAC	480
ACAAGTATGC	CAGAGAAAAGC	TTATCGCTAC	CCTCTACCAA	CAAAATATTA	CACAGAAAAC	540
AAGGTTTCGT	AATACGGTGC	TCATGGTACA	AGTCACCAGT	TTGTAGCAGG	AGAAGCTGCA	600
AAACTCTTGG	GACGTCCATT	AGAAGACTTG	AAGTTAATTA	CCTGTCATAT	TGGTAACGGA	660
GGCTCAATTA	CAGCTGTGAA	AGCCGGCAAA	TCTGTAGACA	CTTCTATGGG	GTTCACTCCT	720
CTTGGTGGTA	TTATGATGGG	AACGCGTACA	GGGGATATTG	ATCCAGCTAT	CATTCCTTAT	780
TTAATGCAAT	ATACAGAGGA	TTTTTAACACA	CCAGAAGATA	TCAGTCGTGT	TCTTAACCGT	840
GAATCAGGTC	TTTTGGGAGT	TTCTGCTAAT	TCTAGCGATA	TGCGCGATAT	AGAAGCAGCT	900
GTAGCAGAA	GGAATCACGA	GGCTAGCTTG	GCTTATGAAA	TGTATGTTGA	CCGTATCCAA	960
AAACATATCG	GTCAGTACCT	TGCAGTGCTA	AATGGAGCAG	ATGCCATTGT	TTTCACAGCA	1020
GGTGTCCGTG	AAAAATGCAGA	GAGTTTCCGT	CGTGATGTAA	TCTCAGGGAT	TTCGTGGTTT	1080
GGTTGTGATG	TTGATGATGA	AAAGAATGTC	TTTGCGGTTA	CAGGAGACAT	CTCAACAGAG	1140
GCAGCTAAAA	TCCGTGTCTT	GGTTATTCCA	ACAGATGAAG	AATTAGTCAT	TGCCCCGTGAC	1200
GTTGAACGCT	TGAAAAAATA	A				1221

(2) INFORMATION FOR SEQ ID NO:1567:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 564 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...564
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1567:

GGAAAATTGC	GAIAAAAAAGT	TAAGAAAAAG	ACCAGAATGG	CGATTGAAAA	TTATATACCA	60
GATTTTGCTG	TGGAAGCAGT	CTATGATCTG	ACAGTCCCAA	GCCTGCAGGC	GCAGGGAATC	120
AAGGCTGTTT	TGGTCGATTT	GGATAATACC	CTCATTGCTT	GGAACAACCC	TGATGGAACG	180
CCAGAGATGA	AGCAATGGCT	ACATGACCTT	CGGGACGCGG	GTATTGGCAT	TATCGTAGTG	240
TCAATAACA	CCAAAAAACG	CGTTCAACGA	GCAGTTGAGA	AATTTGGGAT	TGATTACGTT	300
TACTGGGCCT	TGAAGCCCTT	CACATTTGGT	ATTGACCGTG	CTATGAAGGA	ATTCCACTAT	360
GACAAAAAGG	AAGTGGTCAT	GGTTGGTGAC	CAGCTCATGA	CAGATATACG	AGCAGCCAC	420
CGTGCAGGGA	TTCGGTCAAT	TTTAGTCAAA	CCCTTGGTCC	AACATGACTC	AATCAAAACG	480
CAGATTAACC	GAATCTGTGA	GCGTCGTGTT	ATGAGAAAAA	TCACTGAAAA	GTACGGACCG	540
ATTACATATA	AAAAAGGAAT	TTAA				564

(2) INFORMATION FOR SEQ ID NO:1568:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1568:

CGGTCCATGC	GGTTTAATTT	TCTTCATCGT	TATATATCTC	CTTCTTTAGC	AACTTCTCTT	60
GTTCAACAAGG	TTATCCACAG	GTTGTGGATA	ATAAACCATG	ATCTAACCGC	CAGCTCTTTC	120
CAACTCCAAC	TGGTAGGCTC	AGGATTTTTC	TCCTCAATAT	TCCCTCTTCA	AACAGCTCTG	180
TCATATGGTT	CTGCTAACAC	CTCTCAGAA	TGCTACTCTCC	ATAATTATTC	TCAGGCTTCT	240
TTCAGGTCAT	TGTGTGAAGA	CCATTCACTC	TCCAGACTTT	TCCACAGATT	GTGA	294

(2) INFORMATION FOR SEQ ID NO:1569:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 549 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1569:

TTATTGATGC	GACGGAAGTA	TAAATCAATC	GCCCTAAAAA	AAGAATTAGC	GAATTATTCT	60
GGTAAAAAGA	AATGCCACGC	TATGAAGGCT	CAAGCGATTG	TCACAAGTCA	AGGGAGAATT	120
GTTTCTTTGG	ATATCACTGT	GAAGTATTGT	CATGATATGA	AGTTGTTCAA	AATGAGTCGC	180
AGAAATATCG	GACAAGCTGG	TAAAATCTTG	ACTGACAGTG	ATTATCAAGG	GCCCATGAAG	240
ATATATCCCTC	AAGCACAAAC	TCCACGTAAA	GCCAGCAAAC	TCAAACCGCT	AACAGCTGAA	300
GATAAAGCCT	GTAACCATGC	ACTATCTAAG	GATAGAAGCA	AGGTTGAGAA	CATCCTTGCC	360
AAAGTAAAAA	CGTTTAAAAAT	GTTTTCAACA	ACCTATCGAA	ATCATCGTAA	ACGCTTCGGA	420
TTACGAATGA	ATTTGATTGC	TGGTATTATC	AATCATGAAC	TAGGATTTTG	GTTTCGCAGG	480
AAGTCTAATG	TAATTTTTCG	AATTCAAGAC	GTTTCGATGA	CTATTCAAGA	TCTGGATGAA	540

(2) INFORMATION FOR SEQ ID NO:1570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1023 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1023

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1570:

AGGGCATCGC	GACAAAGACC	GCAGAAAGGA	AACGGTAAAC	CGTTCATGAG	AAAACCAAAG	60
ATAACGGTGA	TTGGTGGAGG	GACTGGAATT	CCCGTCATTC	TAAAAAGTCT	GCGGGAAAAA	120
GATGTGGAAA	TCGCAGCTAT	CGTGACGGTG	GCAGATGATG	GTGGTTCTTC	AGGTGAACTC	180
CGAAAAATA	TGCAACAGTT	GACACCGCCA	GGTGATCTTC	GTAATGTCCT	TGTGGCCATG	240
TCGGATATGC	CTAAGTTTTA	TGAGAAGGTC	TTTCAGTATC	GGTTCTCTGA	GGATGCCGGA	300
GCCTTTGCTG	GCCATCCATT	GGGAAATCTC	ATCATTGCTG	GCTTGTCAGA	AATGCAGGGT	360
TCAACCTATA	ATGCCATGCA	GTTATTGAGC	AAATTTTTCC	ATACAACAGG	GAAAATTTAT	420
CCTTCCAGTG	ACCATCCTTT	GACCC TTCAT	GCAGTCTTTC	AGGATGGGAC	AGAAGTGGCT	480
GGAGAGAGTC	ATATTGTAGA	CCATCGAGGC	ATAATTGACA	ATGTCTATGT	GACCAATGCC	540
CTAAACGATG	ATACGCCTCT	GGCCAGCCGT	CGAGTAGTGC	AGACCATCCT	TGAAAGTGAC	600
ATGATTGTCC	TAGGGCCAGG	TTCCCTCTTT	ACCTCTATTT	TGCCCAATAT	CGTGATTAAAG	660
GAAATTGGGC	GGGCTCTTTT	GGAAACCAAG	GCAGAAATTG	CCTATGTCTG	CAATATCATG	720
ACCCAACGTG	GGGAGACGGA	ACACTTTTACA	GATAGCGACC	ACGTGGAAGT	CTTGCATCGT	780
CACCTTGGTC	GCCCTTTTAT	CGACACTGTC	TTGGTGAATA	TTGAAAAAGT	GCCTCAGGAA	840
TACATGAATT	CCAACCGTTT	TGATGAATAC	TTGGTGCAAG	TGGAACACGA	TTTTGTAGGT	900
CTTTGTAAAGC	AAGTTTCGCG	CGTGATTTCA	TCTAACTTCC	TTCGTCTGGA	AAATGGCGGT	960
GCCTTCCACG	ATGGAGATTT	GATTGTGGAC	GAGTTGATGC	GCATTATACA	GGTGAAAAAA	1020
TGA						1023

(2) INFORMATION FOR SEQ ID NO:1571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1571:

TATAGTAAGC	GCGTCATAAC	AAGGTATCTA	TCATTCATGG	AGCTCCTCCT	GTATACTATT	60
AGTAAAGTAA	AACTATTGGA	GGATATTTTA	ATGCCACAAC	CTATTGTTCC	TGTAGAGATT	120
CCACAATCTC	GTCTTTTGA	TTCTAAAAAG	AGAAATGATA	TTCTGCTTAA	AATTCGTATT	180
GGCAAGCTTG	AAGTAAGTTT	TTTTCAATCT	CTCAATCTCG	AAATGGTAGA	ACAGCTTTTG	240
GATAAGGTGT	TGCTCTATGA	CAATTCATCT	ATCTAG			276

(2) INFORMATION FOR SEQ ID NO:1572:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 429 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1572:

CACGGCAAGC	GCCGGCGGTT	TCCGCGCGCG	TCGCGGCGTC	CACGCAAGCC	CGGGAGCCGG	60
CCAGCGTTTC	GGCGCTCCG	GTCGACGAAC	CGCCGCTGGT	GCCGGTGTCC	TCCCACCCGC	120
AAATCGCAGG	TCGACGCAT	GAGCGGCCAC	AGCCCGGCCC	CGGCTTCCCG	GCGAAAACCG	180
CAGCCGAGGT	CGCGTCCACG	GCGCAGGCCA	GTGTCCAGGT	CTCGCCGCCC	GCGCCGACAG	240
CGGGCGGCGA	AGGCCGCGGA	GAGGAGCGTC	GGCAACCCGG	AGAAACCGAT	CCATCCGCAC	300
TGCCCCCGGA	CGACCAAGCG	CCTGTGCCAT	TGCCTGCCAT	GCAAACCCCG	GGCGACCGCC	360
TGCTGGCACG	CCTGCTGGCA	TCGAGCGGGA	GCCGGCCACT	GCCGCTGGCC	GATCTCGCGC	420
GCCTGCTAG						429

(2) INFORMATION FOR SEQ ID NO:1573:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 648 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1573:

TTTCACTGGC	GATCACGTGG	TGTAAAGCTC	AATTCCGATT	TCGTCGCCAC	CAGCATCGCC	60
GAGTATATCC	GCGACCAGGG	ACGCCGCGTC	CTGCTGCTGA	TGGACTCGCT	GACCCGCTTC	120
GCCAGGGCCC	AGCGCGAAAT	CGGCCTGGCG	GCCGGTGAAC	CGCCCACCCG	CCGCGGCTAT	180
CCGCCATCGG	TGTTCGCCGC	GCTGCCACGC	TTGATGGAGC	GTGCCGGGCA	ATCCGAGCGG	240
GGCTCGATCA	CCGCGCTCTA	CACCGTGCTG	GTGGAAGGCG	ACGACATGAG	CGAGCCGGTG	300
GCCGACGAGA	CCCGCTCGAT	TCTCGACGGG	CACATCGTGC	TGTCGCGCAA	GCTGGCCGCC	360
GCCAAACCACT	ATCCGGCCAT	CGACGTGCTG	CACTCGGTGA	GCCGGGTCAT	GAACCAGATC	420
GTCGACGACG	ATCAGCGCCA	TGCGGCCGGA	CGCTTGCGCG	AATGGCTGGC	GAAGTACGAG	480
GAAGTCGAGT	TGCTGCTGAA	GATCGGCGAA	TACCAGAAAG	GCCAGGACAG	CGAAGCCGAC	540
CAGGCCATCG	AGAAGATCGC	GGCGATCCGC	CAGTGGCTGC	GCCAGGGTAC	CCACGAAACC	600
AGCGATTACG	CACAGGCCTG	CGCGCAGTTG	CGGAGCCTCT	GCGCATGA		648

(2) INFORMATION FOR SEQ ID NO:1574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1574:

CTAGACTGGC	GGGAGAGAGT	CGTCGATAGT	GGACACCATA	TCCGATTCCA	AAATCGTTGC	60
TATATCCCTA	CCGAGCAAGG	AAAAGAAAGT	CATTTTCATCA	GAAAGACAAA	AGCATTAGTT	120
ATAAAAGCAT	TTGATGGTGA	CATCTACCTC	AATATCGCTG	ACAAAATCTA	TCACACAAAG	180
GAGCTACTAA	ATCATGAACT	CTATTCGAAA	AAC TTTGAAC	AAGAACCAGA	ACAAAAA	240
GAAAGACGCA	AGTATATCCC	TCCACAAACC	CATCCGTGGA	AACTCACATC	TTTCAAACAA	300
TATCTTCATA	AAAAATAAAAA	GGATTATGAA	GAGTTTAAAG	GAGGATTTTT	CAGTACGTGC	360
TGA						363

(2) INFORMATION FOR SEQ ID NO:1575:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 252 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...252
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1575:

ACACTACGGC	GTTTACCTTT	ACGACCCTAC	ACGAGTTGTA	AAATTCGGTG	GCGCGTAAGA	60
GGTGACGATA	TGAGTTTATT	GCTACGACGT	CATTATATTC	AAGAAGAGCA	GGTTAACCAG	120
TATTCTGATT	TAGAGAATAA	AACTCTAGAA	GAGTTGAAGG	ATCTAGCGAA	AGAAGCAGGT	180
GTAGCAGGCG	CTTATAAGTT	GACAAAAGCC	GAAATTGTAG	AAGTTTTGGA	GGAACATAAA	240
AGTGAAATTT	AA					252

(2) INFORMATION FOR SEQ ID NO:1576:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...192
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1576:

TTCCGCGGGC	GCGTCAACAG	CTCTAGAGAT	CCGCCTACCT	TTCACGAGTT	GCGCAGTTTG	60
TCTGCAAGAC	TCTATGAGAA	GCAGATAAGC	GATAAGTTTG	CTCAACATCT	TCTCGGGCAT	120
AAGTCGGACA	CCATGGCATC	ACAGTATCGT	GATGACAGAG	GCAGGGAGTG	GGACAAAATT	180
GAAATCAAAT	AA					192

(2) INFORMATION FOR SEQ ID NO:1577:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...234
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1577:

GCTAAAGGGC	GTATTACAGG	GATTCAGCCC	TACGGTGCCT	TTGTTGAGTT	AGAGACGGGT	60
GATACGGGGC	TGATTCACAT	TTCAGAAATT	CGGACAGGAT	TTATTGAAAA	TATTCACGAA	120
ACCTTGAAAG	TCGATGAAGA	AGTTCAAGTT	CAGGTAGTGG	ATTTAGATGA	ATTTACGGGG	180
GAAAGCCAGT	CTTTCTATCC	GCACTTTGGA	GGAAGAAAAG	TACCAGTTTC	CTAG	234

(2) INFORMATION FOR SEQ ID NO:1578:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 924 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...924
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1578:

TACAATATTT	TTAACAAAAT	TTTATTGTTT	GTTAACTTTT	TTCACGAAAA	GGAGAAAATC	60
ATGCGTTATG	ATTTCCGAAA	GGTCTATAAA	GAAATACGTG	AGTCAAAGGG	GCTGACCCAA	120
GAAGAGGTCT	GTGGGGGTGT	TCTCTCAAGA	ACCAGCTTAT	CAAAAATCGA	AAGTGGCAAG	180
ACAACCCCAA	AATATGAAAA	TATGGAATTT	CTTCTCCGTC	AAATCAATAT	GAGTTTTGAA	240
GAGTTTGAAT	ATATCTGTCA	ACTTTATCAA	CCAAGTCAAC	GCACAGAGAT	TATGCAAACC	300
TATCTCAATA	TGCGTTCCAT	TATCGGGACC	AGCGATCTTG	TCAATTTATT	TCAAAAATGC	360

CAAGACTACC	TCAAGACCCA	CCACGATCTC	CCTATAGAAG	AAATCAGAGA	TATGCTTGAA	420
GTTGTTATTT	ATCTCCGTCA	ACACGGGGCA	GGGGAACAT	CAAAACACGC	AGAACAGGTT	480
GTCAAAAAAC	TTTGAAAAAA	AATTGAAAAA	CAAGATACAT	GGTATGAGAG	TGATCTAAAA	540
ATCCTCAATA	CCATTCTTTT	CAGTTTTCCC	ATTGAATACC	TCCATCTCAT	CACTGGAAAA	600
ATATTGCAAC	GCCTAGAAGT	CTATAAAAAA	TATCAACATT	TATATGACTT	GCGAATGACA	660
ATTCTATTAA	ACCTTTCCAC	ACTCTATCTA	TACAATCAAG	ATAAAAAACAT	GTGTAAGCAA	720
ATCTGCTACA	CTTTACTAGA	GGACGCCAAG	AATAAGAAAA	GCTACGATAG	GCTGGCTATC	780
TGCTATGTCC	GTATTGGGAT	TTGTACAGAC	GATTCTAAAC	TTATCCAAAA	AGGGTTCTCC	840
CTTCTGGAGC	TAACCGAGGA	AACTTCTATG	CTGTCTCATC	TCAAAAAAGA	AGTAGAGATC	900
TATTACCAAG	CGAAGGAAAG	ATAA				924

(2) INFORMATION FOR SEQ ID NO:1579:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 402 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...402
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1579:

ATGTCACAGC	TGCTCCTGGT	AGAGAAGCTA	GAAGTACACG	ACGAAGAGAG	TTACCAAGAG	60
TTGTACCGTA	GCCACGTTCA	AGTGGTTCGA	TTACAAACTT	GCCATAATCT	TTATTTTCAT	120
CAATTTTTGT	TATATTTGGT	TTTTCAAACT	CGATCATTTA	GTTACTCCCT	CTTAAACGAA	180
AAGCAGTGTA	ATGCGATGAT	TATACACGGC	GACGTTTTGG	AGGACGAGCA	CCATTGTGTG	240
GGCACTGGAG	TCACATCACG	AATTGCTGTT	ACTTCAAGAC	CAGCGGCAGC	AAGCGCACGA	300
ATAGCTGACT	CACGACCAGA	ACCTGGACCT	TTTACAGTAA	CTTCAACTGA	TTTAAGACCG	360
TGTTCTTGTTG	CAGATTTAGC	AGCAGCTTCA	GAAGCCATTT	GA		402

(2) INFORMATION FOR SEQ ID NO:1580:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1580:

AAAAATAAGC	TAGTAAGAAT	CACTCTTATT	TTAGCGAAAA	ATTACAGAAA	TGAATGGTTT	60
TTCTTGATGA	AACAGAGAAA	AGAATTGTAC	CTCTTTCTTG	GTCGGACAGC	CTTGTATTTT	120
CTTATCTTTC	TAGGGCTGCT	TTACTTCTTT	AGCTATCTTG	GTCAGGGTCA	AGGAAGCTTT	180
ATCTATAATG	AATTTTAA					198

(2) INFORMATION FOR SEQ ID NO:1581:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1518 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1581:

AGAGTCAAGC	TCAAAAAGAA	AGAGATGAGG	AAACTTCGAA	TGTCTAATTG	GGACACTAAA	60
TTTTTGAAAA	AAGGTTTTAC	CTTTGATGAT	GTATTGCTTA	TTCCAGCTGA	AAGTCATGTG	120
TTGCCTAACG	ATGCAGATTT	AACAACATAA	TTGGCAGATA	ATTTGACTTT	AAATATCCCA	180
ATTATTACCG	CTGCCATGGA	CACAGTTACA	GAGAGTCAAA	TGGCCATTGC	TATTGCTCGT	240
GCAGGCGGTC	TCGGAGTTAT	CCATAAAAC	ATGTCAATTG	CTCAACAAGC	AGACGAGGTT	300
CGTAAGGTAA	AACGTTCTGA	AAATGGAGTT	ATTATTGATC	CGTTCTTCTT	GACGCCTGAA	360
CATACAATTG	CTGAAGCAGA	TGAGCTTATG	GGTCGTTACC	GCATCAGTGG	TGTTCCAGTT	420
GTTGAAACAC	TTGAAAATCG	TAAATTGGTT	GGTATTTTGA	CAAACCGAGA	TCTTCGTTTT	480
ATTTTCAGATT	ATAATCAACC	AATTTCAAAC	CATATGACTA	GTGAAAATCT	TGTTACTGCT	540
CCTGTGGGTA	CGGATCTTGC	AACGGCTGAG	AGTATTCTTC	AAGAGCATCG	TATTGAAAAA	600
CTTCCGTTGG	TCGATGAAGA	AGGCAGTCTT	TCTGGTTTGA	TCACTATCAA	AGATATTGAA	660
AAAGTTATTG	AGTTTCCAAA	TGCGGCTAAA	GATGAGTTTG	GTCGTCCTCT	AGTTGCAGGT	720
GCAGTAGGTG	TTACTTCAGA	TACATTTGAA	CGTGCAGAGG	CTCTTTTGA	GGCAGGAGCG	780
GATGCGATTG	TTATTGATAC	TGCACATGGT	CATTCTGCAG	GTGTCTTGCG	TAAAATTGCC	840
GAGATTCTGT	CTCATTTCCC	AGATCGGACT	TTGATTGCTG	GAAATATTGC	TACTGCTGAA	900
GGTGACCGTG	CCCTTTATGA	AGCGGGTGTA	GACGTTGTTA	AGGTTGGTAT	TGGACCAGGT	960
TCTATCTGTA	CTACTCGTGT	GATTGCTGGT	GTTGGTGTTT	CGCAAGTAAC	AGCTATCTAC	1020
GATGCTGCAG	CTGTTGCGCG	CGAATATGGT	AAAACGATTA	TTGCTGACCG	TGGGATCAAG	1080
TATTCTGGAG	ATATTGTAAG	AGCACTTGCT	GCAGGTGGAA	ATGCTGTTAT	GCTTGGATCT	1140
ATGTTTGCTG	GAAGTATGTA	AGCTCCAGGC	GAAACTGAAA	TCTTCCAAGG	ACGTAAATTC	1200
AAGACTTACC	GTGGTATGGG	ATCAATTGCT	GCTATGAAGA	AAGGTTCAAG	CGACCGTTAT	1260

TTCCAAGGTT	CTGTCAATGA	AGCAAACAAG	CTTGTTCCAG	AAGGAATTGA	AGGTCGTGTT	1320
GCTTATAAAG	GAGCGGCAGC	TGATATTGTT	TTCCAAATGA	TTGGTGGTAT	TCGCTCTGGT	1380
ATGGGTACT	GTGGTGCAGC	TAACCTTAAA	GAACACACG	ATAATGCTCA	ATTTATTGAA	1440
ATGTCTGGTG	CTGGTTTGAA	AGAAAGCCAT	CCTCATGATG	TGCAAATTAC	TAATGAGGCA	1500
CCAAATTATT	CTATGTAA					1518

(2) INFORMATION FOR SEQ ID NO:1582:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...228
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1582:

TCTTTTTTTTA	GCAAGTGGA	AAGCGAGCGC	CATGCAAGGA	CAAATCTTGA	CAATAGATGG	60
TGGCTGGTCT	TTGAAGTAGG	AGGAGTTGGA	TGGAATCAA	AAATCACTTT	GGGGTCTACT	120
GTGTTTGCTT	TGAAATGGA	AAGTTACTTT	GTATTGAAAA	AACGAGAGGC	CCTTATCAAC	180
ATCGGTATGA	TCTACCTGGA	GGCAGTCAGC	AACTTGGTGA	AGGACTGA		228

(2) INFORMATION FOR SEQ ID NO:1583:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 486 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...486
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1583:

AGATATTTTA	GAAGAGTATT	AATGATAGAT	AAAGTGGTCA	GGAACCTACT	CCTGACCTTT	60
TTCTTTTGCA	AAATGACAAA	AATCATAAAC	TTTTTGACAA	CTATACTTGT	CAAAAAGAAA	120
AAGATGTGTT	ACAATGTAAG	CAAGTTAAGA	GAAAAGAAGA	AAGGAGCTAT	GATGTGGGTA	180
CTAGGGTTTA	TACTATTTCT	GATTTTCTTT	TATTCTAATG	ATTCTAAAAA	AATCAAGAAA	240
CTAGAGAAGA	AAATCAAAAAG	ACTTGAGCGA	AAAGAGAAAAG	GAAATGCAGA	AATGTTCGAGA	300
TTATTACAAG	AAATGATTGG	AAAGGAACCA	ATTATAACGG	GAGTGTATAT	TGGGCCAGAT	360
AACTGGGAAG	TTGTGGATGT	TGATGAGGAA	TGGGTAAAGC	TACGACGTGT	AGATAATACG	420
GGAAAAGAAA	AATTCAAGTT	GCAACGTATT	GAGGATATCC	AAACCGTTGA	ATTTGACGGA	480
GAGTAG						486

(2) INFORMATION FOR SEQ ID NO:1584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1584:

GGACATTTTA	GAAGAAGAGG	AAGGAAAAAA	ATGAGTCGTT	TACTAGTTAT	TGGTTGTGGG	60
GGCGTTGCCC	AAGTTGCTAT	TTCAAAGATT	TGTCAAGATA	GCGAAACATT	TACAGAGATT	120
ATGATTGCTA	GCCGTACCAA	GTCAAAATGC	GATGACTTGA	AAGCGAAGCT	AGAAGGCAAA	180
ACAAGTACTA	AAATTGAAAC	TGCAGCACTT	GATGCTGACA	AGGTTGAAGA	AGTGATTGCC	240
CTGATTGAAA	GCTACAAACC	AGAAGCTGTT	TTGAATGTAG	CTCTGCCTTA	TCAAGATTTA	300
ACCATTATGG	ATGCTTGTTT	GGCAACAGGT	GTTCACTATA	TCGATACAGC	CAACTACGAA	360
GCAGAAGACA	CAGAAGACCC	TGAGTGCGCT	GCTATCTACG	AAAAACGTTG	TAAGGAACTT	420
GGTTTTACAG	CCTACTTTGA	CTACTCATGG	CAGTGGGCTT	ATCAAGAGAA	ATTCAAAGAA	480
GCAGGCTTGA	CTGCTCTTCT	TGGTTCTGGT	TTTGACCCAG	GTGTAACTAG	TGTCTTTTCA	540
GCTTATGCCC	TCAAACACTA	TTTTGATGAA	ATCCATTATA	TCGACATTTT	AGACTGTAAT	600
GGCGGTGACC	ACGGTTATCC	ATTTGCAACC	AACTTTAATC	CAGAAATTAA	TCTCCGTGAG	660
GTTTCTGCGC	CAGGTTCTTA	CTGGGAAGAT	GGGAAATGGG	TCGAAGTCGA	AGCTATGTCT	720
ATCAAGCGTG	AGTATGATTT	CCCTCAAGTT	GGACAAAAAG	ATATGTATCT	CCTTCACCAT	780
GAAGAAATCG	AATCATTGGC	CAAGAACATT	CCAGGTGTCA	AACGCATTCT	TTTCTTTTATG	840
ACTTTTGGTC	AATCTTACTT	GACGCACATG	AAATGTCTTG	AAAATGTTGG	ACTCCTTCGT	900
ACGGATACCA	TTAACTTTAA	CGGCCAAGAA	ATTGTTCCAA	TTCAATTTTT	GAAAGCCTTG	960
CTTCCAGATC	CTGCTAGCCT	TGGCCCACGT	ACAGTCGGAA	AAACCAATAT	TGGATGTATC	1020
TTTACAGGTG	TCAAAGATGG	CGTTGAAAAG	ACTATCTACA	TCTACAATGT	TTGCGACCAT	1080
CAAGAGTGCT	ATGCAGAAGT	CGGGTCACAA	GCAATTTTCA	ACACGACAGG	CGTTCCAGCC	1140
ATGATTGGGA	CAAAATTAGT	CATGAACGGA	ACTTGGA AAC	AAGCTGGAGT	GTATAACCTT	1200
GAGGAGTTAG	ATCCAGATCC	ATTCATGGAA	GCTTTGAATG	AGTATGGTTT	GCCATGGGTT	1260
GTGGTTGAAA	ATCCACAAAT	GGTGGACTAA				1290

(2) INFORMATION FOR SEQ ID NO:1585:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...297
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1585:

AACGATTTTA	GCACACGGAA	AAAGCTGTTT	AGCCAAGTCA	TAGTAAGGAC	TAAACATATC	60
CATCGTAATG	ATTTTCAC TT	GACAACGAAC	GGCTCTATCG	TAGCGAAGAA	AGTGATTTCG	120
GATGACAGCT	TGTGTTCTGC	CTTCAAGAAC	AGTGATAATA	TTAAGATTAT	CAAAATCTTG	180
CGCAATGAAA	CTCATCTTTC	CCTTAGTGAA	GGCATACTCA	TCCCAAGACA	TAATCTTTGG	240
AAGCCGAGAA	AAATCATGCT	CAAAGTGAAA	GTCATTGAGC	TTGCGAATGA	CAGTTGA	297

(2) INFORMATION FOR SEQ ID NO:1586:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 858 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...858
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1586:

GGTTGGAAGC	TGTATTCCAA	CCTCTTATTT	TGGGAGAAAA	GAATGAAATT	TTTAACACTC	60
AATACTCACA	GTTGGATGGA	GAAAGAAGCA	GAGGAAAAAT	TCCAGATTTT	GCTTGAAGAT	120
ATTCTTGAAA	AGGACTATGA	TTTGATTGTG	TTTCAAGAAA	TCAATCAGGA	GATGACCTCG	180
TCAGAGGTGG	AGGTTAATGA	CCTTTATCAA	GCTTTGCCAG	CAGCTGAGCC	TATTCACCAA	240
GACCATATAT	TTAGACTCTT	GGTTGAAAAG	TTGTTAGAGC	AAGGGAAAAA	TTACTACTGG	300
ACCTGGGCTT	ATAACCATAT	CGGCTATGAC	CGCTACCACG	AAGGTGTGGC	TATCTTGTCT	360

AAAACACCTA	TTGAAGCCAG	AGAAATTTTG	GTTTCAGATG	TGGATGATCC	AACAGACTAT	420
CATACTCGCC	GTGTTGCCCT	AGCTGAAACT	GTAGTCGATG	GCAAGGAGCT	AGCAGTTGCC	480
AGTGTTCATC	TCTCTGGTG	GGATAAAGGT	TTCCAAGAAG	AATGGGCACG	ATTTGAGGCT	540
GTCTTGAAAA	AATTGAACAA	GCCACTTTTA	CTAGCTGGAG	ATTTTAACAA	CCCAGCAGGT	600
CAGGAAGGTT	ACCAAGCTAT	TTTAGCTAGT	CCATTAGACT	TACAAGACGC	ATTTGAAGTT	660
GCTCAAGAGA	AAAGTGGTAG	CTATACTGTT	CCGCCTGAAA	TTGATGGCTG	GAAAGGGAAC	720
ACTGAACCCC	TTCGAATCGA	TTATGTCTTT	ACTACCAAAG	AGTTAGCGGT	GGAAAATTTA	780
CATGTCGTAT	TTGATGGTAA	CAAGAGTCCA	CAAGTGAGTG	ATCACTATGG	CTTGAATGCT	840
ATGTTAAACT	GGAAATAA					858

(2) INFORMATION FOR SEQ ID NO:1587:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 252 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1587:

CAGAGGAAGC	TGTTCAAAAT	CTTCCACCTA	TTCCAGAAGA	AAAGTGGGTG	GAACCAGAAA	60
TCATCCTGCC	TCAAGCTGAA	CTTAAATTCC	CTGAACAGGA	AGATGACTCA	GATGACCAAG	120
ATGTTTCAGT	CGATTTTTC	GCCAAAGAAG	CCCTTGAATA	CAAAC TTCCA	AGCTTACAAC	180
TCTTTGCACC	AGATAAACCA	AAAGATCAGT	CTAAAGAGAA	GAAAATTGTC	AGAGAAAATA	240
TCAAAATCTT	AG					252

(2) INFORMATION FOR SEQ ID NO:1588:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 744 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1588:

AATAGGATTA	GAATTATTAA	GAAAGTTGGT	TCTTTATTGG	AAACGATAGT	ATTTTAAATC	60
TCTGTTTTTC	TAGCAGGTGT	TTTATCCTTT	TTTTCTCCTT	GTATTTTTCC	TCTTCTGCCA	120
GTCTATGCTG	GGATTTTATT	GGATGATCAA	GAAAGTGCAA	AAAGCTTTTC	TTTGTTTGGG	180
AGAAAGGTTT	TCTGGTCAGG	CTTGATTCTG	ACACTTTGCT	TTATCGCTGG	TATCTCTCTC	240
ATTTTCTTTA	TTCTAGGCTT	TGGTGCTGGT	TACTTTGGTC	ATATTCTCTA	TGCAAATTGG	300
TTTCGATATG	GCATGGGAGC	TATTATTATC	ATTTTGGGTC	TTCACCAGAT	GGAAATTTTT	360
CATTTGAAGA	AATTAGAAGT	TCAAAAAAGT	TTTACCTTTA	AAAAATCAGA	TTCTAATCGT	420
TATTGGTCAG	CTTTTTTACT	TGGTATTACC	TTTAGCTTTG	GTTGGACACC	TTGTATTGGT	480
CCAGTTTTAA	GTTCTGTTTT	AGCACTTGCG	GCTTCTGGAG	GCAATGGCGC	TTGGCAAGGA	540
GCGATTTATA	CTCTCATTTA	CACTCTGGGC	ATGGCCCTTC	CTTCTTTGGT	ATTGGCACTA	600
GCTTCAGGTC	TAGTCATGCC	ATATTTTAGT	AAAATCAAGC	GTCATATGAT	GCTACTAAAG	660
AAAATTGGTG	GTTTCTCAT	TGTTTAAATG	GGAATTTTGT	TACTATTAGG	ACAAGTAAAT	720
GTTCTAGCTG	GAATTTTGA	ATAA				744

(2) INFORMATION FOR SEQ ID NO:1589:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1230 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1589:

AGAAGAGTTA	GAAGCGATTG	TTGCCGAGTT	TCCCGACTCC	CTTTCACCTTG	TATGATGAGA	60
ANGGGAATCG	TGAGAAGGCA	ANAACCGTCN	ACCAAGCTTT	TTCGTGGAAA	CAAGGGCTTT	120
AAGGAATATT	TTGCAGTTAA	GGCTACTCCA	ACTCCAGCTA	TTTTGAAAAT	TCTCCAAGAA	180
GAAGGTTGTG	GTGTGGACTG	CTCTAGTTAT	GTAGAGCTTT	TGATGAGCCA	TAAACTGGAC	240
TTTCTGGGTT	CTGAGATTAT	GTTCTCTTCC	AACAACACGC	CAGACAAGGA	ATACGCCTAT	300
GCACGTGAAT	TGGGTGCGAC	CATTAACCTG	GATGCCCTTG	AAGATATTGA	ACATCTGGAG	360
AGAGCAGCAG	GTATTCCAGA	AATCATCTCT	TGTCGTTATA	ATCCTGGAGG	CGTTTTTGAA	420
CTGGGGACAG	ACATTATGGA	CAATCCTGGG	GAGGCTAAGT	TTGGCATGAC	CAAGGACCAG	480
CTCTTTGAAG	CCTTTGCTAT	CTTGAAGGAA	AAAGGAGCCA	AGACTTTTGG	GATTCACCTC	540
TTCTAGCGT	CCAATACCGT	GACCCATCTC	TATTATCCAG	AGTTGGCTCG	TCAGCTCTTT	600
GAAGTGGCTG	TTGAAATCAA	GGAAAAGTTG	GGCATTGTGC	TAGACTTTAT	CAATCTTTCT	660
GGCGGTATTG	GTGTTAATTA	TCGTCCAGAC	CAGGAGCCGA	ACGATATCGC	CTTGATTGGT	720
GAGGGAGTTC	GTAAGGTGTA	TGAAGAAGTT	CTTACGTCAG	CAGGTCTTGG	TCAGGTCAAG	780
ATTTTCACCG	AATTGGGTCG	TTTTATGCTG	GCACCTCACG	GTGCTCTAGT	CACAAGAGTG	840
ACTCATAAGA	AGGAAACCTA	CCGTACCTAT	CTAGGTGTGG	ATGCCCTCAG	AGTCAACCTC	900

ATGCGTCCAG	CTATGTACGG	AGCTTACCAT	CATATTAGCA	ACGTGACCCA	TCCAGATGGA	960
CCAGCTGAAG	CGGTAGATGT	GGTTGGTTCA	CTCTGTGAAA	ACAATGATAA	ATTTGCAGTC	1020
AATCGCGAAC	TGCCTCATAC	AGAAATCGGT	GATTTGCTGG	TAATTCATGA	TACAGGTGCC	1080
CACGGATTTT	CAATGGGCTA	CCAGTATAAT	GCCAAATTAC	GTTCTGCGGA	AATCCTCTAT	1140
ACCGAAGAAG	GTAAAGCCCG	TCAAATCCGC	CGTGCAGAGC	GCCCTGAGGA	CTATTTTGCA	1200
ACCTTATATG	GCTTCGATTT	TGAAGAATAA				1230

(2) INFORMATION FOR SEQ ID NO:1590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2163 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1590:

ATGGGAGTTA	GGATAGAGAA	TAATCTATTT	TATGTTGAGA	GTAAAAATCT	AAGTTTGATT	60
ATTGAAAATC	GAAATGGCTA	CTTACTTTTT	AAACATTTAG	GAAAGACTAT	TAAGAACTAT	120
AAAGGTTCCA	ATAGTGTTTA	TGAACGAGAC	CATGCCTTTT	CAGGAAATCC	AACGGCTACT	180
AATCGAACCT	TTAGTTTAGA	TACTCAGCGA	CAGATTTTTG	GACAACATGG	CTTAGGAGAT	240
TTTAGGAAAC	CAACCATACA	GGTTCAGCAT	AGTGTAAC TG	AAGTAACAGA	CTTTCGATTT	300
GTAGAAGCAA	AGATTTTAAA	AGGTCAGAAT	GGTCCACAGG	GCTTACCTTC	TCCACATAGC	360
ATGGACGATA	CAGAGACTCT	TGTCTTAATG	TTAGAAGATT	CTAAGGCTCA	ACTTAGTCTG	420
ACTTTGTATT	ATACTACTTT	TAATAATGAT	GCGACTATTG	CTAGCTACAG	TAAATTAGAT	480
AATAATAGTA	ATCAGGAAGT	TGTCATCCAT	AAAGATTTTT	CTTTTATGGC	TGATTTTCCA	540
GCTGCAGATT	ACGAAATAGT	AACTCTGCAG	GGTGCTTATG	CTCGTGAAAA	GACTGTTAGA	600
CGTCAACAGG	TAGAACAAGG	AATCTTTTCG	ATTAGCTCAA	ACCGAGGTGC	TTCTGGTCAT	660
GCTCAACAC	CAGCTCTTCT	ACTATGCGAA	CAAGGAGTCA	CAGAGGATGC	TGGGAATGTG	720
TTTGCTATT	AACTAATGTA	TAGTGGCAAC	TTTGAAGCTT	TTGTTCAAAA	AAATCAATTG	780
AATGAAGTTC	GGGTGGCTAT	TGGCATTAAT	CCAGAAAAC	TTTCTTGGA	GTTAGCCCT	840
GAGGAATACT	TTGAAACACC	GGTAGCTTTA	GTGACTCAT	TGACTCAGG	ATTAACGGT	900
ATTAGTCATG	AAAGTCAGAA	TTTTGTACTG	AAGCACATTA	TTCTAAGTGA	ATTTTCTAAA	960
AAAGAACGTC	CAATTCTAAT	CAATAACTGG	GAAGCTACTT	ACTTTGACTT	TCAGAGAGAA	1020
AAACTGTTAG	AGTTAGCAGA	TGAAGCTAAG	AAAGTTGGCA	TTGAACCTTT	TGTATTAGAT	1080
GATGGTTGGT	TTGGCAATCG	TTTTGATGAT	AATCGTGCTT	TAGGTGATTG	GGTTGTTAAT	1140
GAGGAAAAAC	TGGGTGGAAG	TCTAGAAAGT	CTGATTTTCA	CTATCCATGA	AAGAGGTTTG	1200
CAGTTTGGAC	TTTGGTTAGA	ACCCGAAATG	ATTTCTGTAG	ATAGTGATTT	GTATCGTCAA	1260
CATCCTGACT	GGGCTATTCA	GGTTCCTGAT	TATGAGCATA	CTTATTCTCG	GAATCAATTA	1320
GTAATTAAAT	TTGCCAATCC	TCAGGTAGTA	GAATACTTGA	AAAGTGCTCT	AGATCAACTC	1380
CTATCTTATC	ATGAGATTGA	TTACATTTAA	TGGGATATGA	ACCGCAATAT	CACTAAGCTA	1440
GGGAATGGAT	TAACCTTATCT	AGAGACACAG	ATGCAATCTC	ATCAGTACAT	GCTGGGGCTT	1500
TACGAACCTG	TTTCTTATCT	GACAGAGAAG	CACAGCCATA	TTCTCTTTGA	GTCTGCTCT	1560
GGTGGTGGTG	GACGAAATGA	TCTTGGTATG	ATGCGCTATT	TCCACACAAG	CTGGGCTAGT	1620

GATAATACAG	ATGCTATTGC	ACGTTTACCA	ATTCAATACG	GTTTCATCCTA	TCTCTATCCA	1680
ACCATTTTCTA	TGGGGGCTCA	TGTGTCAGCA	GTACCGAATC	ATCAGATGGG	GCGAACGACA	1740
CCATTAGAAA	CACGTGGACA	TGTAGCAATG	ATGGGAAAT	TGGGCTATGA	GCTTGATTG	1800
ACAAGTTTAT	CAGATGAAGA	GAAAGCTGAG	ATTGCTAATC	AGGTGAACTT	GTATAAAGAA	1860
TTACGACCAG	TAGTTCAGTT	AGGACAACAG	TATAGACTAA	TTAATCCTGA	TACTGCATCC	1920
AATGAAGCTG	CTGTACAATT	TAATTACAAA	AATCAAACGA	TTGTAACCTA	CGTTCGCGTT	1980
TTGTCAGTTG	TAGAGACCAT	GGAAACAAC	TTAAAGTTAA	AAGATTTGGA	TGAAGAGGGA	2040
CTATATGAAT	TACAGGAAAA	TGGCGAAGTT	TACTCAGGTG	CAGAACTCAT	GTATGCGGGT	2100
TTAACTGTTA	TTTTATCCCA	AGGAGATTTT	TTGAGTAAAC	AGTATATTTT	TAGAAGACTA	2160
TAA						2163

(2) INFORMATION FOR SEQ ID NO:1591:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 255 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...255
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1591:

GCTTGTTCTA	GTGGATTGAA	ATTGACTTTA	AGTGAGTTTG	GAAATAATAT	CCAAGCTCAT	60
TTTTTCTCAG	ACTGCAAGCA	GTTTCATCAAT	AAGATTTATA	CTCTTCGAAA	ATCTCTTCAA	120
ACTACGTCAG	CTTCACCTTG	CCGTAGGTAT	ATGATACTGA	CTCTGTCAGT	TCTATCCACA	180
ACCTCAAAAC	AGTGTTTTGA	GCAACCTGCG	GCTAGCTTCC	TAGTTTGCTC	TTTGATTTTC	240
ATTGAGTATA	AGTAG					255

(2) INFORMATION FOR SEQ ID NO:1592:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 504 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1592:

ACTGTATCTA	GAAAGGGGAA	AATTATGATT	AAAGAATTGT	ATGAAGAAGT	CCAAGGGACT	60
GTGTATAAGT	GTAAGAAATGA	ATATTACCTT	CATTTATGGG	AATTGTCGGA	TTGGGACCAA	120
GAAGGCATGC	TCTGCTTACA	TGAATTGATT	AGTAGAGAAG	AAGGACTGGC	AGACGATATT	180
CCACGTTTAA	GGAAATATTT	CAAAACCAAG	TTTCGAAATC	GAATTTTGA	CTATATCCGT	240
AAGCAGGAAA	GTCAGAAGCG	TAGATACGAT	AAAGAACCCT	ATGAAGAAGT	GGGTGAGATC	300
AGTCATCGTA	TAAGTGAGGG	AGGTCTCTGG	CTAGATGATT	ATTATCTCTT	TCATGAAACA	360
CTAAGAGATT	ATAGAAACAA	ACAAAGTAAA	GAGAAACAAG	AAGAACTAGA	ACGCGTCTTA	420
AGCAATGAAC	GATTTTCGAGG	GCGTCAAAGA	GTATTAAGAG	ACTTACGCAT	TGTGTTTAA	480
GAGTTTACTA	TCCGTACCCA	CTAG				504

(2) INFORMATION FOR SEQ ID NO:1593:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 639 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1593:

AACATTCCTA	GAAGTTGCTT	TGATTTACCT	AATCTATTTA	TGCAAATTTT	ATGTTATTTT	60
ACTATAACAG	TTGTTGCTAA	TCCAAATAAT	AGTGGGGAAG	TTCATTTAGA	TGTAAGCATT	120
GAAGATAATC	AGGGAGGTAG	TGGGTATAAT	TTCAGTTCTG	TTTCAAGTAG	CTCACAAACA	180
GCTAAATATG	AAGGAGCTGG	TTATAATAAC	AATTCATCAT	TATATATAAC	GATTGATAAA	240
ACGTCTGATG	CAACAGCTCT	TTTGAAATTA	AAGTTGAATA	ATGTTAATAA	TCAACCTGCT	300
ACTGAAGTTC	CTAGTTCAGG	AATTACTGTA	AAATTAAATG	CTAAAGATAA	TGCTGGAAAC	360
TGGACAAGTG	CTTCGAATAA	AAAAGAAGTA	ACAGTAAAAA	TTGTTTCTGC	TAAACCGACA	420
TATCCAGACA	AAATTTTAGT	GAAAAATCCT	GATAATATAA	AAGATACAGA	AAAAAATGCC	480
ATTATTGAAA	AATTGAAAAG	GGCAAATAAA	AATCATCCAG	CAGGAGCTCC	AACCTTTGCT	540
AAAGGTGAAG	GAGAGCATGC	AAATGATATT	GTAGCAACTT	ATTGAGATGG	TACAACTTAT	600
TATGTACCGT	TAAATGATGT	GACAAAATAT	GCGAGGTAG			639

(2) INFORMATION FOR SEQ ID NO:1594:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 618 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1594:

ACCGATCCTA	GAAACAGCCT	AGAGGTGACT	ATGGAACCTTA	ATACACACAA	TGCTGAAATC	60
TTGCTCAGTG	CAGCTAATAA	GTCCCACTAT	CCGCAGGATG	AACTGCCAGA	GATTGCCCTA	120
GCAGGGCGTT	CAAAATGTTGG	TAAATCCAGC	TTTATCAACA	CTATGTTGAA	CCGTAAGAAT	180
CTCGCTCGTA	CATCAGGAAA	ACCTGGTAAA	ACCCAGCTCC	TGAACTTTTT	TAACATTGAT	240
GACAAAGATGC	GCTTTGTGGA	TGTGCCTGGT	TATGGCTATG	CTCGTGTTTC	TAAAAAGGAA	300
CGTGAAAAGT	GGGGGTGCAT	GATTGAGGAG	TACTTAACGA	CTCGGGAAAA	TCTCCGTGCG	360
GTTGTCAGTC	TAGTTGACCT	TCGTCATGAC	CCGTCAGCAG	ATGATGTGCA	GATGTACGAA	420
TTTCTCAAGT	ATTATGAGAT	TCCAGTCATC	ATTGTGGCGA	CCAAGGCGGA	CAAGATTCCT	480
CGTGGTAAAT	GGAACAAGCA	TGAATCAGCA	ATCAAAAAGA	AATTAAACTT	TGACCCAAGT	540
GACGATTTCA	TCTCTTTTTT	ATCTGTCAGC	AAGGCAGGGA	TGGATGAGGC	TTGGGATGCA	600
ATCTTAGAAA	AATTGTGA					618

(2) INFORMATION FOR SEQ ID NO:1595:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 222 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1595:

ACACTACCTA	GAATCAAACC	ATTTACGAGT	TGTTGGAGCA	TAAGATTCAC	TCTCTCTATT	60
TATAATTCCG	AGGGTTTTTC	CTCACTTTTT	GATAGGTTCT	TATACTCAAT	GAAAATCAAA	120
GAGCAAACCTA	GGAAACTAGC	CGCAGGTTGC	TCAAAGCACT	GCTTTGAGGT	TGTAGATAAG	180
ACTGACGAAG	TCAGTCACAT	ATATAATCCA	AGGCGACGTT	GA		222

(2) INFORMATION FOR SEQ ID NO:1596:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 474 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...474
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1596:

CCCTTGCCTA	GGTTGGGAAA	ATACAGAGGC	CTTGGTAGAA	GAGATTTATG	TTACCTTGAC	60
AAAATAAGTG	AAAAGGATGG	AGTTGGGGAA	TCTCAACTCC	TTTTGATGAG	AATGATAGTT	120
GGACACGGAA	TTGACATCGA	AGAATTGGCT	TCGATAGAAA	GCGCAGTTAC	ACGACATGAA	180
GGATTTGCTA	AGCGTGTA	CTACTGAC	GAAATGGAGC	GCTTCACCAG	TCTCAAAGGA	240
CGCAGGCAAA	TAGAATATTT	AGCTGGTCGC	TGGTCGGCTA	AGGAGGCCTT	TTCCAAGGCT	300
ATGGGAACGG	GCATTAGCAA	GCTCGGTTTT	CAGGATTTGG	AAGTCTTGAA	CAATGAACGT	360
GGGGCGCCTT	ATTTTAGTCA	GGCACCATTT	TCAGGAAAGA	TTTGGCTGTC	TATCAGCCAC	420
ACCGATCAGT	TTGTGACAGC	CAGTGTCA	TTGGAGGAAA	ATCATGAAAG	CTAG	474

(2) INFORMATION FOR SEQ ID NO:1597:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 660 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...660
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1597:

ATTAAGCCTA	GAAGACCTTC	TTATGGCCAC	TCTTCATATG	TGCGAGAATA	TCGAACTTAT	60
GAACAAATTG	CGGCTGATTT	TGGTATTAC	GAAAGCAACT	TTATCCGTCG	GAGCCAATGG	120

GTTGAAGTAA	CTCTTGTTCA	AAGTGGTGT	ACGTNTCAAG	CACTCCTCTC	AGCTCTGAGG	180
ACACGGTATG	ATATGATGCG	ACGGAAGTAC	AAATCAATCG	CCATAAAAAA	AGAATTAGCG	240
AATGATTCTG	GTAAAAAGAA	ATGCCACGCT	ATGAAGGCTC	AAGCGATTGT	CACAAGTCAA	300
GGGAGAAATTG	TTTCTTTGGA	TATCACTGTG	AACTATTGTC	ATGATATGAA	GTTGTTCAAA	360
ATGAGTTGCA	GAAATATCGG	ACAAGCTGGT	AAAATCTTGG	CTGACAGTGG	TTATCAAGGA	420
CTCATGAAGA	TATATCCTCA	AGTACAAACT	CCACGTAAAT	CCAGCAAAC	CAAGTCGCTA	480
ATAGCTGAAG	ATAAAGCCTA	TAACCATGCG	CTATCTAAGG	AGAGAAGCAA	GGTTGAGAAC	540
ATCTTTGCCA	AAGTAAAAAC	GTTTAAAAATG	TTTTCAACAA	CCTATCGAAA	TCATCGTAAA	600
CGCTTCGGAT	TACGAATGAA	TTTGAGTGCT	GGTATTATCA	ATCATGAACT	AGGATTCTAG	660

(2) INFORMATION FOR SEQ ID NO:1598:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...294
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1598:

CCCGAGCCTA	GAAACGAAAA	AGCGAGGGTT	CCAAAAGCGC	TTGAGCGCCC	GATACTCCAA	60
GGATTTTCGG	TCAAATTGGT	TCATGATTTG	GATTCGTA	CTCGGCTCAG		120
ATGTTGGACA	ATGTGGAAGC	GGTCAAGAAC	AATCTTCGCC	TTTGGAAAGA	GTTGCTTAGC	180
GAGCCGATAA	TAAGGGCTGT	ACATGTCCAT	GGTGATGACC	TCGACCAGCT	CCCGAACCTC	240
TCTCTGATAG	CGTTGGAAAT	GGTTTCGAAT	CACCGCATGA	GTTCCGCCGT	CTAA	294

(2) INFORMATION FOR SEQ ID NO:1599:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 812 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1599:

ACAGTTGCTA	GAAATGTAGA	GGTATTGACC	ATGTATCAAG	ATTTACTAAG	AAAAATAGCA	60
GAAGAAAAAC	CAAATTATAA	CCAGGAAGAA	ATCCAGTGGT	TGTTTGATCA	TTTGGGAAAT	120
CCTTCTCCAG	AAATTCGTGA	TGACCTTATT	TTTACAAGCT	TTGCTAAGGG	GATTCAGGAA	180
GAGCTATTTA	TACAGGAGCA	ATTTTCATTTT	ATTGCTGAAG	GGGTTTCATC	TGATGTAGGA	240
CTAGATAAAG	AGATTGATAA	GGTAGGCCCTG	CCAACACTGG	AACGTTCTTT	TAGGGCACTT	300
GTTTATGCAA	ATCTCTTGTC	TGCAGATGCT	AACCAGCAAT	CGGTTTTTTA	TCAGGGATTA	360
CAATCAGAAA	TTCGTGATGA	TCTTTCAAAT	CAAGGCTTGC	ACTATCTTTC	AAAAGAAAAG	420
GATACAACAG	GTTTCTCAAG	TCAGTATGGT	TGGGTTTCATT	CTTTTGCACA	TGGAGCCGAT	480
TTACTGACAG	AGGTGGTTTG	TCATCCAGAC	TTTCCTAAAA	ACAGAGTTCA	TGAAGTATTT	540
GATATACTTG	GCCAACTATT	TAAAAGAATG	TCGATTGCT	TTACAGATGA	TGAGGATTGG	600
CGTTTAGCAA	GAGTGATCTA	TGAACCTATT	TTACAAGGGA	AGTTGGAGCA	AGAACAAGTA	660
GCTTCTTGGA	TAAAACTGT	TGATTTTCCG	ATAGAAGAAA	GGGAGGATTT	TTCCAAATTT	720
TCCAACTTTA	GATCCTGTCT	GGTGGAAGTC	TATGTCCAAC	TTGACCAGAG	AAATAGTTTA	780
CAAGATGAGT	TGAAAGAAGC	TATCCAGTCT	TT			812

(2) INFORMATION FOR SEQ ID NO:1600:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1600:

AGAAATGCTA	GAAGACTTTT	AGATGACAGT	TACCAAGAGG	GTCTAATTTT	CACTGCTACT	60
TATGCAGTGG	GAATTGGACC	TTTTTATATA	AGCAAATTCT	ATTTCAAAAT	TGGTTACCAA	120
GAAAGACTTC	TTTTCCTGT	TAAGTATAAG	AGGGTAATTT	ATAGAATTTT	GTTACATCAA	180
GATAAATATT	TTCTGATGGT	CAAATTTTAA				210

(2) INFORMATION FOR SEQ ID NO:1601:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 756 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1601:

TTGGAGGCTA	GCATGCAGCA	GTATTTTGTA	AAAGGCAGTG	CTATCTCTCC	TGTCACTATC	60
GAGGACAAGG	AAACCAGTAA	GCATATGTTT	CAGGTTATGC	GCTTGAAAGA	AGAGGATGAG	120
GTTACCTTAG	TCTTTGATGA	TGGCATCAAG	CGCTTGGCGC	GCGTGCTGGA	TATGGAAAAT	180
CGTCAGTTTG	AGTTGGTCCA	AGAATTAAAT	GACAATGTGG	AACTACCAGT	CCAAGTGACC	240
ATCGCATCTG	GATTTCCCAA	GGGAGACAAG	CTGGAGTTCA	TCGCTCAAAA	AGTAACCGAA	300
CTGGGTGCTA	GCCAAATCTG	GGCCTTTCCT	GCAGACTGGT	CAGTTGCCAA	GTGGGATGGC	360
AAGAAATTGG	GTAAAAAAGT	TGAAAAACTA	GAAAAAATTG	CCCTTGAGC	AGCCGAGCAA	420
AGCAAGCGTA	ATATTGTACC	AAGTATTAAA	CTTTTCGAGA	AAAAAGCAGA	TTTTCTAGCT	480
CAGCTGGACC	AGTTTGACTC	TATCATAGTA	GCCTATGAAG	AATCAGCTAA	AGAAGGAGAA	540
GCCGCTGCGC	TTCTGCAAGC	AGTCACTGGT	CTTGAAACAG	GAGCCAAACT	GCTCTTTATC	600
TTTGGTCCAG	AAGGTGGTCT	GTCACCTGCA	GAAATCGAAA	GTTTTGAAGC	TAAAGGAGCA	660
GTTTTGGCAG	GCCTAGGTCC	TCGTATTTTG	CGAGCAGAAA	CAGCACCGCT	TTACGCCTTA	720
TCAGCCCTTA	GTGTTTTAGT	AGAATTAGAG	AAATAA			756

(2) INFORMATION FOR SEQ ID NO:1602:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1602:

ATACAAGAGC	TGCTAAACAC	TACTATGCAA	GAGCTCAAAA	AAACGGAACA	GTTGAACAAC	60
AGTATTTTAA	TTGATCTTGA	GAAATTTTAC	CAACCCACCA	GTCTTTTGAT	TGGACTGGGT	120
AGCCTAAAAAC	TAAACAATCA	AGCACGCACT	GCTTGGCGAA	ACTATGATAA	AATCCATTAC	180
GAGCATGTCA	AACACGTACT	AAGTTTTTAT	GGACCTGTTT	TTGGATTTTA	G	231

(2) INFORMATION FOR SEQ ID NO:1603:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1701 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1603:

ATTTTTTATA	GGAGGAGTTT	TATGGATAAG	CTAGTCGCTG	CCATTGAAAA	GCAACAAGGG	60
AAATTTGAAA	AAATTTCTAC	TAATAACTAT	ATGATGGCTA	TTAAAGATGG	ATTCATTGCT	120
ACTATGCCTT	TAATTATGTT	TTCAAGCTTT	TTGATGATTA	TTATTATGAT	TCCTAAAAAT	180
TTCGGAGTAG	AGTTACCGAG	TCCAGCTATT	GTCTGGATGA	GAAAAGTGTA	TATGTTAACC	240
ATGGGAGTTT	TGGGTATTAT	TGTTTCAGGG	ACTGTTGGAA	AGTCATTAGT	TGGAAATGTT	300
AACAGAAAAA	TGCTCACGG	AAAGGTAATA	AATGATACTT	CTGCAATGTT	GGCAGCCATA	360
TGTAGTTATC	TGGTATTAAC	TGTAACGCTT	GTAGTTGATG	AGAAGACGGG	ATCTACAAGT	420
TTGTCGACAA	ACTATTTAGG	ATCTCAAGGA	TTGATAACTT	CGTTTGTCAG	TGCCTTTATT	480
ACTGTAAATG	TTTACCGATT	CTGTATTAAG	CGAGACATTA	CTATTCATTT	ACCTAAGGAA	540
GTTCTGGGG	CTATATCACA	AGCTTTTAGA	GATATTTTTT	CTTTTTCTTT	TGTTTTACTT	600
ATTAGTGGTT	TGTTAGATAT	TGTATCTCGG	TTTAGTTTAG	ATGTTCCCTT	TGCCCAAGTA	660
TTTCAACAAC	TATTGACTCC	TATTTTTAAG	GGGGCAGAAT	CATATCCTGC	TATGATGTTG	720
ATTTGGTTTA	TGTGTGCTTT	GCTTTGGTTT	GTTGGAATTC	ATGGACCATC	TATTGTCTTA	780
CCTGCTGTTA	CAGCTTTACA	ACTGAGCAAT	ATGGAAGAGA	ATGCTCAACT	TC'TTGCAAT	840
GGGCAGTTCC	CTTATCATTC	TTTAACACCT	AATTTTCGGGA	ATTATATCGC	TGCTATTGGA	900
GGAACGGGGG	CTACCTTTGT	TGTACCATTT	ATTTTGATTT	TC'TTTATGCG	GTCTAAACAA	960
TTAAAATCGG	TAGGTAAAGC	TACAATTACT	CCTGTTTTAT	TTGCGGTAAA	TGAACCTCTT	1020
CTATTTGGTA	TGCCTGTTAT	TTTGAATCCC	TATCTTTTTG	TCCCTTTTTT	GATGACTCCA	1080
CCAGTAAATG	TATTTCTAGG	AAAGGTATTT	ATTGATTTCT	TTGGAATGAA	TGGATTTTAT	1140
ATCCAGTTAC	CTTGGGCTTT	TCCTGGTCCC	TTGGGATTGT	TAATTGGAAC	GAATTTTCAA	1200
CCTATCTCCT	TTGTGCTTTT	ATCTTTGATG	TTAGTTGTCG	ACATATTGAT	TTATTTGCCA	1260
TTCTGTAGAG	CGTATGATAG	ACAGTTACTG	ATGAAAGAAG	ATGTTGCAAG	CTCAAATGAT	1320
ATTATTTTAG	AGGAGGATAC	AAGTGAAATA	ATGCCTGGTG	AGATAGATGT	AATAAAAAGT	1380
AAGGAGTTGA	AAGTACTGGT	TCTTTGTGCA	GGGTCTGGAA	CAAGTGCGCA	ATTAGCCAAT	1440
GCAATTAACG	AGGGCGCTCA	ATTAGCAGAA	GTTAGAGTGA	TTGCGAATTC	AGGAGCGTAC	1500
GGAGCTCATT	ATGATATTAT	GGGTGTTTAT	GATTTAATTA	TTCTGGCTCC	ACAAGTTCGG	1560
AGTTATTATA	GAGAGATGAA	GGTGGATGCA	GAAAGATTAG	GTATTCAGAT	AGTTGCTACC	1620
AGAGGAATGG	AATATATTCA	TTTAACAAAG	AGTCCAAGTA	AATCCTTACA	ATTTGTATTG	1680
GAGCATTACC	AAGCTGTGTA	G				1701

(2) INFORMATION FOR SEQ ID NO:1604:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 849 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1604:

TTCTTATATA	GATGCTTGGA	AGTACGGCTT	CCGAACAGGG	TAATCTTTCA	AAAAAGTACG	60
ATGAGAAACA	CAAAGAAACT	AAGACAATTT	GGAATATTTT	TGCTTATTAT	TTTACTATCT	120
ACCTATTTAC	CACAAACAAT	TAGATTGTAT	GTGACGATCA	TTTTAGGGTT	AGGAGCTGAT	180
GTCTATTCTC	TTATTTTAAC	AATGGGATTA	GTGGGAAGTT	TCCTTCTATT	AATTTGGAGG	240
TTAAAAAGA	AAAAGATGCT	CTTTATCTTT	GAGAAAAAGA	GCTGGAACG	GTCATTTGTC	300
TTCTACTTAT	TTGCAACTTA	TGTGGTTTAT	CAGATTCTCG	GTAATTTTGT	GGCACGCTAT	360
GCTCATTTGA	TTAATCATAG	GAATATTCAT	GATGAGTATT	TTACCGTGGT	TCTTTCAAAT	420
GGACAACCAA	CCTTTTTTATC	GACTATCTTA	TCTTTTGTCC	TGCCTGTAAT	CATCGATCCT	480
GTTTTTGAGG	AGACTCTTGA	TAGAGGGTAT	TTTATGAATA	CCTTCTTTCC	TAAGTCAAAG	540
TACTATTTAG	ATGTCATCTT	ATCAGGCCTT	ATCTTTGGGC	TTAGTCATTT	GATACTATCT	600
CACAGAGATC	CAATTAGTTT	ATTATATTAT	AGTTTGATTG	GTTTCTTTTT	TGCCCTTGTT	660
TATCGTTCTA	CCGACAATCT	GAGATTAACG	ATTCTCTGCC	ATAGTTTTTT	AACTTTCTCA	720
ATCATGCAAA	ACCTATCTGG	ATTTTTGTTT	ACAATTATAT	CTATTATCAT	TTTTTTAGAT	780
AGTGGGAGGC	AAAGAAAAAA	GTGTTTGATA	TCTATCAAAC	ACTTTTTTCTT	TTTATTGTTG	840
GCTCTATAA						849

(2) INFORMATION FOR SEQ ID NO:1605:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1605:

ACAACATATA GAACCGGACT GACGAATAGA AACATAAATT CAATTGGTTC TGTAATACCG	60
GTAATAAAAAG ATGTTAAAGC AACTCCAAAA AACAAACCCG CGTATTTTTT ACGACGATTT	120
TTAGGAACAC TATGGTACAT CGCTAAACAG GCAGCCGGTA AACCGAACAT CATTGTTGAG	180
AAACGACCTG CAAAAACCT TGTTCCTTCT GTAAATAATC CAGAATGGGC CGGATCGGCT	240
AATTGA	246

(2) INFORMATION FOR SEQ ID NO:1606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1606:

AAAGCATATA GAGTAGCTGG CGTTAAAAGC TCCTGTCTTG CTTTTTTGAC CTATAGTCAC	60
ATCTATCAAG TATTGTTCTT GCCTAAGCTA TCAATAAAAA GGTGGCATT TTTAGGCTTG	120
GTGTTAGTGA ATTTTGCCTT ATCCTATCTA AGTCATTTTCG AGCTTTTTTAT GGTACAATGG	180
AAACATGTTA TTCAAATTAT CTAA	204

(2) INFORMATION FOR SEQ ID NO:1607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1607:

AAGCAATATA	GGAGAAAATC	TATGTCAGAT	TTGAAAAAAT	ACGAAGGTGT	CATTCCAGCC	60
TTCTACGCAT	GTTATGATGA	TCAAGGAGAA	GTAAGCCCAG	AACGTACGCG	TGCCTTGGTT	120
CAATACTTCA	TTGATAAAGG	TGTTCAAGGT	CTTTATGTCA	ATGGTTCTTC	TGGTGAATGT	180
ATCTACCAAA	GCGTTGAAGA	TCGCAAGTTG	ATTTTGGAA	AAGTCATGGC	GGTAGCCAAA	240
GGTAAATTGA	CCATTATTGC	TCATGTTGCC	TGCAACAATA	CTAAAGACAG	TATGGAACCT	300
GCTCGCCATG	CTGAAAGCTT	GGGAGTAGAT	GCTATTGCAA	CGATTCCACC	AAATTTATTC	360
CGCTTGCCAG	AATACTCAGT	TGCCAAATAC	TGGAACGATA	TCAGTTCTGC	AGCTCCAAAC	420
ACAGACTACG	TGATTTACAA	CATTCTCTCA	TTGGCAGGGG	TTGCTTTGAC	TCCAAGCCTT	480
TACACAGAAA	TGTTGAAAAA	TCCTCGTGTT	ATCGGTGTTA	AGAACTCTTC	TATGCCAGTT	540
CAAGATATCC	AAACCTTTGT	CAGCCTTGGT	GGGGAAGACC	ATATCGTCTT	TAATGGTCCT	600
GATGAGCAGT	TCCTAGGAAG	ACGCCTCATG	GGTGCTAGGG	TGGTATCGGT	GGTACTTATG	660
GTGCTATGCC	AGAACTCTTC	TTGA				684

(2) INFORMATION FOR SEQ ID NO:1608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1608:

GGTATGCATA	GAAAAACAGT	GATTGATTTT	AGGACTTTGG	GGGAGAGATA	TACCTTTACC	60
AAGCCTATTA	AAGAGTTGAA	AACGAGAAAT	GTAGAAGAAG	TGGCAGATTT	GCTGGCACAA	120
GTGGAAAGCT	ACCAAGAGCA	AGGTATTAT	GTGGTGGGGT	ATGTCAGCTA	CGAGGCTGCA	180
CCTGCTTTTG	AGGAAAAATT	AGCAGTTCAC	AAGGATCCCC	TACTGGGAGA	GTACCTGCCT	240
TATTTTACTG	TTCATGATAG	CGTAGAAACT	TCCTCTATTC	CTCTGACTTA	TGAGGATATT	300
GATTTGCCCT	CAAATTGGCA	GGAAGTAACG	TCTGCAGCAG	ACTATGAAAA	GGCCATTGCC	360
CAAATTCACC	ATCATTTACG	GCAGGGAGAT	ACCTATCAGG	TCAACTACAC	CGTCCAACCT	420
AAGCAAAAGT	TAAATGCCAA	TCCTTTTGCC	ATCTACAATC	GTATGGTGGT	AGAGCAGGAG	480
GCGGGCTACA	ATGCCTATGT	GGAACATGAC	GAGATGGCAG	TGATTTCCAT	GAGCCCAGAG	540
CTCTTTTTTG	AGCAAAATGA	TCGCGAGTTG	ACAACACGAC	CAATGAAGGG	GACGACTCAG	600
CGTGGGGTAA	CTGACCAAGA	AGATCTTGAA	CAGGCCAGTT	GGTTGGAACA	GGATCCCAAA	660
AATCGCTCTG	AAAATATGAT	GATTGTGGAC	CTCTTGCGCA	ATGATATGAA	CCGTATTTCT	720
GAAGTTGGGA	GCGAGCACGT	GGAGCGTCTG	TGTCAGGTAG	AGCAGTATTC	AACTGTTTGG	780
CAGATGACTT	CGACCATCAA	GAGTCAGTTG	CGAGAGGATG	TGGACCTTGT	TGAAATCTTC	840
CGCTCACTCT	TTCCTTGTTG	TTCCATAACG	GGTGCACCGA	AAATTGCGAC	AATGGAGATT	900
ATCAAGGACT	TGGAGCCTCA	ACCGCGTGGA	GTCTACTGTG	GAACGATTGG	TCTCTTGCTT	960
CCAAATGGAC	GACGGATTTT	TAATGTGGCC	ATTTCGTACCA	TTCAACTTCA	CAAAGGTCAA	1020

GCCATTTATG	GAGTTGGCGG	AGGGATTACT	TGGGATAGCA	CATGGGAATC	TGAATACCGA	1080
GAGGTTTCATC	AAAAGGCAGC	AGTTCTTTAT	CGTAAACAAG	CTCGCTTCCA	ACTGATTACG	1140
ACAGGGGAAA	TCAGCCAGAA	GAACCTGTTG	TTTGAAGATC	AACATCTGGA	AAGACTGAGA	1200
AAAGCTAGTC	GTTATTTTGC	CTTTCCTTTT	GATGCAGAAG	ACTTGGGACA	CAAGATTGAG	1260
GAAGAGTGTC	AGGATTGTGA	AGCTAATCGA	GATTACCGCT	TGCGAATCAG	CCTTAGCAAA	1320
TCTGGAGAGA	TAGAAGTCAA	TCGTCAAGTA	TTAACCCTC	TCAGTACAAG	CTTTTGTGAG	1380
GCCCAAGTCT	GCCTTCAGGA	AGCTGCTTTG	AATCAATCCT	TTACCTACTT	TAAAACCACT	1440
CACCGACCGC	ATTTGAGCCT	AGGAGAACAA	GAGAAGATTT	ACCACAATAA	GTCAGGAGAA	1500
CTGCTTGAAA	CCTCTATAGG	AAATTTGGTT	CTGAAAATCG	CTGGAAAAC	CTACACACCG	1560
CCTATCCGAC	TTGGAATCTT	GCCAGGAATT	TACCGTCAGT	ATTTGCTAGA	AACAGGACAG	1620
GTAGAAGAGA	AAGTCTTGAC	CTTGGCAGAT	TTAGCCCAAG	CAGAAGCTAT	TTACGGCTGT	1680
AATGCAGTGA	GAGGCTTGTA	TGAGTTGCAA	GTGATAGGAT	TGTGA		1725

(2) INFORMATION FOR SEQ ID NO:1609:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...225
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1609:

GATAGTATTT	TAAAACGAAA	GGACTATAAA	AGCTCATTTT	CTTCGCACTT	ATTTTATAGA	60
GATCTATCAT	TATACTCTTT	AGAAATCAAA	AAGCAACACA	CCTTGTCATC	GTTTTATCGT	120
AAACCTGTTA	ATGAGGGGCT	AGTCTTATCT	GCAATCTCAA	ATCAGTGTTT	TGAGCTGAAT	180
GGCACTCGTT	TTCTAGTTTG	CTCTTTGATT	TTAATTGGGC	CTTAG		225

(2) INFORMATION FOR SEQ ID NO:1610:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1191 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1610:

GAGAACAAATA	GAAAGGAAAGT	ATTTATGGAG	CAAAAAGAGA	AACATTTTATG	CCTATCTTGG	60
TTTTTCAAGT	GGTTTTTAGA	TAACAAGGCA	ATTACGGTAT	TTTTAGTAAC	CTTATTATTG	120
GGACTGAATC	TTTTTATTTT	AAGTAAGATT	AGTTTTCTAT	TTTCACCTGT	TTTAGACTTT	180
TTAGCAGTTG	TGATGTTGCC	AGTCATTTTG	TCTGGTTTGT	TATATTATTT	GTTGAATCCT	240
ATTGTTGATT	GGATGGAGAA	GCATAAGGTT	AATCGTGTTA	TAGCTATCAC	TATTGTCTTT	300
GTTATCATCG	CTCTCTTTAT	CATTTGGGGC	TTGGCAGTCG	CCATTCCAAA	TCTGCAACGT	360
CAGGTTTTGA	CCTTTGCAAG	AAACGTTCCCT	GTTTACTTAG	AAGATATAGA	TAGGATTGTT	420
AATGGATTGG	TAGCCCAGCA	CCTGCCAGAT	GATTTCAGAC	CTCAATTAGA	GCAAGTTTTG	480
ACCAATTTTT	CTAGCCAGGC	TACAGTTTTG	GCAAGTAAGG	TTTCATCTCA	GGCAGTCAAC	540
TGGGTGAGTG	CCTTTATTAG	CGGGGCTTCT	CAAGTGATTG	TTGCCTTGAT	TATCGTTCCT	600
TTCATGCTCT	TTTATCTCTT	GCGTGATGGG	AAAGGCTTGC	GTAACATTTT	GACCCAATTC	660
ATTCCAAGAA	AATTGAAGGA	ACCTGTTGGA	CAAGTTTTAT	CAGATGTGAA	TCAACAGTTG	720
TCCAACATATG	TTCGAGGGCA	AGTGACAGTG	GCTATTATTG	TAGCAGTAAT	GTTTATCATC	780
TTCTTCAAGA	TTATTGGTCT	ACGCTATGCG	GTTACGCTGG	GGGTTACTGC	TGGTATTTTA	840
AATCTGGTCC	CTTATCTTGG	TAGCTTTCTA	GCCATGCTTC	CTGCTCTAGT	ATTGGGTTTG	900
ATTGCTGGTC	CAGTCATGCT	TTTGAAAGTA	GTGATTGTCT	TTATCGTAGA	ACAACTATT	960
GAAGGCCGTT	TTGTCTCTCC	ATTGATTTTG	GGAAGTCAAT	TAAACATCCA	CCCTATTAAT	1020
GTTCTCTTTG	TTTTGTAAAC	TTCAGGATCT	ATGTTTGGTA	TCTGGGGAGT	TTTACTTGGT	1080
ATTCCGGTTT	ATGCCTCTGC	TAAGGTTGTC	ATTTACAGCCA	TTTTCGAATG	GTATAAGGTA	1140
GTCAGTGGTC	TATATGAATT	AGAGGGTGAG	GAAGTCAAGA	GTGAACAATA	G	1191

(2) INFORMATION FOR SEQ ID NO:1611:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4392 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...4392

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1611:

ATGTCAAATA	GTTTTGAAAT	TTTGATGAAT	CAATTGGGGA	TGCCTGCTGA	AATGAGACAG	60
GCTCCTGCTT	TAGCACAGGC	TAATATTGAG	CGAGTTGTGG	TTCATAAAAT	TAGTAAGGTA	120
TGGGAGTTTC	ATTTTCGTATT	TTCTAATATT	TTACCGATTG	AAATCTTTTT	AGAATTAAAG	180
AAAGGTTTGA	GCGAAGAAAT	TTCTAAGACA	GGCAATAAAG	CTGTTTTTGA	AATTAAGGCT	240
CGGTCTCAAG	AATTTTCAAA	TCAGCTCTTG	CAGTCTTACT	ATAGGGAAGC	TTTCTCTGAA	300

GGTCCATGTG	CTAGTCAAGG	TTTTAAGTCC	CTTTATCAAA	ATTTGCAAGT	TCGTGCTGAG	360
GGTAATCAGC	TATTTATTGA	AGGATCTGAA	GCGATTGATA	AGGAACATTT	TAAGAAGAAT	420
CATCTTCCTA	ATTTAGCCAA	ACAACCTGAA	AAGTTTGGTT	TTCCAACTTT	TAACGTGCAA	480
GTCGAGAAGA	ATGATGTCC	GACCCAAGAG	CAGGAAGAGG	CCTTTCATGC	TGAAAATGAG	540
CAGATTGTTT	AAGCTGCCAA	TGAGGAAGCG	CTCCGTGCTA	TGGAACAAC	GGAGCAGATG	600
GCACCTCCTC	CAGCGGAAGA	GAAACCAGTC	TTTGATTTTC	AAGCGAAAA	AGCTGCAGCT	660
AAACCCAAGC	TGGATAAGGC	GGAGATTACT	CCTATGATCG	AAGTGACGAC	AGAGGAAAA	720
CGTCTGGTAT	TTGAAGGGGT	TGTTTTTGAT	TGGGAGCAAA	AAGTGACTAG	AACAGGTCGT	780
GTTTTAATCA	ACTTTAAAA	GACGGACTAT	ACTTCAAGTT	TTTCTATGCA	AAAGTGGGTT	840
AAAAACGAGG	AAGAGGCCCA	GAAGTTTGAC	CTCATCAAGA	AGAATTCCTG	GCTCCGAGTT	900
CGAGGGAATG	TGGAGATGAA	TAACCTCACA	CGCGATTTGA	CTATGAACGT	ACAGGATCTG	960
CAGGAAGTTG	TTCACATATG	GCGGAAGGAT	TTGATGCCAG	AAGGTGAGCG	TCGGGTTGAG	1020
TTTCATGCTC	ATACTAACAT	GTCGACTATG	GATGCTTTGC	CAGAGGTCGA	AGAGATTGTT	1080
GCAACAGCTG	CTAAGTGGGG	ACACAAGGCG	GTTGCTATCA	CGGACCATGG	GAATGTCCAG	1140
TCCTTTCCAC	ATGGCTATAA	GGCGGCTAAG	AAAGCGGGAA	TCCAGCTGAT	CTATGGGATG	1200
GAAGCCAATA	TCGTGGAGGA	CCGTGTCCCT	ATCGTCTATA	ACGAAGTGGA	GATGGACTTG	1260
TCAGAAGCAA	CCTACGTGGT	CTTTGACGTG	GAAACGACGG	GACTTTCAGC	TATCTATAAT	1320
GACTTGATTG	AGGTTGCGGC	CTCTAAGATG	TACAAGGGGA	ATGTTATTGC	TGAATTTGAT	1380
GAATTTATCA	ATCCTGGGCA	TCCCTTGTC	GCCTTTACTA	CAGAGTTAAC	TGGAATTACA	1440
GATGATCATG	TCAAAAAATG	CAAACCACTA	GAACAAGTTT	TGCAAGAATT	CCAAGAATTT	1500

TGCAAGGATA	CGGTCCTAGT	TGCCCCAAT	GCTACCTTTG	ACGTTGGCTT	TATGAATGCT	1560
AATTATGAGC	GGCATGATCT	TCCAAAGATT	AGTCAGCCAG	TTATTGATAC	GCTGGAGTTT	1620
GCTAGAAACC	TCTATCCTGA	GTATAAACGC	CATGGTTTGG	GGCCTTTGAC	CAAGCGTTTT	1680
GGTGTGGCCT	TGGAACATCA	TCACATGGCC	AACACGATG	CGGAAGCGAC	TGGTCTCTG	1740
CTTTTCACT	TTATCAAAGA	GGTAGCAGAA	AAACATGGTG	TGACCGATTT	AGCTAGACTC	1800
AACATTGATC	TAATCAGTCC	AGATTCTTAC	AAAAAAGCTC	GGATCAAGCA	TGCGACCATC	1860
TATGTCAAGA	ATCAGGTAGG	TCTAAAAAAT	ATCTTTAAGC	TGGTTTCCTT	GTCTAATACC	1920
AAGTATTTTG	AAGGAGTGCC	ACGGATTCCG	AGAACGGTTC	TAGATGCCCA	TCGAGAGGGC	1980
TTGATTTTAG	GTTTCAGCCTG	TTCAGAGGGT	GAAGTTTTTG	ACGTGGTTCG	TTCTCAAGGT	2040
GTGGATGCGG	CGGTTGAGGT	GGCCAAGTAT	TATGACTTTA	TCGAGGTCAT	GCCACCGGCT	2100
ATCTATGCGC	CCTTGATTGC	CAAAGAGCAG	GTCAAGGATA	TGGAGGAAC	CCAGACCATT	2160
ATCAAGAGTT	TGATAGAGGT	TGGAGATCGC	CTTGGCAAGC	CTGTTCTGGC	TACGGGAAAT	2220
GTTCACTATA	TCGAACCGGA	AGAAGAGATT	TATCGTGAAA	TTATCGTCCG	TAGTTTGGGA	2280
CAGGGTGCGA	TGATTAACCG	AACATATCGT	CATGGTGAAC	ATGCCCAACC	AGCACCACCT	2340
CCAAAGGCTC	ATTTTCGAAC	GACTAATGAG	ATGTTGGATG	AATTTGCCTT	TTTGGGAGAG	2400
GAACCTGGCTC	GTAAACTGGT	TATTGAAAAC	ACCAATGCCT	TGGCAGAAAT	ATTTGAACCC	2460
GTTGAAGTCG	TTAAGGGTGA	TTTGTATACG	CCTTTCATCG	ACAAGGCTGA	AGAAACAGTT	2520
GCTGAGTTGA	CCTATAAGAA	AGCTTTTGAG	ATTTATGGAA	ATCCGCTGCC	AGATATTGTT	2580
GATTTGCGGA	TTGAAAAAGA	ATTAACATCC	ATACTGGGGA	ATGGATTTGC	TGTGATTTAT	2640
CTGGCATCGC	AGATGCTGGT	GCAACGTTCT	AATGAACGGG	GTTATTTGGT	TGGTTCCTCG	2700
GGGTCTGTCT	GATCTAGTTT	CGTTGCGACC	ATGATTGGGA	TTACGGAGGT	CAATCCTCTC	2760
TCTCCTCACT	ATGTCTGTGG	TCAGTGTCCG	TACAGTGAGT	TTATCACAGA	TGGTTCGTAC	2820
GGTTCAGGAT	TTGATATGCC	CCATAAGGAC	TGTCCAAACT	GTGGTCACAA	ACTCAGTAAA	2880
AACGGACAGG	ATATTCCGTT	TGAGACCTTC	CTTGGTTTTG	ATGGGGATAA	GGTTCCTGAT	2940
ATTGACTTGA	ACTTCTCGGG	AGAAGATCAG	CCTAGCGCCC	ACTTGGATGT	GCGTGATATC	3000
TTTGGTGAAG	AATATGCCCT	CCGTGCGGGA	ACGGTTGGTA	CGGTAGCTGC	CAAGACTGCC	3060
TATGGATTTG	TCAAGGGTTA	CGAGCGAGAT	TATGGCAAGT	TTTATCGTGA	TGCAGAAGTA	3120
GAACGCCCTCG	CTCAAGGAGC	GGCGGGTGTC	AAGCGGACAA	CAGGCCAACA	CCCGGGGGGA	3180
ATCGTTGTTA	TTCCGAAC	CATGGATGTC	TACGATTTTA	CGCCTGTCCA	GTATCCAGCA	3240
GATGATGTCA	CGGCTGAATG	GCAGACCACT	CACTTTAACT	TCCACGATAT	CGATGAGAAC	3300
GTCTCTAAAC	TCGATGTACT	GGGACATGAT	GATCCGACCA	TGATTCGAAA	ACTTCAGGAT	3360
TTGTCTGGTA	TTGACCCTAA	TAAAATTCCCT	ATGGATGACG	AAGGCGTGAT	GGCACTCTTT	3420
TCTGGGACTG	ATGTGCTAGG	GGTAACACCT	GAACAAATTG	GAACGCCTAC	GGGTATGTTG	3480
GGGATTCCAG	AGTTTGGAAC	AAATTTCTGTA	CGTGGAATGG	TAGACGAAAC	CCATCCGACA	3540
ACCTTTGCGG	AATTGCTTCA	GCTGTCTGGT	CTGTCCCACG	GTAAGTACGT	TTGGTTGGGG	3600
AATGCTCAGG	ATCTGATTAA	GCAAGGAATA	GCGGACCTAT	CGACTGTTAT	CGGTTGTCTG	3660

GACGACATCA	TGGTTTACCT	CATGCATGCG	GGTCTGGAAC	CTAAGATGGC	CTTTACCATT	3720
ATGGAACGGG	TACGTAAGGG	TTTGTGGCTA	AAGATTTCAG	AAGAGGAGAG	AAATGGCTAT	3780
ATCGAAGCCA	TGAAGGCTAA	TAAGGTGCCA	GAGTGGTATA	TCGAATCCTG	TGGGAAAATT	3840
AAGTACATGT	TCCCTAAGGC	CCATGCGGCA	GCCTACGTTA	TGATGGCCTT	GCGTGTAGCT	3900
TACTTCAAGG	TTCACCATCC	TATTTATTAC	TACTGTGCTT	ACTTCTCCAT	TCGTGCTAAG	3960
GCTTTTGATA	TCAAGACCAT	GGGTGCGGGC	TTGGAGGCCA	TCAAGCGCAG	AATGGAAGAA	4020
ATCTCTGAAA	AACGGAAGAA	CAATGAAGCC	TCTAATGTGG	AAATCGATCT	CTATACAAC	4080
CTTGAGATTG	TCAATGAGAT	GTGGGAACGA	GGTTTCAAGT	TTGGCAAATT	AGATCTCTAC	4140
CGTAGTCAGG	CGACAGAGTT	CCTCATCGAC	GGGGATACCC	TTATCCCACC	ATTTGTAGCA	4200
ATGGATGGTC	TGGGAGAGAA	CGTTGCCAAG	CAACTGGTGC	GGGCGCGTGA	AGAGGGAGAA	4260
TTCCTCTCTA	AAACAGAACT	ACGCAAGCGT	GGTGGACTCT	CATCAACCTT	GGTTGAAAAG	4320
ATGGATGAGA	TGGGTATTCT	TGGAAATATG	CCAGAGGATA	ACCAGTTGAG	TTTGTTTGAT	4380
GAGTTGTTTT	AA					4392

(2) INFORMATION FOR SEQ ID NO:1612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1612:

AAGGAAAATA	GGATGATTGA	ACTAAAGAAT	ATATCTAAAA	AATTTGGAAG	CCGTCAACTA	60
TTTTCAGATA	CAAACTTTCA	TTTTGAAGGT	GGGAAAATTT	ATGCCTTAAT	CGGTACAAGT	120
GGCTGTGGTA	AGACAACATT	CTTGAATATG	ATTGGACGAT	TAGAGCCATA	TGACAAAGGA	180
CAAATCATCT	ATGATGGTAC	TTCTCTTAAG	GACATCAAGC	CTTCTGTTTT	CTTTAGAGAT	240
TACTTGGGAT	ATTTATTTCA	AGATTTTGGC	TTAATTGAAA	ACCAAACCGT	CAAAGAGAAT	300
CTCAATCTGG	GTTTAGTTGG	TAAAAAGTTG	AAGGAAAAAG	AGAAAATCTC	TTTGATGAAA	360
CAAGCTCTAA	ACCGTGTAAG	CCTCTCTTAT	TTGGATTTGA	AGCAACCTAT	ATTTGAGTTA	420
TCAGGAGGAG	AAGCACAACG	TGTTGCATTA	GCGAAGATAA	TTTTAAAGGA	TCCACCTTTG	480
ATTCTCGCAG	ATGAACCAAC	CGCTTCACTA	GACCCCAAAA	ACTCTGAGGA	ATTACTTTCC	540
ATCCTAGAAT	CTCTAAAAAA	TCCGAATCGG	ACCATTATTA	TTGCGACCCA	CAATCCTCTG	600
ATTTGGGAGC	AAGTGGATCA	GGTCATTTCG	GTTACCGATT	TATCACATAG	ATGA	654

(2) INFORMATION FOR SEQ ID NO:1613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1613:

ATCTGGAATA	GTCCATCGAG	CTTTCTAATA	CTCTTCGAAA	ATCTCTTTCAA	ACCACGTCAA	60
CGTCGCCCTT	CCGTGCGTAT	GGTTCATACT	ACGTCAGATC	TATCCACAAC	CTCAAAACAG	120
TGTTTTGAGC	AACCTGAGGC	TAGTTTCCTA	GTCTGCTCTT	TGGTTTTTCAT	TGAGTATAAC	180
ACATTGTTAG	AAGTTGGTTT	AAATTCCTTA	ATCAGTTTGT	TCACATTTAC	CTTCGATATA	240
TTATATCCCA	TAGTTAAGGT	TGGTCATACA	GATGATTATA	GTCATGGAGC	CGTAAACTT	300
AGTGTTCCTT	TAGTTGACAA	AGATGTCATG	AAAAAATAT	CTGTAACTGT	AATAGGATAT	360
TTTGAAATAA	ATATAGATGA	AAATATCACC	GATATTCTAT	ACGTAAATGG	TACTGCTATT	420
CTTTATCCTT	ATTTACGTTT	TATTGTTTCA	ATAGTTTCGG	CAATTGATAG	CAGTGAAGCA	480
ATGTTGCTAC	CTACCATTAA	TGTTTTAGAG	TTACTAGATA	AATCTCAACC	TTTTGAAGAA	540
GAATAA						546

(2) INFORMATION FOR SEQ ID NO:1614:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 663 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1614:

GTGAGGAATA	GAATGCCAAT	TACATCATTA	GAAATAAAGG	ACAAGACTTT	TGGAACTCGA	60
TTCAGAGGTT	TTGATCCAGA	AGAAGTCGAT	GAATTTTTAG	ATATTGTGGT	TCGTGATTAC	120
GAAGATCTTG	TGCGTGCGAA	TCATGATAAA	AATTTGCGTA	TTAAGAGTTT	AGAAGAGCGT	180
TTGTCTTACT	TTGATGAAAT	AAAAGATTCA	TTGAGCCAGT	CTGTATTGAT	TGCTCAGGAT	240
ACAGCTGAGA	GAGTGAAACA	GGCGGCGCAT	GAACGTTCAA	ACAATATCAT	TCATCAAGCA	300
GAGCAAGATG	CGCAACGCTT	GTTGGAAGAA	GCTAAATATA	AGGCAAACGA	GATTCTTCGT	360
CAAGCAACTG	ATAATGCTAA	GAAAGTCGCT	GTTGAAACAG	AAGAATTGAA	GAACAAGAGC	420
CGTGTCTTCC	ACCAACGTCT	CAAATCTACA	ATTGAGAGTC	AGTTGGCTAT	TGTTGAATCT	480

TCAGATTGGG AAGATATTCT CCGTCCAACA GCTACTTATC TTCAAACCAG TGATGAAGCC	540
TTTAAAGAAG TGGTTAGCGA AGTACTTGGA GAACCGATTC CAGCTCCAAT TGAAGAAGAA	600
CCAATTGATA TGACACGTCA GTTCTCTCAA GCAGAAATGG CAGAATTACA AGCTCGTAAT	660
TGA	663

(2) INFORMATION FOR SEQ ID NO:1615:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 186 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...186
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1615:

AAACTTGATA GTATGCCTTT TATGATGGAA AAATCTTCTA ATACTCTTCG AAAATCTCTT	60
CAAGCCACGT CAACGTCGCC TTACCGTAGG TATATGATAC TGACTCTGTC AATTCTATCC	120
ACAACCTCAA AACAGTGTTT TGAGGTTGTG GATAGCTTCC TAGTTTGCTC TTTGATTTTC	180
ATTAG	186

(2) INFORMATION FOR SEQ ID NO:1616:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...321
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1616:

AAAATTGATA GAGATAAATT AAAAATCTAT ATTGAAACTC ATCCCGATGC TTATTTGACT	60
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GAAATAGCTG	CTGAATTCAA	CTGTCCTCCA	ACAACTATTC	ATTACGCTCT	AAAGGCTATG	120
GGATATAGTC	TAAAAAAGAG	CCGTACCTAC	TGCGAACAAAG	ACCCAGAAAA	AGTAAATCGG	180
TTCCTTAAAG	AATTGAATCA	CTTAAGCTAC	CTGACTCCTA	TTTATATTTA	TGAGACAGGG	240
GTTGAGACCT	ATTTTATCT	CGAATATGAT	CGAGCCTTGA	GCAGGCAGTT	AGTCTCTCTG	300
AAAGAAGATA	TAATTATTTG	A				321

(2) INFORMATION FOR SEQ ID NO:1617:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 726 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...726
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1617:

AGAAAAGATA	GAAATGAAGT	GAAAAATATG	CTACCTGCTT	ATATGAAAAT	CCATGATCAG	60
ATAAAAAAGG	ATATTGACGA	GCACCGTTGG	GCTATTGGTG	AGAGGCTTCC	CAGTGAAAGA	120
GATTTAGCTG	AGCAGTTTGC	GGTCAGTCGC	ATGACCCTCC	GCCAAGCCGT	ATCTCTATTA	180
GTCGAAGAAG	GCGTCTTAGA	GCGCCGTGTA	GGAAGCGGCA	CCTTTGTTTC	CAGTACTCGA	240
GTACAAGAAA	AGATGCGAGG	GACAACCAGT	TTTACTGAAA	TTGTCAAATC	CCAAGGTAAA	300
GTTCCCTCTA	GCCAGCTCAT	TTCCTACAAA	AAAACCATTC	CCAATGAGCA	AGAAGTTGCC	360
AAGCTAGGAA	TTTTTCCAAC	GGACAATATT	ATCCGAATGG	AGCGGGTCCG	CTATGCCGAC	420
CAAGTTCCCC	TAGTTTATGA	AGTTGCTTCT	ATTCCTGAAA	AATTCATTAA	GGACTTTTAAA	480
AAAGAAGAAA	TCACCAGTCA	TTTCTTCCAA	ACCTTGCAAA	AACATGGGCTA	TCGTATCGGC	540
AAATCTCAAC	AGACCATCTA	TGCTCGCCTT	GCTAAAGAAA	AGATTGCCCA	CTATTTGGAA	600
GTTGAAAAAG	GACATGCTAT	TCTTGGATTG	ACACAGGTTT	CCTACCTAGA	AGATGGTACT	660
GCTTTTGAAT	ACGTAAAAAG	TCAATATGTA	GGCGAACGCT	TTGAATTTTA	TCTTGAAAAT	720
AATTAG						726

(2) INFORMATION FOR SEQ ID NO:1618:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1011 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1618:

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ATGAAGGATA GATATATTTT AGCATTTGAG ACATCCTGTG ATGAGACCAG TGTCGCCGTC      60
TTGAAAAACG ACGATGAGCT CTTGTCCAAT GTCATTGCTA GTCAAATTGA GAGTCACAAA      120
CGTTTTTGGTG GCGTAGTGCC CGAAGTAGCC AGTCGTCACC ATGTCGAGGT CATTACAGCC      180
TGTATCGAGG AGGCATTGGC AGAAGCAGGG ATTACCGAAG AGGACGTGAC AGCTGTTGCG      240
GTTACCTACG GACCAGGCTT GGTCTGAGCC TTGCTAGTTG GTTTGTCAGC TGCCAAGGCC      300
TTTGCTTGGG CTCACGGACT TCCACTGATT CCTGTTAATC ACATGGCTGG GCACCTCATG      360
GCAGCTCAGA GTGTGGAGCC TTTGGAGTTT CCCTTGCTAG CCCTCTTGGT CAGCGGCGGA      420
CACACAGAGT TGGTCTATGT TTCTGAGGCT GGCGATTACA AGATTGTTGG GGAGACACGA      480
GATGACGCGG TTGGCGAGGC CTATGATAAG GTCGGCCGTG TCATGGGCTT GACCTATCCT      540
GCAGGTCGTG AGATTGACGA GCTGGCTCAT CAGGGGCAGG ATATTTATGA TTTCCCCCGT      600
GCCATGATTA AGGAAGATAA TCTGGAGTTT TCATTCTCTG GTTTGAAGTC AGCCTTTATC      660
AATCTTCATC ACAATGCCGA GCAAAAGGGA GAAAGCCTGT CTACAGAAGA TTTGTGTGCT      720
TCCTTCCAAG CAGCAGTTAT GGACATTCTC ATGGCAAAAA CCAAGAAGGC TTTGGAGGAA      780
TATCCTGTTA AAACCCTATT TGTGGCAGGT GGTGTGGCAG CCAATAAAGG TCTCAGAGAA      840
CGCTTAGCAG CCGAAATCAC AGATGTCAAG GTTATCATCC CCCCTCTGCG ACTCTGCGGA      900
GACAATGCAG GTATGATTGC CTATGCCAGC GTCAGCGAGT GGAACAAAGA AAACCTTCGCA      960
GGCTGGGACC TCAATGCCAA ACCAAGTCTT GCCTTTGATA CCATGGAATA A      1011
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(2) INFORMATION FOR SEQ ID NO:1619:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 873 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1619:

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TGTTATCGTA GCGCGATGCT TCCTGATGTT CGAGATGGCT TAACACCTGT TCACCGTCGC      60
ATTCTCTACG GAATGAATGA ATTGGGTGTG ACCCAGAACA AACCCCATAA TACATCTGCT      120
CGTATTACAG GGGATGTCAT GGGTAAATAT CACCCACACG GGGATTCCCTC TATTTATGAA      180
GCCATGGTCC GTATGGCTCA ATGGTGGAGC TACCGTTACA TGCTTGTAGA TGGTCATGGG      240
AATTTTGGTT CCATGGATGG AGATAGTGCT GCCGCTCAAC GTTATACCGA GGCACGTATG      300
AGCAAGATTG CTCTGGAAAT GCTTCGTGAT ATCAACAAAA ATACAGTTGA TTTCGTTGAT      360
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AACTATGATG	CCAATGAACG	GGAACCCCTTG	GTCTTGCCAG	CGCGTTTTTC	AAACCTTTTG	420
GTTAATGGAG	CAACTGGTAT	CGCGTTTGGG	ATGGCAACCA	ATATTCCACC	TCATAATCTG	480
GGTGAAACCA	TTGATGCAGT	GAA GTTGGTC	ATGGATAATC	CTGAAGTGAC	TACCAAGGAC	540
TTGATGGAAG	TCTTGCCTGG	ACCAGATTTT	CCA ACTGGTG	CTCTTGTCAT	GGGGAAATCA	600
GGTATCCATA	AGGCTTATGA	AACAGGTAAA	GGTTCGATTG	TCCTACGTC	TCGTACAGAG	660
ATTGAAACGA	CTAAGACTGG	TCGTGAGCGC	ATCGTTGTAA	CAGAATTTCC	TTACATGGTC	720
AATAAAACCA	ATGTGCATGA	GCATATTGTT	CGCTTGGTTC	AGGAAAAACG	CATTGAGGGT	780
ATCACAGCAG	TACGTGATGA	GTCAAACCGT	GAAGGTGTTT	GATTTGTTAT	TGAAGTCAAG	840
CGCGACGCCT	CAGCCAATGT	TATTCTCATA	TAA			873

(2) INFORMATION FOR SEQ ID NO:1620:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 858 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...858

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1620:

TTCAATAGTA	GAATTGATAT	AATAGTAGTT	ATGGAGAAAA	AGAAATTACG	CATCAATATG	60
TTGAGTTCAA	GTGAGAAAGT	AGCAGGACAG	GGAGTTTCAG	GTGCTTACCG	TGAATTAGTT	120
CGTCTTCCTC	ACCGTGCTGC	CAAGGACCAA	TTGATTGTTA	CAGAAAATCT	TCCAATCGAG	180
GCAGATGTGA	CTCACTTTCA	TACGATTGAT	TTTCCCATT	ATTTATCAAC	CTTCCAAAAG	240
AAACGCTCAG	GGAGAAAGAT	TGGCTATGTG	CATTTCTTGC	CAGCTACACT	TGAGGGGAAGT	300
TTGAAAATTC	CATTTTTCTT	AAAGGGAATT	GTGAAACGCT	ATGTATTTTC	TTTTTACAAC	360
CGGATGGAGC	ACTTGGTTGT	GGTCAATCCT	ATGTTTATTG	AGGATTTGGT	AGCAGCTGGT	420
ATTCCACGTG	AAAAAGTGAC	CTATATTCCT	AACTTTGTCA	ACAAGGAAAA	ATGGCATCCT	480
CTACCACAAG	AAGAGGTAGT	TAGACTGCGC	ACAGATCTTG	GTCTTAGTGA	CAATCAGTTT	540
ATCGTAGTAG	GTGCTGGGCA	AGTTCAGAAA	CGTAAAGGGA	TTGATGACTT	TATCCGTCTG	600
GCTGAGGAAT	TGCCTCAGAT	TACCTTTATC	TGGGCTGGTG	GCTTCTCTTT	TGGTGATATG	660
ACAGATGGTT	ATGAACACTA	TAAGAAAATT	ATGGAAAATC	CCCCTAAAAA	TTTGATTTTTT	720
CCAGGCATTG	TATCGCCAGA	GCGGATGCGC	GAATTGTATG	CTCTAGCGGA	TCTTTTCTTG	780
TTGCCTAGCT	ACAATGAGCT	CTTTCCTATG	ACTATTTTAG	AAGCTGCGAG	TTGTGAGGCT	840
CGCTATTATG	TTGCGTGA					858

(2) INFORMATION FOR SEQ ID NO:1621:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 789 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1621:

GATAGTAGTA	GGAAACGAGG	TGATAATATG	CTCAAACAAG	AAAAATTAAC	CAAAATTTTA	60
GAGATAGTAA	ATAGTAAAGG	AACCATAACA	GTAAACAGA	TTATGGACGA	AATAGCCGTT	120
TCAGATATGA	CTGCAAGGCG	CTATTTACAG	GAATTAGCTG	ATAAAGATTT	GCTGATTCGT	180
GTGCATGGTG	GAGCTGAAAA	ACTTCGAACC	AACTCCCTTT	TGACTAATGA	GCGATCAAAT	240
ATTGAAAAAC	AAGCCCTCCA	AACGGCAGAA	AAACAAGAAA	TAGCCCATTT	TGCAGGCAGT	300
CTAGTAGAAG	AAAGAGAAAC	TATTTTCATT	GGACCAGGAA	CAACATTAGA	GTTTTTTGCG	360
CGTGAGTTGC	CTATTGACAA	TATCCGCGTC	GTAACCAACA	GTCTACCTGT	TTTTCTGATT	420
TTAAGCGAAC	GAAAATTAAC	AGATTTGATT	TTAATAGGTG	GAAATTATCG	CGATATTACA	480
GGTGCTTTTG	TTGGTACATT	GACCCACAAA	AATCTCTCTA	ATCTCCAATT	TTCTAAAGCT	540
TTCGTTAGCT	GTAATGGTAT	TCAAAACGGA	GCTCTAGCTA	CTTTTAGCGA	GGAAGAGGGA	600
GAGGCTCAAC	GCATCGCTTT	AAATAATTCT	AATAAAAAAT	ATTTACTCGC	AGATCATAGT	660
AAGTTCAATA	AGTTTGATTT	TTTACTTTTT	TATAATATAT	CAAATCTTGA	TACTATTGTT	720
TCAGATTCTA	AACTAAGTGA	TTCAATCCTT	TTTAAGCTAT	CTAAACACAT	TAAAGTCATC	780
AAGCCTTAA						789

(2) INFORMATION FOR SEQ ID NO:1622:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 753 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1622:

ACTTTAAGTA	GGATGAAGTT	CTCCGGTGCT	TGTGTTAAGA	TTCAATTTTT	TAAGCTTGTT	60
GTAAAAACCA	TTGCTCGCAA	ACACGGACTT	TACGCAACAT	TTATGGCGAA	GCCAAAATTT	120
GGTATTGCTG	GATCAGGTAT	GCACTGTAAT	ATGTCCTTGT	TTGATGCAGA	AGGAAATAAC	180
GCTTTCCTTG	ATCCAAATGA	TCCAAAAGGA	ATGCAGTTGT	CAGAAACAGC	TTACCATTTT	240

CTAGGCGGTT	TGATCAAGCA	TGCTTACAAC	TATACTGCCA	TCATGAACCC	AACAGTTAAC	300
TCATACAAAC	GTTTGGTTCC	AGGTTATGAA	GCGCCTGTTT	ACATTGCTTG	GGCTGGTCGT	360
AACCGTTCGC	CACTTGTGCG	CGTACCTGCT	TCACGTGGTA	TGGGAACTCG	TCTTGAGTTG	420
CGTTCAGTGG	ATCCAATGGC	GAACCCTTAC	GTTGCTATGG	CTGTTCTTTT	GGAAGTTGGT	480
TTGTATGGTA	TTGAAAAATA	AATCGAAGCA	CCAGCTCCTA	TCGAAGAAAA	TATCTACATC	540
ATGACAGCAG	AAGAGCGCAA	GGAAGCTGGT	ATTACAGACC	TTCCATCAAC	TCTTCACAAC	600
GCTTTGAAAG	CTTTGACAGA	AGATGAAGTG	GTTAAAGCTG	CTCTCGGAGA	TCACATCTAT	660
ACTAGCTTCC	TTGAAGCCAA	ACGAATCGAA	TGGGCAAGTT	ATGCAACCTT	CGTTTCACAA	720
TGGGAAATTG	ATAATTATTT	AGACCTTTAC	TAA			753

(2) INFORMATION FOR SEQ ID NO:1623:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 834 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...834
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1623:

TATAAAGGTA	GGGATATGAA	CCGTTTAAAA	AAATCAAAAT	ATGTCATTAT	TGTTTTTGTG	60
ACTGTTCTGC	TTGTGTCAGC	TCTCTTAGCG	ACGACTTATT	CAAGTACAAT	TGTGACAAAA	120
TTAGGAGATG	GAACTCTCAT	GGTTGATAGA	GTTGTACAAA	AACCTTTTCA	GTGGTTTGAT	180
TCTGTCAAAT	CAGATTTGGC	TCATTTGACA	CGAACATATA	ATGAAAAATGA	AAGTTTGAAG	240
AAACAGCTTT	ACCAATTAGA	AGTTAAATCA	AATGAGGTGG	AAAGTTTAAA	GACAGAAAAAT	300
GAACAACTGC	GCCAATTGCT	TGATATGAAG	TCTAAATTGC	AAGCCACAAA	GACTTTTAGCA	360
GCAGATGTTA	TTATGCGTTC	TCCGGTATCT	TGGAAGCAGG	AGTTGACCTT	AGATGCAGGT	420
AGATCAAAAAG	GTGCTTCTGA	GAACATGTTA	GCTATTGCAA	ATGGTGGCTT	GATTGGGAGT	480
GTTTCAAAAAG	TAGAGGAGAA	ATCTACTATA	GTCAACCTTC	TGACAAATAC	GGAAAAATGCT	540
GATAAGATTT	CTGTTAAAAAT	TCAACATGGC	TCTACTACAA	TTTATGGAAT	TATTATTGGC	600
TATGACAAGG	AAAATGACGT	TCTTAAAAAT	AGCCAATTAA	ATAGTAATAG	CGATATTAGT	660
GCGGGAGATA	AGGTGACTAC	TGGTGGATTA	GGAAACTTTA	ACGTTGCTGA	TATTCCTGTT	720
GGTGAAGTGG	TTGCCACAAC	GCATAGTACA	GACTATTTGA	CACGAGAAGT	AACTGTTAAA	780
TTGAGTGCAG	ATACTCATAA	TGTAGATGTG	ATAGAATTAG	TGGGGAATTC	ATAA	834

(2) INFORMATION FOR SEQ ID NO:1624:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1624:

AAGATGTTCA	GTAAACTTAA	AAAAACATGG	TATGCGGATG	ACTTTAGTTA	TTTATCCGC	60
AACTTCGGTG	TCTTCACCCT	GATTTTTTCT	ACAAAGACTC	TGATTATTTT	ACAAGTCATG	120
CATTTCGAGTC	TTTATACTTC	GGTGGACGAT	AAGCTTCATG	GACTGAGTGA	AAATCCTCAA	180
GCAGTTATTTC	AGCTGGCTAT	AAATAGGGCA	ACAGAAGAGA	TTAAAAGATT	AGAAAATGCT	240
AGGGCGGACG	CTAGTAAAGT	AGAAAATAAA	CCTAATGTCA	GTTCCAATAC	GGAAGTCATT	300
CTCTTTGATA	AAGACTTTAC	TCAACTTCTT	TCTGGAAAATC	GATTTTTTGGG	CTTGGATAAG	360
ATTAAGTTAG	AAAAGAAAAGA	ACTAGGACAT	ATCTACCAGA	TTCAGGTTTT	TAATAGCTAT	420
GGGCAGGAAG	AAATCTATCG	TGTGATTTTG	ATGGAGACCA	ATATTAGTTC	GGTTTCAACC	480
AATATCAAGT	ATGCTGCTGT	CTTGATTAAT	ACCAAGTCAGT	TGGAGCAGGC	TAGTCAAAAG	540
CATGAGCAAT	TGATTGTGGT	CGTGATGGCT	AGTTTCTGGA	TTTTGTCTTT	ACTTGCCAGT	600
CTCTATCTAG	CTAGGGTCAG	TGTTAGGCC	CTGCTTGAGA	GTATGCAAAA	GCAACAGTCT	660
TTTGTGGAAA	ATGCCAGTCA	TGAGTTACGA	ACTCCACTCG	CAGTTTTGCA	AAATCGCTTA	720
GAGACCTTTT	TTCGTAAGCC	AGAAGCTACC	ATTATGGATG	TGAGCGAAAG	CATTGCATCG	780
AGTTTGGAAG	AAGTCCGAAA	TATGCGTTTT	TTAACGACAA	GCTTGCTGAA	CTTAGCTCGG	840
AGAGATGATG	GGATTAAGCC	GGAGCTTGCA	GAAAGTTCCAA	CTAGCTTTTT	TAATACAACT	900
TTCACAAACT	ACGAGATGAT	TGCTTCGGAA	AATAATCGTG	TCTTCCGTTT	TGAAAATCGT	960
ATCCATCGAA	CAATTGTCAC	AGATCAGCTT	CTTCTGAAAC	AACTGATGAC	CATTCTTTTC	1020
GATAATGCCG	TCAAGTATAC	TGAGGAGGAT	GGTGAAATTG	ATTTTCTTAT	CTCGGCGACC	1080
GATCGCAATC	TTTATTTACT	TGTTTCTGAT	AATGGAATCG	GTATTTTCGAC	AGAAGATAAA	1140
AAGAAAATTT	TTGACCGTTT	TTATCGAGTA	GACAAAGCTA	GAACCCGGCA	AAAAGGTGGT	1200
TTTGGTTTAG	GATTATCCCT	AGCCAAGCAA	ATTGTAGATG	CTCTAAAAGG	AACTGTTACT	1260
GTCAAAGATA	ATAAACCCAA	GGGAACAATC	TTTGAAGTGA	AGATTGCCAT	TCAGACACCA	1320
TCTAAAAAGA	AAAAATAA					1338

(2) INFORMATION FOR SEQ ID NO:1625:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1625:

TCTGGACTCA GTTGGCATGT GGGACATCGA GACAAACGCT TGGGTTCTCT ATCTGGGGGA	60
CAAAAGCAGC GAGCGGTGAT TGC GCGTATG TTTGCTTCTG ACCCTGATGT GTTTATCCTA	120
GACGAGCCGA CAACGGGGAT GGATGCAGGA AGTAAAAATG AATTTTACGA ACTCATGCAC	180
CACAGCGCCC ATCATCATGG CAAGGCTGTT TTGATGATTA CCCATGACCC TGAAGAAGTT	240
AAGGATTATG CGGATCGCAA TATTCATCTA GTCCGTAACC AAGACTCGCC ATGGCGTTGT	300
TTCAATGTTC ATGAGAATGG CCAGGAGGTG GGCCATGCTT AG	342

(2) INFORMATION FOR SEQ ID NO:1626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1626:

CCTAAGCTCA GTTTAAAAAA GCGAGGGTGG TTATTTTCTC AAAGTTTGA AGGAGCTAAA	60
GCAAGAGCTA TTATTATGAG TTTGTTGGAA ACAGCTAAAC GTCATCAACT AAATAGTGAG	120
AAATATCTAT CCTATCTTCT AGAATGTCTT CCAAACGAGG AAACCTCTCGT AAACAAAGAG	180
GTTTTAGAGG CCTATTTACC ATGGACTAAA GTTGTAACAAG AAAAGTGCAA ATGA	234

(2) INFORMATION FOR SEQ ID NO:1627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1627:

AAGTGGCTCA	GAAATCCATC	GTGTAGAAGA	TACCATGATT	CGAATCGCGA	TTCGCAGGGG	60
ATTGTGGATT	GCAATGTCCT	TGCCATGCCT	GCCGCTATCT	TTTTCTCTAT	TGAAAATACC	120
AATATTTTCG	GCATGAAGCG	CGTGACCTCC	TCTTCTTATA	ACATCGAAAA	AGTCTGCGAT	180
GTGAACCAGA	TTTCTCGTCA	GCTAGTTGGG	GGGCAGATTG	ACTTAGAAAC	AGCCTTTAAG	240
CAATTGACGG	CCTTGCAAGC	TCAACCCCTT	CCCTATACTA	AGTTGCAGGT	AACTCTGGCT	300
GCGACCTTTA	GTGCTCCTTT	CTTTTCAGTT	ATGTTTAGCG	GAAATATCTA	CGACGCACTT	360
GGGGCAGGAG	TGGCGACCTT	ATTTGGTTTT	GCCTTTTCCC	TCTATGTGGA	AAAATTTATC	420
CGAATTCCCT	TTGTGACAGC	CTTTGCTGGA	GCCTTTGTCT	TTGGGATAAT	TGCCCAGTTT	480
TGGGCTCGCT	ACACAGGTTT	TCCTTCAACG	GCAGATTTGA	TTATAGCTGG	TGCGGTCATG	540
CCGTTTGTAC	CAGGTATTGC	CTTGACCAAT	GCGGTCCGTG	ATATTATGAC	CAACCACATA	600
AACTCTGGTA	TGAGTAAGAT	GTTTGAATCC	CTGCTCATTA	CCCTCGCTTT	AGGGGCAGGA	660
ACTTCTGTCG	CCTTGGTATT	GATGAACTAA				690

(2) INFORMATION FOR SEQ ID NO:1628:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1628:

GTGCCTATCA	GTGGAAGTGG	TTCTACAGTT	TCTACAAATG	CAAAACCTAA	TGAAGTAGTG	60
TCTAGTCTAG	GCAGTCTTTC	AAGCAATCCT	TCTTCTTTAA	CGACAAGTAA	GGAGCTCTCT	120
TCAGCATCTG	ATGGTTATAT	TTTAAATCCA	AAAGATATCG	TTGAAGAAAC	GGCTACAGCT	180
TATATTGTAA	GACATGGTGA	TCATTTCCTT	TACATTCCAA	AATCAAATCA	AATTGGGCAA	240
CCGACTCTTC	CATACAATAG	TCTAGCAACA	CCTTCTCCAT	CTCTTCCAAT	CAATCCAGGA	300
ACTTCACATG	AGAAACATGA	AGAAGATGGA	TACGGATTTG	ATGCTAATCG	TATTATCGCT	360
GAAGATGAAT	CAGGTTTTGT	CATGAGTCAC	GGAGACCACA	ATCATTATTT	CTTCAAGAAG	420
GACTTGACAG	AAGAGCAAAT	TAAGGCTGCG	CAAAAACATT	TAGAGGAAGT	TAAAAC TAGT	480
CATAATGGAT	TAGATTCTTT	GTCATCTCAT	GAACAGGATT	ATCCAGGTAA	TGCCAAAGAA	540
ATGAAAGATT	TAGATAAAAA	AATCGAAGAA	AAAATTGCTG	GCATTATGAA	ACAATATGGT	600
GTCAAACGTG	AAAGTATTGT	CGTGAATAAA	GAAAAAATG	CGATTATTTA	TCCGCATGGA	660
GATCACCATC	ATGCAGATCC	GATTGATGAA	CATAAACCGG	TTGGAATTGG	TCATTCTCAC	720
AGTAACTATG	AACTGTTTAA	ACCCGAAGAA	GGAGTTGCTA	AAAAAGAAGG	GAATAAAGTT	780
TATACTGGAG	AAGAATTAAC	GAATGTTGTT	AATTTGTTAA	AAAAATAGTAC	GTTTAATAAT	840
CAAAACTTTA	CTCTAGCCAA	TGGTCAAAAA	CGCGTTTCTT	TTAGTTTTCC	GCCTGAATTG	900
GAGAAAAAAT	TAGGTATCAA	TATGCTAGTA	AAATTAATAA	CACCAGATGG	AAAAGTATTG	960

GAGAAAGTAT	CTGGTAAAGT	ATTTGGAGAA	GGAGTAGGGA	ATATTGCAAA	CTTTGAATTA	1020
GATCAACCTT	ATTTACCAGG	ACAAACATTT	AAGTATACTA	TCGCTTCAAA	AGATTATCCA	1080
GAAGTAAGTT	ATGATGGTAC	ATTTACAGTT	CCAACCTCTT	TAGCTTACAA	AATGGCCAGT	1140
CAAACGATTT	TCTATCCTTT	CCATGCAGGG	GATACTTATT	TAAGAGTGAA	CCCTCAATTT	1200
GCAGTGCCTA	AAGGAACTGA	TGCTTTAGTC	AGAGTGTTTG	ATGAATTTCA	TGGAAATGCT	1260
TATTTAGAAA	ATAACTATAA	AGTTGGTGAA	ATCAAATTAC	CGATTCCGAA	ATTAAACCAA	1320
GGAACAACCA	GAACGGCCGG	AAATAAAATT	CCTGTAACCT	TCATGGCAAA	TGCTTATTTG	1380
GACAATCAAT	CGACTTATAT	TGTGGAAGTA	CCTATCTTGG	AAAAAGAAAA	TCAAACTGAT	1440
AAACCAAGTA	TTCTACCACA	ATTTAAAAAG	AATAAAGCAC	AAGAAAACTC	AAAACCTTGAT	1500
GAAAAGGTAG	AAGAACCAAA	GACTAGTGAG	AAGGTAGAAA	AAGAAAAACT	TTCTGAAACT	1560
GGGAATAGTA	CTAGTAATTC	AACGTTAGAA	GAAGTTCCTA	CAGTGGATCC	TGTACAAGAA	1620
AAAGTAGCAA	AATTTGCTGA	AAGTTATGGG	ATGAAGCTAG	AAAATGTCTT	GTTTAAATATG	1680
GACGGAACAA	TTGAATTATA	TTTACCATCA	GGAGAAGTCA	TTAAAAAGAA	TATGGCAGAT	1740
TTTACAGGAG	AAGCACCTCA	AGGAAATGGT	GAAAATAAAC	CATCTGAAAA	TGAAAAAGTA	1800
TCTACTGGAA	CAGTTGAGAA	CCAACCAACA	GAAAATAAAC	CAGCAGATTC	TTTACCAGAG	1860
GCACCAAACG	AAAAACCTGT	AAAACCAGAA	AACTCAACGG	ATAATGGAAT	GTTGAATCCA	1920
GAAGGGAATG	TGGGGAGTGA	CCCTATGTTA	GATCCAGCAT	TAGAGGAAGC	TCCAGCAGTA	1980
GATCCTGTAC	AAGAAAAATT	AGAAAAATTT	ACAGCTAGTT	ACGGATTAGG	CTTAGATAGT	2040
GTTATATTCA	ATATGGATGG	AACGATTGAA	TTAAGATTGC	CAAGTGGAGA	AGTGATAAAA	2100
AAGAATTTAT	CTGATTTTCAT	AGCGTAA				2127

(2) INFORMATION FOR SEQ ID NO:1629:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1629:

TTAACTATCA	GAAACGAAGG	AAAGAGTATG	ATTTTTGACG	ATTTGAAAAA	CATCACCTTT	60
TACAAAGGGA	TTCATCCTAA	TTTAGACAAAG	GCTATCGACT	ATCTCTACCA	ACATCGTAAG	120
GATTCTTTTCG	AATTAGGAAA	GTATGATATT	GATGGAGATA	AAGTCTTTCT	AGTTGTTCAG	180
GAAAAATGTCC	TCAATCAAGC	TGAAAATGAT	CAATTTGAGT	ATCATAAGAA	CTATGCAGAT	240
TTGCATTTGC	TGGTAGAAGG	ACATGAATAT	TCGAGCTACG	GTTACCGTAT	CAAAGACGAG	300
GCAGTAGCAT	TCGACGAAGC	GAGTGACATT	GGCTTTGTTC	ATTGTCATGA	ACACTACCCA	360
CTCTTGTTGG	GTTATCACAA	TTTTGCGATT	TTCTTCCCAG	GTGAGCCACA	TCAGCCAAAT	420
GGTTATGCAG	GCATGGAAGA	AAAGGTTCGA	AAATATCTCT	TTAAAAATTT	GATTGATTAA	480

(2) INFORMATION FOR SEQ ID NO:1630:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 759 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1630:

ATCGAAATCA	GATAGTCGTA	TAAAGTGAAA	AGGAAGGATT	TCAATATGAC	AAGTTTAAAA	60
TTATTAAAAAG	AAAAAGCACC	ATTGGTCATT	TGTATAACCA	ATGATGTAGT	AAAAAATTTTC	120
ACAGCAAATG	GATTAGTAGC	ACTGGGCGTC	TCACCAGCCA	TGAGTGAGTT	TCCAGCAGAT	180
TTAGAGGATT	TGTTAAAGTA	TGCTGGTGGT	TTATTAATAA	ACATAGGAAC	ATTGACAGAT	240
GAAAAATTGGA	AATTATACCA	AGCTGCTCTG	AAAATTGCGG	AGAAATATAA	TGTCCCAGCA	300
GTTTTAGATC	CTGTAGCCTG	TGGAGCAGGA	GAATATAGAA	AAAAAGTAGC	AGATGATCTA	360
ATCAACAATT	ATAAACTAGC	AGCGATTAGA	GGAAATGCTG	GCGAGATTGC	CTCTTTAGTA	420
GGAATAGATG	TGGCATCTAA	AGGAGTAGAT	AGTGCGGGCG	TAGATAATAT	TGACGAAATT	480
GCTCTAGCAG	CAATGAGAA	GTTCAATATT	CCAATAGTAG	TAACAGGTGA	AGTGGATGCC	540
ATTGCTGTTA	ATGGAGAAGT	GGTAACGATT	CATAATGGTA	GTGCTATGAT	GCCGAAAGTC	600
ATTTGGGACA	GGATGCTTAT	TAGGAGCTGT	AGTAGCAAGC	TTTATCGGAC	TAGAAAAAGG	660
TCAAGAATTG	AAATCATTAG	AAACAGCAAT	GTTAGTTTAC	AATATCGCTG	GAGAAATGGC	720
AGAAAAACGT	CCAAATGGAC	ATCTTCCTGG	GACATTTAA			759

(2) INFORMATION FOR SEQ ID NO:1631:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1221 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1631:

ACTAGAATCA	GGAGTGGAAG	TATGAGAAAT	ATGTGGGTTG	TAATCAAGGA	AACCTATCTT	60
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CGACATGTCA	AGTCATGGAG	TTTCTTCTTT	ATGGTGATTT	CGCCGTTTCCT	CTTTTTAGGA	120
ATCTCTGTAG	GAATTGGGCA	TATCCAAGGT	TCCTTCTATGG	CTAAAAATAA	TAAAGTGGCA	180
GTAGTGACAA	CAGTGCCATC	TGTAGCAGAA	GGACTGAAGA	ATGTAAATGG	TGTTAACTTC	240
GACTATAAAG	ACGAAGCAAG	TGCCAAAGAA	GCAATTAAAG	AAGAAAAATT	AAAAGGTTAT	300
TTGACCATTG	ATCAAGAAGA	TAGTGTTCCTA	AAGGCAGTTT	ATCATGGCGA	AACATCGCTT	360
GAAAATGGAA	TTAAATTTGA	GGTTACAGGT	ACACTCAATG	AACTGCAAAA	TCAGCTTAAT	420
CGTTCAACTG	CTTCCCTTGTC	TCAAGAGCAG	GAAAAACGCT	TAGCGCAGAC	AATTCAATTTC	480
ACAGAAAAGA	TTGATGAAGC	CAAGGAAAAAT	AAAAAGTTTA	TTCAAACAAT	TGCAGCAGGT	540
GCCTTAGGAT	TCTTTCTTTA	TATGATTCTG	ATTACCTATG	CGGGTGTAAC	AGCTCAGGAA	600
GTTGCCAGTG	AAAAAGGCAC	CAAAATTATG	GAAGTCGTTT	TTTCTAGCAT	AAGGGCAAGT	660
CACTATTTCT	ATGCGCGGAT	GATGGCTCTG	TTTCTAGTGA	TTTTAACGCA	TATTGGGATC	720
TATGTTGTAG	GTGGTCTGGC	TGCCGTTTTG	CTCTTTAAAG	ATTTGCCATT	CTTGGCTCAG	780
TCTGGTATTT	TGGTTCACCT	GGGAGATGCT	ATCTCACTGA	ATACCCTGCT	CTTTATTTTG	840
ATCAGTCTTT	TCATGTACGT	AGTCTTGGCA	GCCTTCCTAG	GATCTATGGC	TTCTCGTCCT	900
GAGGACTCAG	GGAAAGCATT	GTCGCCTTTG	ATGATTTTGA	TTATGGGTGG	TTTTTTTTGGA	960
GTGACAGCTC	TAGGTGCAGC	TGGTGACAAT	CTCCTCTTGA	AGATTGGTTC	TTATATTCCC	1020
TTTATTTTCGA	CCTTCTTTAT	GCCGTTTCGA	ACGATTAATG	ACTATGCGGG	GGGAGCAGAA	1080
GCATGGATTT	CACCTTGCTAT	TACAGTGATT	TTTGCGGTGG	TAGCAACAGG	ATTTATCGGA	1140
CGCATGTATG	CTAGTCTCGT	TCTTCAAACG	GATGATTTAG	GGATTTGGAA	AACCTTTAAA	1200
CGTGCCTTAT	CTTATAAATA	G				1221

(2) INFORMATION FOR SEQ ID NO:1632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1632:

CTGGATTCCA	GCAGTGTATT	GGCTGTCTTT	AAAAAACAGT	CAATTAGTCC	TCACAAACAT	60
AATATACTAC	TATTGTTTGA	AGAAGTCAAT	AGTTTGTGTT	TGTTTTTGTT	ATTTATTTTT	120
TACTTTTTTA	TAAAACTTCT	ATCTCAAACC	CTAATTCTTC	AACCTGATTG	GCTTCTAAGA	180
GACAAACATT	CTTCTTATCT	TCTAAATGAT	CTCCTTCTTC	AAGGAATGTT	GACAAGCCAG	240
ACCATGGTTC	AAAGGTAA					258

(2) INFORMATION FOR SEQ ID NO:1633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1633:

GTCATCCCCA	GAGCAAGAGC	TTCATCTCGT	AATTTTTTCAA	CATCACTAAC	CGTAGGTCGC	60
CATCCTTCAA	TCATATTTGT	ACTTAAAGCA	TACCAAACAC	TCTTAAAAAC	GGATCGGTTT	120
TCAAAAGCTA	TTCCCATGAT	TGTCATCTTT	TCTTTATCTA	TATCTAAGGA	CATATGCTAC	180
CTCCTTTAG						189

(2) INFORMATION FOR SEQ ID NO:1634:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1152 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1634:

GAATCGTGGC	TGGTCGTTTA	TTGGAAGAAT	TGGGGACAGA	CAGTCATTGT	TCTTAATATA	60
GATGACGGTC	GTGCCAAGGG	CAGTGCTCGT	ATTGTGGAAC	CGGTCGATAT	TTTTGAAGCT	120
CTGGATCCCC	ATCGAGACCT	CTTCATCGCC	TTTGGAGGTC	ATGCAGGTGC	AGCGGGTATG	180
ACGCTGGAAG	TTGAGCAACT	CTCAGATTTA	TCTCAGGTTT	TGGAAGATTA	TGTTTCGTGAA	240
AAAGGTGCAG	ATGCTGGTGG	CAAGAATAAG	TTAAACCTAG	ATGAAGAGTT	GGATTTGGAG	300
GCACTTAGCT	TGGAACGGT	CAAAAGTTTT	GAACGTTTAG	CTCCTTTTGG	AATGGATAAT	360
CAGAAACCTA	TTTTTTATAT	CAAGAATTTT	CAGGTCGAAA	GTGCTCGTAC	TATGGGGGCA	420
GGTAATGCCC	ATCTAAAGCT	GAAAAATTCC	AAGGGTGAGG	CGAGTTTGA	AGTGGTAGCC	480
TTTGGTCAAG	GCAGATGGGC	GACAGAGTTT	TCTCAAACCA	AGAATCTAGA	GTTAGCGGTT	540
AAATTGTCTG	TCAACCAATG	GAATGGCCAA	ACTGCCCTCC	AGTTGATGAT	GGTGGATGCG	600
CGAGTGGAAG	GTGTTCAACT	TTTTAACATT	CGTGAAAAAA	ATGCAGTCTT	GCCAGAAGGT	660
GTTCCAGTCT	TGGATTTTCC	TGGAGAACTG	CCAAATCTTG	CGGCTAGTGA	AGCTATTGTC	720
GTAAAAAACA	TTCCAGAGGA	TATTACTCAG	CTGAAGACCA	TTTTTCAGGA	ACAGCATTTT	780

TCTGCTGTCT	ATTTCAAAAA	TGATATTGAC	AAGGCCTATT	ATCTGACAGG	TTATGGGACT	840
AGAGATCAGT	TTGCCAAATT	GTACAAGACT	ATTTACCAGT	TCCCAGAGTT	TGATATTCGC	900
TACAAGCTGA	AAGATTTGGC	TGCATATCTT	AATATTCAAC	AAATCTTGCT	GGTCAAGATG	960
ATTCAAGTAT	TTGAAGAACT	AGGCTTTGTG	ACGATAAAAG	ATGGTGTGAT	GACAGTCAAT	1020
AAAGAGGCGC	CAAAGCGGGA	GATAGGAGAA	AGTCAAATTT	ACCAAAATCT	CAAACAAACC	1080
GTTAAAGACC	AAGAAATGAT	GGCGCTGGGT	ACGGTGCAAG	AAATTTATGA	TTTTTTGATG	1140
GAAAAAGAGT	AG					1152

(2) INFORMATION FOR SEQ ID NO:1635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1635:

AAAAAGTGGC	TCTTAACAGC	AGGAGTGGTC	CTGAGCACGT	CAGCTATTTT	AGTGGCTTGT	60
GGAAAACTG	ATAAAGAAGC	AGATGCACCG	ACAACATTTT	CTTATGTCTA	TGCAGTAGAT	120
CCAGCATCAT	TGGGCTACAG	TATAGCGACT	CGAACATCGA	GGACAGACGT	TATTGGAAAT	180
GTTATTGATG	GTTTGATGGA	AAATGATAAA	TACGGCAATG	TTGCTCCTTC	TCAAAAAGAC	240
TATGATTTGA	ACAGTACAGG	ATGGGCTCCA	AGCTATCAAG	ATCCAGCGTC	TTACTTGAAT	300
ATTATGGATC	CAAAATCTGG	TTCTGCCATG	AAACACCTTG	GCATTACGAA	AGGAAAAGAT	360
AAGGATGTTG	TAGCTAAACC	TGGTTTGGAT	AAATATAAGA	AATTGTTAGA	AGATGCTGTT	420
TCTGAGATCA	CTGACCTAGA	GAAGAGATAT	GAAAAATATG	CCAAAGCTCA	AGCTTGGTCG	480
ACAGATAGTT	CATTATTGAT	GCCAACAGCT	TCATCTGGTG	GTTTTCCAGT	TGTAAGTAAC	540
GTAGTACCAT	TCTCAAAACC	ATACTACAA	GTTGGTATTA	AGGGGGAACC	ATATATCTTT	600
AAAGGAATGA	AATTGCAAAA	AGATATTGTT	ACAACAAAAG	AATATAACGA	GGTTTTTAAA	660
AAATGGCAAA	AAGAAAAATT	GGAATCCAAT	AGCAATACC	AAAAAGAACT	AGAAAAATAC	720
ATTAAATAA						729

(2) INFORMATION FOR SEQ ID NO:1636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...780

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1636:

CGCTCTACCA	GCAGCATTGA	TGGATATGAA	AGATCAGAAT	GGCGTTATAA	AGGCTCAAGC	60
AGGTGTTGCT	CTAGTAATGA	TTGTTATTCA	CATATTCTTA	ATGTACTTTC	TCGCATTTTA	120
GTAAAGGAAA	ATAAAATGAA	AATATTGGTT	ACAGGTTTTA	ATCCTTTTGG	AGGTGAAAAG	180
ATTAATCCAG	CTTTGGAGGC	TGTAAAATTA	TTACCATCTG	AGATTAATGG	GGCTGAAGTT	240
CGCTGGGTAG	AAATTCCAAC	GGTTTTTTAT	AAGTCGTCAG	AAGTTTTAGA	GGCAGAAATA	300
TTACGATATC	AACCAGATGC	TGTACTTTGT	ATTGGACAAG	CAGGCGGCAG	GACCGGCTTA	360
ACACCTGAAC	GAGTGGCTAT	TAATCAAGAT	GATGCTCGCA	TACCTGATAA	CGAAGGCAAT	420
CAACCAATTG	ATACACCGAT	TCGTATTGAT	GGAGCATCGG	CCTATTTTAG	TAGTTTACCT	480
ATCAAAGCGA	TGGTACAAGC	TATCAAAAAA	CAGGGACTTC	CGGCAGTTGT	ATCCAATAGT	540
GCAGGAACCT	TTGTTTGCAA	TCATTTGATG	TACCAAGCTC	TTTATTTAGT	GGATAAAAAA	600
TTCCCTAATA	TGAGAGCAGG	TTTCATGCAT	ATTCCATATA	TGATGGAACA	AGTAGTAAAT	660
AAGCCGAATA	CTGCAGGAAT	GAGTCTATGT	GATATTGTAA	GAGGCATAGA	GGTAGCTATT	720
GAAGCTATTG	TAGACTACAA	AGATAAGGAT	TTGCAGTTAG	TAGGCGGTGA	GACTCACTGA	780

(2) INFORMATION FOR SEQ ID NO:1637:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1637:

CTTGGCACCA	GCTGTCTTGG	TAGGCGGCGC	AGCCCTTCAA	CAAGTTTGGA	TTTTCATCCT	60
TGCACCAATC	GCTGGTGGAG	TTCTTGACAG	CCTTGTTGCA	AAAAATTTC	TTGGAACAGA	120
AGAATAATTG	AAACTCAAAA	AGCCTTGCTC	CTCATCTTGA	GGAACAGGGC	TTTTTCGTAT	180
GATACTCTTC	GAAAATCTCT	TCAAACCACG	TCAGCTTCAC	CTTGTCGTAG	GTATGGTTAC	240
TGA						243

(2) INFORMATION FOR SEQ ID NO:1638:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...273
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1638:

AAGACAACCA	GTCTACTTC	TCTAAATAAA	AGAGAGGGTA	GAAAAAATAA	ATACAAAGGA	60
GGTGAGGAAA	TGAGACCAAG	ACGATATCCG	TATAGTGGGA	AAAAAGAGTC	CACCTTTGTA	120
AAGGCAGACC	CTGAGTTAGT	TGAAAAACTT	TTAAGAAACA	CTAGTTTCT	TGAGCGTTTA	180
CAAAAAAAGC	CTATCAATTT	TCAGATAGAC	TCAGAAGAAT	TTAAGCGTCT	TAGCTATGAA	240
GCCATTTCATG	ATACTTCTCA	AGTAACTCAA	TAG			273

(2) INFORMATION FOR SEQ ID NO:1639:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 516 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...516
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1639:

GAGTGTGCCA	GAAGTTTACT	CTGTCAAACG	GACCAACGGC	TAGTTGTCCT	AGCTCTTACT	60
AGAAAGGCTA	TTATGAAAAT	CATTATCCAA	CGGGTTAAAA	AAGCCAAGT	GAGTATAGAA	120
GGCCAGATTC	AGGGAAAAAT	CAATCAGGGA	CTTTTATTGC	TGTTGGTGT	TGGACCAGAG	180
GACCAAGAGG	AAGATTTGGA	CTATGCTGTG	AGAAAACTGG	TCAATATGCG	GATTTTTTCA	240
GACGCAGAAG	GCAAGATGAA	CCTGTCTGTC	AAAGATATTG	AAGGAGAAAT	CCTCTCTATT	300
TCTCAGTTTA	CCCTCTTTGC	GGATACTAAG	AAAGGCAATC	GTCCAGCCTT	TACAGGGGCA	360
GCTAAACCTG	ATATGGCATC	AGACTTCTAT	GATGCTTTCA	ATCAAAAAAT	AGCGCAAGAA	420

GTGCCCCGTTT	AGACAGGCAT	CTTTGGAGCA	GATATGCAGG	TTGAGCTGGT	TAATAACGGA	480
CCTGTTACCA	TTATCCTAGA	TACTAAAAAG	AGATAA			516

(2) INFORMATION FOR SEQ ID NO:1640:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 546 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1640:

TTAGATTACA	GTAAGAAAGG	TAAGTTAAAA	ATGAGAATTG	CAATTGGATG	CGACCACATC	60
GTAACAGATG	AAAAAATGGC	GGTTTCAGAA	TTTTTGAAAT	CAAAAGGATA	TGAAGTCATT	120
GACTTTGGTA	CATATGACCA	TACACGGACT	CACTACCCAA	TCTTTGGTAA	AAAAGTAGGG	180
GAAGCTGTAA	CTAGCGGCCA	AGCTGATCTT	GGGGTATGTA	TCTGTGGTAC	TGGTGTGGT	240
ATCAACAACG	CTGTAAATAA	AGTTCCAGGT	GTTTCGTTCTG	CCTTGGTTTCG	TGATATGACA	300
ACAGCCCTTT	ATGCTAAAGA	GCAATTGAAC	GCTAACGTTA	TCGGCTTTGG	TGGTAAGATT	360
ACTGGTGAAT	TGCTTATGTG	TGATATCATC	GAAGCTTTCA	TTCATGCTGA	ATACAAACCA	420
TCTGAAGAAA	ACAAGAAATT	GATTGCGAAA	ATTGAACACC	TTGAAAGTCA	CAATGCTCAA	480
CAAACAGACG	CAAACTTCTT	TACAGAATTC	CTTGAAAAAT	GGGATCGCGG	AGAATACCAC	540
GACTAA						546

(2) INFORMATION FOR SEQ ID NO:1641:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1641:

CCAATTCGGC	TCATATCTAT	AAAGGAGATT	CTTATGAAAC	TATTCAAACC	ACTCTTAAC	60
GTTTTAGCAC	TTGCCTTTGC	CCTTATCTTT	ATCACTGCTT	GTAGCTCAGG	TGGAAACGCT	120
GGTTCATCCT	CTGAAAAAAC	AACTGCCAAA	GCTCGCACTA	TCGATGAAAT	CAAAAAAAGC	180
GGTGAAC	TGC GAATCGCCGT	GTTTGGAGAT	AAAAAACCGT	TTGGCTACGT	TGACAATGAT	240
GGTTCCTTACC	AAGGCTACGC	TACGATATTG	AACTAG			276

(2) INFORMATION FOR SEQ ID NO:1642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1642:

GTCTTATACA	GAATACAAGG	GAGAATATGG	TGGCTAAAAA	AAAAATCTTA	TTTTTTTATGT	60
GGTCTTTTCC	TCTTGGAGGT	GGTGCAGAGA	AGATTCTATC	AACCATTGTT	TCAAATCTGG	120
ATCCAGAAAA	GTATGATATT	GATATTCTTG	AAATGGAGCA	CTTTGACAAG	GGATATGAAT	180
CTTTTCCAAA	GCATGTACGC	ATTTTATGAT	CCCTATCAGG	ATTATCGCCA	AACCAGATGG	240
TTACGAGCTT	TTTTGTGGAG	AATGAGAATT	TTATTTTCCA	AGACTGGCTC	GTCGTTTGCT	300
TGTAAATGA						309

(2) INFORMATION FOR SEQ ID NO:1643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 738 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1643:

GATAGGCACA	GTATGCGTTT	AGATAATTTA	TTAGCCCAAG	AAAAAATCAG	CCGAAAGGCC	60
ATGAAGCAAG	CACTCCTCAG	AGGGGAAATT	CTAGTCGATG	GTTGCCCAGC	CCGCTCCCTA	120
GCTCAAAATA	TCGATACAGG	ACTACAAGAA	CTCCTTTTTC	AGGATCGAAT	CATTCAAGGC	180
TATGAACACA	CCTATCTTAT	GCTTCATAAA	CCTGCTGGTG	TCGTTACAGC	CAACAAAGAC	240
AAGGAACTTC	CGACCGTCAT	GGACCTGCTT	CCATCTGACA	TCCAGTCTGA	CAAGCTCTAT	300
GCCGTCGGCC	GACTGGACCG	AGATACAACA	GGACTCCTTC	TCTTGACCGA	TAACGGTCCC	360
TTGGGCTTCC	AACTCCTCCA	TCCCCAATAT	CATGTCGATA	AGACTTACCA	AGTCCAGGTT	420
AATGGACTTC	TAACACCTGA	CCATATCCAA	ACCTTTCAAA	AAGGAATTGT	CTTTTTAGAT	480
GGCACTATCT	GTAAACCTGC	AAGACTAGAG	ATTCTATCAG	CAAGTCCTTC	CTTCAGTCAA	540
GCCTCTATCA	CCATTTCAGA	AGGAAAATTT	CATCAAATCA	AGAAAATGTT	CCTCTCGGTT	600
GGTGTTAAGG	TGACTAGCCT	CAAGAGAATC	CAATTTGGGG	ACTTCACATT	GAACCCAGAT	660
TTAGCAGAAA	GTAAC TACCG	CCCTTTGAAC	CAAAAAGAGT	TACAAATCAT	TAAAAACTAT	720
TTAGAGATGA	GTCGATAA					738

(2) INFORMATION FOR SEQ ID NO:1644:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1644:

TTACATAACA	GCTTCATATC	AATCCAGCTC	AACCAAACTG	GATTAACCGC	GACCGCTTTA	60
TTCTTTTCAGC	AGGTCATGGT	TCAATGCTCC	TTTATGCTCT	TCTTCACCTT	TCTGGTTTTG	120
AAGATGTCAG	CATGGATGAG	ATTAAGAGCT	TCCGTCAATG	GGGTTCAAAA	ACACCAGGTC	180
ACCCAGAATT	TGGTCATACG	GCAGGGATTG	ATGCTACGAC	AGGTCCTCTA	G	231

(2) INFORMATION FOR SEQ ID NO:1645:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1645:

AAAGCAAACA	GCCTTGAAAT	CAATGTTGAC	TGCGATTATG	AACCTGAATC	AGCCCCCTCAA	60
AAGGGACTGT	ATATGAATGA	ACGTTACCAG	TGTTTAAAAA	CTAAAGAATA	TCAGGCACTT	120
TTATCTTCCA	AGGGTAGACA	AATTTTCGCT	AAACGTAAGA	TTGATATGAA	ATCTGTCTTT	180
GGGCAGATAA	AGGTTTGTTC	GGGTTATAAG	AGATGTCATC	TGAGAGGTAA	GCGTCAAGTG	240
AGAAATTGACA	TGGGATTCGT	ACTCATGGCC	AACAACCTGC	TGAAATATAA	TAAGAGAAAAG	300
AGGCAAAATT	AA					312

(2) INFORMATION FOR SEQ ID NO:1646:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 780 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...780

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1646:

AGAAAAAACA	GAGGTGTTCA	AATGTCAGAA	GCAGGTCATA	AGTTTTTTAGC	AAAATTGGGG	60
AAAAAACGCT	TACGTCCAGG	TGGAAAGCGT	GCTACAGATT	GGTTAATTGTC	AGAAGGAGGA	120
TTGTCAAAAAG	AAAAGAGAAT	ACTAGAGGTT	GCGTGTAAATA	GGGGAACTAC	AGCAATTGAG	180
TTGGCACAGC	GTTTTGGTTG	CAAGATAACT	GCTGTTGATA	TGGATGCTCA	AGCTTTAGAA	240
GTGGCTAAAA	AATCTGCTGG	AACGGCAGGT	GTTGCTCATT	TAATCAGTTT	TGAAAGAGCA	300
AATGCAATGA	AACCTCCTTA	TCAAGATGCT	AGTTTTGATA	TTGTTATAAA	TGAAGCTATG	360
CTGACTATGC	AAGCCGATCA	AGCTAATAAA	AAATGTGTAA	TGGAATATCT	AAGGGTATTA	420
AAACCTGGAG	GTCTTCTTTT	GACACATGAT	GTGCTTCTTA	AGGAAGCTAA	AGAGTCTATC	480
AGACAGGAAT	TATCACAAGC	AATTCATGTA	AATGTAGGTC	CTTTAACTCA	AGATGGTTGG	540
GAACAGGTGA	TGATAGAATC	AGGTTATTGT	GATGTGAAAG	TATTGACTGG	TGAAATGACA	600
TTAATGAAAT	TATCGGGTAT	GATTTATGAC	GAAGGTTGGC	TAGGAACTTT	GAAAATTTGT	660
GTAAATGCTT	GTAAAAAGGA	GAATAGAAAAG	CAGTTTTTAA	CTATGTATAA	AATGTTTGCT	720
AAGAATAAAC	AGAAATTGGG	CTTTATTGCG	ATGGCTAGTT	ATAAATCGTC	AAAACGTTAG	780

(2) INFORMATION FOR SEQ ID NO:1647:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 459 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...459
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1647:

AGAATGAACA	GAAGAGAGGC	AGTCGAATTT	GTTAACATGT	GTATGATTAA	AAACGGAGAT	60
AAGGTCCTGG	TCCAAGACCG	AGTTAGTCCC	GACTGGTCTG	GCATTACTTT	TCCTGGTGGT	120
CATGTTGAAC	GTGGCGAATC	CTTTGTCGAT	GCTGTCAATC	GTGAAGTGAA	AGAAGAAACT	180
GGTCTGATCA	TTTCCAAACC	CCAACTCTGT	GGTATCAAAA	ACTGGTATGA	CGACAAGGAT	240
TATCGTTATG	TCGTCCTTTT	TTACAAGACA	GAACACTTTA	CTGGTGAACT	CCAGTCTTCA	300
GACGAAGGGA	AAGTTTGGTG	GGAGGACTTT	GAAAATCTTT	CTCATCTAAA	ACTTGCAACC	360
GATGATATGT	CTGATATGCT	TCGTGTGTTT	CTAGAAGAAG	ATCTCAGTGA	ATTCTTTTAC	420
TACAAAAACG	GTGACGACTG	GCTTTATGAT	TTGAAGTAA			459

(2) INFORMATION FOR SEQ ID NO:1648:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...462
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1648:

TGCCTTGACA	GAGTAAGGTC	TGCATACTGC	AGTAGAGTCT	GTGAAGGCTG	GGCTGCCTTG	60
GA	CTCTCTCA	AAGATGTGAA	AGCAAATGCT	AGCGACAGCA	AGCCTGCACA	120
GATGCA	AAAAAC	AAGGAACGGA	AGATAGTAAG	GATTCAGATA	AGATGACTGA	180
GTTCCGGCAG	GAGTGATTGT	GGTCAGTCTA	CTTGCCCTCC	TAGGCGTGAT	TGCCTTCTGG	240
CTGATT	TCGCC	GTAAGAAAGA	GTCAGAAATC	CAGCAATTAA	GCACGGAATT	300
CTAGGACAGC	TAGATGCAGA	AAAAGCGGAT	AAAAAAGTCC	TTGCCAAAGC	CCAAAACCTT	360
CTCCAAGAAA	CCCTTGATT	CGTGAAAGAA	GAAAATGGCT	CAGCAGAGAC	AGAAACTAAA	420
CTAGTAGAGG	AGCTTAAAGC	AATCCTTGAC	AAACTCAAGT	AA		462

(2) INFORMATION FOR SEQ ID NO:1649:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1649:

GCAAAGGACA	GAGCCTCTAC	TACAAATGAA	ATGACCGCAA	CTACTAGTAA	CGAAACAAAG	60
CCTGAAGCAG	GAAAGGCGAT	AGAAAGTATT	CAAGAGACAG	CACTAACGCA	GGCTACCGAA	120
AGTCCTGAGC	AACCTCCATT	AAAGGCGCAA	CCTACTGGTC	CGTTAGTGCC	ACCAACACCT	180
GGTCGGGGGT	TTAATACACC	GATTTATCAA	AGCGTTCATA	AAGGAGAACT	TTTTTCAACG	240
GGAAATACCA	ACTTAAAAAT	TGCGAATGAA	AATACGGCGG	CTGCACAAAC	ATTTTAAAC	300
ACACGAGGAG	CAAGTAGTGG	TTATGCAATT	AACAATTTTC	CTTTAGAATT	TGCAGATGTT	360
GACAAATGATC	CAAAATACGTA	TAACTCTAGT	CGGGCTTATA	TTGATTTAAA	TGGTGCAAAA	420
GAGATTGCTT	GGGCGGGCTT	ATTTTGGAGT	GCATCTAGAT	ATAAAGGCC	TGCTTACGGA	480
ACAAATCTTT	CTGATGAAGA	AATTAGTGCA	CCAGTTCAAT	TACTACACC	AAATGGAACC	540
GTACAGCGTG	TTTCGCCCCA	AAGGTACCAT	CGTATCGATC	AAGATGCAAC	AAACCCAGGA	600
CAACGTTTCG	GGTACAATA	CACTGGATTT	TCTAATTATG	CAGATGTAAC	TTCAATTTTA	660
CAAGGGGATA	AAAGTGCGAC	AGGGAGTTAT	ACGTTGGCAG	ATATTCCTAT	GACAAGTAGT	720
TTAAATGGTC	AATATCAATA	TTATAACTTT	AGTGGTTGGA	GTTTGTTTGT	TGTTACAAAG	780
GATCAGGCAA	GTAAGTCAAG	AGCTTTTAGT	ATTTACTATG	GAGCACGTGG	TAATGCTGCT	840
GGAACCAATA	ATGAATTTAC	TATGAGCAAC	TTTTTAACAG	CAAAACAAGG	AAATCTTGAT	900
CCAATTGTGA	CCTGGTTTAC	TGTTCAAGGA	GATAAATACT	GGACTGGAGA	CAACGCACAA	960
ATTAAAAATA	GCGCAGGAAC	TTGGGTAAAT	ATTTCGAACA	CGCTCAATCC	AGTTAACAAT	1020
GCTATGAACG	CAACTGTGAC	CGATAACGAT	GAACATTTGG	TAAAACAATA	TCCAGGGATA	1080
TTTGCGCCGG	GATCATCCTA	A				1101

(2) INFORMATION FOR SEQ ID NO:1650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...210
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1650:

CCATTTTGCA	GGACTAAAT	CAAATCTGCA	TGGACAACTG	CACTGAGGCG	ATGGGCAGTG	60
ATAATGGTTG	TCTTGTCCTT	TCGCGTCTCC	TTGAGGTTGT	CGATAATCGC	ATACTCTGTC	120
TTGGCATCTA	CGGCGGATAA	GGAATCATCC	AAAATCAAGA	TATCAGGGTC	TAAAATCATA	180
GCCCGACTCA	TAGCCAACCG	TTGCTTTTGA				210

(2) INFORMATION FOR SEQ ID NO:1651:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1035 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1035
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1651:

TTCCCTAGCA	GACTGGGGAC	AATTACTAAA	AGAGGAAAAG	AAATGAAAAA	AATCGCAGTA	60
GATGCCATGG	GGGGCGATTA	CGCACCTCAG	GCCATTGTTG	AGGGTGTCAA	TCAAGCCCTA	120
TCTGACTTTT	CAGATATCGA	GGTTCAACTT	TACGGAGATG	AAGCTAAAAT	CAAGCAATAT	180
CTGACAGCGA	CAGAGCGCGT	CAGCATTATC	CATACGGATG	AGAAGATTGA	TTCGGATGAT	240
GAACCTACGA	GAGCTATTAG	GAATAAGAAA	AATGCCAGTA	TGGTATTGGC	AGCCAAGGCT	300
GTCAAAGATG	GTGAAGCAGA	CGCTGTCCTT	TCGGCTGGGA	ATACAGGTGC	CTTGTTGGCT	360
GCTGGATTCT	TCATCGTGGG	TCGTATCAAG	AATATCGACC	GTCTTGGGCT	TATGTCGACT	420
TTGCCGACTG	TAGATGGGAA	GGGATTTGAC	ATGCTAGACC	TCGGTGCCAA	TGCGGAAAAT	480
ACAGCCCAGC	ACCTCCATCA	ATACGCGGTT	CTAGGATCCT	TCTATGCTAA	AAATGTTTCGT	540
GGCATTGCGC	AACCACGTGT	TGGCTTGCTC	AATAACGGAA	CAGAGAGTAG	CAAGGGCGAT	600
CCGCTTCGTA	AGGAAACTTA	TGAATTACTA	GTGGCTGATG	AAAGTTTGAA	CTTTATCGGA	660

AATGTGGAAG	CGCGTGATTT	GATGAATGGT	GTTGCAGATG	TTGTTGTGGC	AGATGGTTTC	720
ACGGGAAACG	CTGTGCTCAA	ATCCATCGAA	GGGACAGCTA	TGGGAATCAT	GGGCTTGCTC	780
AAGACAGCTA	TTACAGGTGG	TGGTCTTCGA	GCGAAACTAG	GTGCCCTCCT	TCTCAAGGAC	840
AGCCTCAGAG	GTTTGAAGAA	ACAGCTCAAT	TATTCAGATG	TTGGTGGAGC	GGTCTTGTTT	900
GGTGTTAAGG	CACCTGTTGT	CAAGACTCAT	GGCTCAAGCG	ATGCCAAGGC	TGTTTATAGT	960
ACGATTCGCC	AGATTCGTAC	CATGCTAGAA	ACAGACGTAG	TTGCCCAGAC	TGCGCGTGAA	1020
TTTTCAGGAG	AATAA					1035

(2) INFORMATION FOR SEQ ID NO:1652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...3651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1652:

TTGACAAGGC	TTGGAACCTTA	TTTACAAAGG	AGAATCATCT	TGGCAGGACA	TGACGTTCAA	60
TACGGGAAAC	ATCGTACCCG	TCGTAGTTTT	TCAAGAATCA	AAGAAGTTCT	TGACTTACCA	120
AATTTGATTG	AAATTCAAAC	TGACTCATTG	AAAGCTTTCC	TAGACCACGG	TCTTAAGGAA	180
GTGTTTGAAG	ATGTATTGCC	AATTTCAAAC	TTCACAGACA	CAATGGAGTT	GGAATTTGTT	240
GGATATGAAA	TCAAGGAACC	AAAATATACG	CTAGAAGAAG	CTCGTATCCA	CGATGCTAGC	300
TACTCAGCAC	CAATTTTTGT	AACCTTCCGT	TTGATCAATA	AAGAAACAAG	CGAAATCAAG	360
ACCCAAGAAG	TTTTCTTTGG	TGATTTCCCA	ATCATGACAG	AAATGGGTAC	TTTCATCATC	420
AATGGTGGTG	AACGTATTAT	CGTTTCTCAG	TTGGTCCGCT	CACCAGGTGT	TTACTTTAAC	480
GACAAAGTAG	ACAAAAATGG	TAAGGTGGGC	TATGGTTCAA	CTGTTATCCC	TAACCGTGGA	540
GCTTGTTGG	AAC TTGAAAG	CGACTCAAAA	GATATCACCT	ACACTCGTAT	CGACCGTACT	600
CGTAAGATTG	CATTTACAAC	CTTGGTTCGT	GCTCTTGTTT	TCTCAGGTGA	TGATGAAATC	660
TTTGATATCT	TTGGTGACAG	CGAATTGGTT	CGCAACACTG	TTGAAAAAGA	TATCCACAAG	720
AATCCAATGG	ACTCTCGTAC	AGACGAAGCC	TTGAAAAGAAA	TTTACGAACG	CCTTCGTCCA	780
GGTGAGCCTA	AGACGGCTGA	AAGCTCACGT	AGCTTGCTTG	TAGCTCGCTT	CCTTGACCCA	840
CGTCGTTATG	ACTTGGCAGC	AGTTGGTCGT	TACAAAATCA	ATAAAAAACT	CAATGTTAAA	900
ACACGTTTGC	TCAACCAAAC	CATTGCAGAG	CCATTGGTAG	ACCC TGAAAC	TGGAGAAATC	960
TTGGTAGAAG	CTGGTACGAT	TATGACTCGT	AGCGTGATTG	AAAGCATTGA	AAGCCATTTG	1020
GATGGCGACT	TGAACAAGAT	TGTCTACATC	CCAAACGATG	CAGCCGTTGT	GACTGAGCCT	1080
GTTGTTCTTC	AAAAATTCAA	GGTTATTGCT	CCAACTGATC	CAGATCGCGT	CGTAACGATC	1140
ATTGGTAATG	CTAACCCAGA	TGACAAGGTT	CGTACGGTGA	CTCCTGCAGA	TATCCTTGCT	1200
GAGATGAGCT	ACTTCCTCAA	CTTGGCTGAA	GGACTTGGCC	GTGTAGATGA	TATCGACCAC	1260
CTTGGAATC	GTCGTATCCG	TGCGGTTGGT	GAATTGCTTG	CCAACCAAGT	ACGTTTGGGA	1320
CTTCTCTCGTA	TGGAACGTAA	TGTCCGTGAA	CGTATGTCTG	TTCAGGACAA	TGAAGTCTTG	1380
ACACCACAAC	AAATTATCAA	TATTCGTCCT	GTAACAGCTG	CAGTTAAAGA	ATTCCTTGGT	1440
TCATCACAGT	TGTCACAGTT	CATGGACCAA	CACAACCCGC	TTTCTGAGTT	GTCTCACAAA	1500
CGCCGTTTGT	CAGCCTTAGG	ACCTGGTGGT	TTGACTCGTG	ACCGTGCCGG	ATATGAAGTG	1560

CGTGACGTGC	ACTACACTCA	CTATGGTCGT	ATGTGTCCAA	TCGAGACACC	TGAAGGACCT	1620
AACATCGGTT	TGATCAATAA	CTTGTCACT	TACGGACACT	TGAACAAATA	TGGTTTTGTT	1680
CAAAACACCAT	ACCGTAAGGT	TGACCGTGAA	ACAGGTGTTG	TCACGAACGA	AATTGTTTGG	1740
TTGACAGCTG	ATGAAGAAGA	TGAATATACT	GTAGCTCAGG	CTAACTCTCG	TCTGAATGAA	1800
GATGGAACCT	TTGCTGAGAA	GATTGTCATG	GGACGTCACC	AAGGGGTCAA	CCAAGAGTAT	1860
CCAGCTAATA	TTGTTGACTA	CATGGACGTT	TCACCAAAAC	AGGTAGTTGC	CGTTGCCGACA	1920
GCAATGTATTC	CTTTCTTGGA	AAACGATGAC	TCCAACCGTG	CCCTCATGGG	AGCCAATATG	1980
CAACGTCAGG	CTGTGCCATT	GATTAAATCCT	CAGGCACCTT	ACGTTGGTAC	TGGTATGGAA	2040
TACCAAGCAG	CCCACGATTC	TGGTGCGGCT	GTGATTGCTC	AGTATGATGG	TAAAGTTACT	2100
TACGCAGATG	CTGACAAGGT	AGAAGTTTCGT	CGTGAAGATG	GTTTCATTGGA	TGTTTACCAC	2160
ATCCAAAAAAT	TCCGTCGTTC	AAACTCAGGT	ACTGCTTACA	ACCAACGCAC	TCTCGTAAAA	2220
GTTGGTGATG	TCGTTGAAAA	AGGCGATTTT	ATCGCTGACG	GACCTTCTAT	GGAAAATGGA	2280
GAAATGGCGC	TTGGACAAAA	CCCAATCGTT	GCCTACATGA	CTTGGGAAGG	CTACAAC TTC	2340
GAGGATGCCG	TTATCATGAG	CGAACGCTTG	GTGAAGGACG	ATGTCTACAC	ATCTGTTTAC	2400
CTTGAAGAAT	ACGAATCAGA	AACGCGCGAT	ACAAAGCTTG	GGCCTGAAGA	AATCACTCGC	2460
GAAATTCCAA	ACGTTGGTGA	AGATGCCCTC	AAAGACCTTG	ACGAAATGGG	GATTATCCGT	2520
ATTGGTGCTG	AGGTTAAAGA	AGGTGATATT	CTTGTAGGGA	AAGTAACACC	TAAGGGTGAG	2580
AAAGATCTTT	CAGCTGAAGA	ACGTCTCTTG	CACGCTATCT	TTGGAGACAA	GTCTCGTGAA	2640
GTGCGTGATA	CTTCTCTTCG	TGTACCACAC	GGTGCCGATG	GTGTCGTTTC	TGATGTTAAG	2700
ATCTTTACAC	GTGTAAATGG	AGATGAGTTG	CAATCAGGTG	TTAACATGTT	GGTTCGTGTT	2760
TACATCGCTC	AAAAACGTAA	GATTAAAGGTC	GGAGATAAAA	TGGCCGGACG	TCACGGAAAC	2820
AAAGGGGTTG	TCTCTCGTAT	CGTTCCTGTA	GAAGACATGC	CTTACCTTCC	AGACGGAAC	2880
CCAGTCGACA	TCATGTTGAA	CCCACTTGGA	GTGCCATCAC	GTATGAATAT	CGGTCAGGTT	2940
ATGGAGCTTC	ACCTTGGTAT	GGCAGCTCGT	ACTCTTGTTA	TTCACATTGC	GACACCAGTC	3000
TTTGATGGAG	CAAGTTCTGA	AGATCTTTGG	TCAACTGTTA	AAGAAGCAGG	TATGGATAGC	3060
GATGCCAAGA	CAATCCTTTA	CGATGGACGT	ACAGGTGAAC	CATTTGATAA	CCGTGTTTCT	3120
GTTGGAGTCA	TGTACATGAT	CAAACTCCAC	CACATGGTTG	ACGATAAATT	GCATGCGCGT	3180
TCAGTCGGAC	CTTACTCAAC	TGTTACCCAA	CAACCACTCG	GAGGTAAAGC	TCAGTTTGTT	3240
GGACAACGTT	TCGGTGAGAT	GGAGGTTTGG	GCTCTTGAA	GCTACGGTGC	GTCAAATGTC	3300
CTTCAAGAAA	TCTTGACTTA	CAAGTCGGAC	GATATCAACG	GACGTTTGAA	AGCCTATGAA	3360
GCTATTACAA	AAGGCAAAAC	AATTCCAAAA	CCAGGTGTTT	CAGAATCCTT	CCGAGTTCTT	3420
GTCAAAGAAT	TGCAATCTCT	TGGTCTTGAC	ATGCGTGTCC	TAGACGAAGA	TGACCAAGAA	3480
GTGGAACCTC	GCGACTTGGA	TGAAGGAATG	GACGAAGATG	TCATCCACGT	AGATGACCTT	3540
GAAAAAGCCC	GCGAAAAAGC	AGCCCAAGAG	GCTAAAGCAG	CCTTTGAAGC	TGAAGAAGCT	3600
GAGAAAGCAA	CAAAAGCGGA	AGCAACAGAA	GAAGCTGCTG	AACAAGAATA	A	3651

(2) INFORMATION FOR SEQ ID NO:1653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1653:

AAAATTTTAA	GGAGAAATGA	CAGAATGTCT	GTATCATTTG	AAAACAAAGA	AACAAACCGT	60
GGTGTCTTGA	CTTTCACTAT	CTCTCAAGAC	CAAAATCAAAC	CAGAATTGGA	CCGTGTCTTC	120
AAGTCAGTGA	AGAAATCTCT	TAATGTTCCA	GGTTTCCGTA	AAGGTCACCT	TCCACGTCCT	180
ATCTTCGATA	AAAAATTTGG	TGAAGAATCA	CTTTACCAAG	ACGTTATGAA	CGCTCTTTTG	240
CCAAACGCTT	ATGAAGCAGC	TGTAAAAGAA	GCTGGTCTTG	AAGTGGTTGC	CCAACCAAAA	300
ATTGACGTAA	CTTCAATGGA	AAAAGGTCAA	GACTGGGTTA	TCGCTGCTGA	AGTCGTTACA	360
AAACCTGAAG	TAAAATTTGG	TGACTATAAA	AACCTTGAAG	TATCAGTTGA	TGTAGAAAAA	420
GAAGTAACTG	ACGCTGATGT	TGAAGAGCGT	ATCGAACGCG	AACGCAACAA	CCTGGCTGAA	480
TTGGTTATCA	AGGAAGCTGC	TGCTGAAAAC	GGCGACACTG	TTGTGATCGA	CTTCGTTGGT	540
TCTATCGACG	GTGTTGAATT	TGACGGTGGA	AAAGGTGAAA	ACTTCTCACT	TGGACTTGGT	600
TCAGGTCAAT	TCATCCCTGG	TTTCGAAGAC	CAATTGGTAG	GTCACCTCCG	TGGCGAAACC	660
GTTGATGTTA	TCGTAACATT	CCCAGAAGAC	TACCAAGCAG	AAGACCTTGC	AGGTAAAGAA	720
GCTAAATTCG	TGACAACTAT	CCACGAAGTA	AAAGCTAAAG	AAGTTCCAGC	TCCTTGACGAT	780
GAAGTTGCAA	AAGACATTGA	TGAAGAAGTT	GAAACACTTG	CTGACTTGAA	AGAAAAATAC	840
CGCAAAGAAT	TGGCTGCTGC	TAAAGAAGAA	GCTTACAAAG	ATGCAGTTGA	AGGTGCAGCA	900
ATTGATACAG	CTGTAGAAAA	CGCTGAAATC	GTAGAACTTC	CAGAAGAAAT	GATCCATGAA	960
GAAGTTCACC	GTTCAAGTAA	TGAATTCCTT	GGGAACCTGC	AACGTCAAGG	GATCAACCCT	1020
GACATGTACT	TCCAAATCAC	TGGAACACT	CAAGAAGACC	TTCAACAACCA	ATACCAAGCA	1080
GAAGCTGAGT	CACGTACTAA	GACTAACCTT	GTTATCGAAG	CAGTTGCCAA	AGCTGAAGGA	1140
TTTGATGCTT	CAGAAGAAGA	AATACAAAAA	GAAGTTGAGC	AATTGGCAGC	AGACTACAAC	1200
ATGGAAGTTG	CACAAGTTCA	AACTTGCTT	TCAGCTGACA	TGTTGAAACA	TGATATCACT	1260
ATCAAAAAAG	CTGTTGAATT	GATCACAAGC	ACAGCAACAG	TAAAAATA		1308

(2) INFORMATION FOR SEQ ID NO:1654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1654:

AAATATTTTAA	GGAGAAAATA	TATGTTGAAA	CACTTAAACT	TAAAAGGTCA	CTTATTGACA	60
GCCATTTTCCT	ATATGATTCC	AATTGTTTGT	GGTGCAGGAT	TCTTAGTTGC	CATTGGTTTA	120
GCAATGGGGG	GTGGTGTTC	TGACGCTCTT	GTAGCAGGAA	AATTCACTAT	CTGGGATGCT	180
TTAGCAACTA	TGGGTGGTAA	AGCCCTTGGT	CTCTTGCCAG	TTGTTATTGC	TACAGGTTTG	240
TCTTACTCGA	TTGCTGGTAA	GCCAGGGATT	GCACCAGGTT	TTGTTGTTGG	TCTAATTGCC	300
AATTCGTGTT	GTTCAAGGTT	TATCGGTGGT	ATCTTGGGAG	GTTATATAGC	TGGTTTCTTG	360
GTTCAAGCGA	TTATTAAAAA	GGTCAAAGTA	CCAAACTGGA	TTAAAGGTTT	AATGCCAACC	420
TTGATTATTTC	CTTTTGTAGC	CTCTTTGGTA	AGTAGTTTGA	TTATGATTTA	TATTATTGGA	480

GCGCCTATCG	CAGCCTTTAC	CAACTGGTTG	ACGAGCTTAT	TACAAAGCTT	GGGAAGTGCT	540
TCAAATGGTT	TGATGGGGGC	AGTTATTGGA	GTTCTCAGTG	CTGTTGACTT	TGGTGGCCCA	600
CTTAATAAAA	CAGTCTATGC	CTTTGTGTTG	ACTTTACAGG	CTGAAGGTGT	GAAAGAACCA	660
TTGACTGCTT	TGCAATTGGT	GAATACTGCT	ACACCAGTTG	GATTTGGATT	GGCCTATTTT	720
ATCGCGAAAT	TACTCAAAAA	AAATATCTAT	ACTCAAGAGG	AAATCGAAAC	ATTGAAATCG	780
GCTGTTCCCTA	TGGGGATTGT	CAATATTGTT	GAAGGTGTAA	TTCCGATTGT	TATGAATAAC	840
TTGGTTCCAG	GTCTCATTGC	AACAGGTATC	GGTGGTGCTG	TTGGTGGTGC	TGTTTCTTTG	900
ACAATGGGTG	CTGATTCTGC	CGTGCCATTT	GGTGGAGTGC	TTATGTTACC	AACCATGACT	960
CGTCCAGTAG	CTGGTATTTG	TGCTTTGTTA	GCCAACATTG	TAGTCACAGG	ACTTGTCTAC	1020
GCGATTTTGA	GAAAACCAAT	AAAACATACA	GAACCAGTTA	TGACTGTTGA	AGAAGAGATT	1080
GATTTGTCAG	ATATTGAAAT	TTTGTAA				1107

(2) INFORMATION FOR SEQ ID NO:1655:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...342
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1655:

TTGGATTTAA	GAAAAGGAGA	AAATATTATG	GCAAAAGCTT	TAATTATTTG	TGCAGCAGGA	60
ATGTCTTCAT	CACTTATGGC	ACAGAAAACA	ACAGAGTTTC	TAAAAGGAAA	AGGGAAAGAT	120
ATTGTAGTTG	ATGCTATTAG	TGCTACTGAA	GGAGGGAAAG	CTATCGCAGC	AGCAGCTTTT	180
GATTTGTATC	TTGTCAGCCC	TCAAAACAAA	ATGTACTTTA	AGCAATTTGA	AGAGGCTGGT	240
TCTAAAGCAG	GAAAACCAAGT	TGTACAAATA	CCTCCTCAAG	CCTATATTCC	TATTCCAATG	300
GGAATTGAAA	AAATGGCTAA	TTTGATTCTT	GAGAATATTT	GA		342

(2) INFORMATION FOR SEQ ID NO:1656:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 561 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1656:

AGTACATTAA	GATTGAAATC	ATTAAAGGAG	GCGAACATGG	CCCAAGATAT	AAAAAATGAA	60
GAAGTAGAAG	AAGTTCAAGA	AGAAGAAGTT	GTGGAAACAG	CTGAAGAAAC	AACTCCTGAA	120
AAGTCTGAGT	TGGACTTGGC	AAATGAACGT	GCAGATGAGT	TCGAAAACAA	ATATCTTCGC	180
GCTCATGCAG	AAATGCAAAA	TATCCAACGC	CGTGCCAATG	AAGAACGTCA	AAACTTGCAA	240
CGTTATCGTA	GCCAGGACTT	GGCAAAAGCA	ATCTTACCAT	CTCTTGACAA	CCTTGAGCGT	300
GCACTTGCAG	TTGAAGGTTT	GACAGATGAT	GTGAAGAAGG	GCTTGGGGAT	GGTGCAAGAA	360
AGCTTGATTC	ACGCTTTGAA	AGAAGAAGGA	ATTGAAGAAA	TCGCAGCAGA	TGGCGAATTT	420
GACCATAACT	ACCATATGGC	CATCCAAACT	CTCCCAGCAG	ACGATGAACA	CCCAGTAGAT	480
ACCATCGCCC	AAGTCTTTCA	AAAAGGCTAC	AAACTCCATG	ACCGCATCCT	ACGCCCAGCA	540
ATGGTAGTGG	TGTATAACTA	A				561

(2) INFORMATION FOR SEQ ID NO:1657:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2076 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1657:

AAAAGATTAA	GGAGGACGTG	CGTGGAATTA	CTGATTTACC	TCATCCTATT	TTTACTGGTT	60
TTGATTGTCT	CAAGTACAAC	CAATAAGCTC	CTGCCCTTTT	TGCCTCTCCC	TTTGGTGCAG	120
ATTCTTTTAG	GAATTGTGAT	TGGTCTCTTT	TTACCCAATA	CTGACTTTCA	CCTTAATACG	180
GAGTTGTTTT	TGGCACTGGT	TATCGGACCC	TTGCTTTTCC	GAGAGGCTGA	AGATACAGAT	240
GTTACGGCTA	TTTTAAAAACA	CTGGCGAATC	ATTGTTTATC	TCATATTTCC	AGTGATTTTT	300
ATCTCGACCC	TGAGTTTGGG	TGGCTTGGCC	CATCTTCTTT	GGTTCAGCCT	TCCCTTGGCA	360
GCTTGCTTGG	CTGTGCTGTC	AGCCCTTGGT	CCTACGGACT	TGGTGGCCTT	TGCCTCTCTT	420
TCGGAGCGTT	TTAGCTTTCC	TAAGCGCGTG	TCCAATATTC	TTAAGGGCGA	AGGACTCTTG	480
AATGATGCTT	CTGCTTTGGT	GGCTTTTCAG	GTAGCTTTGA	CAGCTTGGAC	AACTGGAGCT	540
TTTTCTCTGG	GGCAAGCTAG	CAGTTCGCTC	ATCTTTTCAA	TCCTAGGCGG	TTTTTTAATT	600
GGATTTTTAA	CAGCCATGAC	CAACCGCTTC	CTCCATACCT	TCTTGCTAAG	TGTGCGCGCA	660
ACGGATATTG	CCAGTGAACT	TTTATTAGAA	TTGAGTTTGC	CTCTAGTGAC	CTTCTTTCTG	720
GCAGAAGAAG	TCCATGTTTC	AGGGATTATT	GCCGTCGTAG	TTGCTGGAAT	TTTAAAGGCA	780
AGTCGCTTCA	AGAAAAACAC	GCTCCTCGAA	GCCCAAGTGG	ATACGGTGAC	CGAGACGGTC	840

TGGCATAACAG	TGACCTTTAT	GCTCAACGGT	TCTGTCTTTG	TGATTTTAGG	GATGGAGTTG	900
GAAATGATAG	CAGAACCTAT	CTTGACCAAT	CCAATCTATA	ATCCTCTACT	TTTATTGCTA	960
TCTCTCATCG	CCCTTACCTT	TGTCCTCTTT	GTCAATTCGTT	TTATTATGAT	CTATGGCTAT	1020
TATGCCATATA	GAACCCGACG	CCTCAAGAAA	AAGCTAAATA	AGTATATGAA	GGACATGTTT	1080
CTCTTGACCT	TTTCAGGTGT	TAAGGGAACG	GTGTCGATTG	CTACGATTCT	CTTGATACCA	1140
AGTAATCTAG	AACAGGAGTA	TCCTCTCTTG	CTTTTCCTTG	TTGCAGGTGT	GACGCTTGTC	1200
AGCTTTTTTAA	CAGGTCTCTT	GGTCTTGCCCT	CATCTTTCCTG	ATGAAGAGGA	AGAAAGCAAG	1260
GATTATCTCA	TGCATATCGC	CATTTTGAAT	GAAGTAACGC	TAGAGTTGGA	AAAAGAGTTG	1320
GAAGACACCA	GAAATAAACT	TCCCCTCTAT	GCGGCTATTG	ACAATTATCA	TGGACGTATT	1380
GAAAATCTCA	TTTTAAGCCA	AGAAAACCAG	GATGATCAAG	AAGATTGGGC	TGCTTTGAAA	1440
CTCTTGATTG	TTAGTATTGA	AAGTGATGGT	TTGGAGCAGG	CCTATGAAGA	GGGGAACATT	1500
AGCAATCGTG	TTTACCGAGT	TTACCAACGT	TATCTGAAAA	ATATAGAACA	AGGAATCAAT	1560
CGTAAACTTG	CCTCAAGACT	GACCTATTAT	TTCTTGTGTT	CTTTGCGGAT	TTTACGTTTT	1620
CTCCTTCATG	AAGTTTTTAC	TCTCGGAAAG	ACCTTCCGTA	GCTGGAAGAA	CAAGGAGCAA	1680
AGCCGTCTCC	GTGCTCTTGA	TTATGACCAA	ATTGCAGAGC	TCTATCTTGC	CAATACGGAG	1740
ATGATTATTG	AAAGTTTGGG	AAACCTGAAG	GGAGTCTACA	GCCGCTCTTT	GATTAGTTTT	1800
ATGCAGGAGT	CTCGTCTTCG	AGAAACAACCT	ATTATTAGCA	GTGGTGCCTT	TGTCGAACGG	1860
GTTATCAATC	GTGTCAAACC	CAACAATATC	AATGAAATGC	TGAGAGGCTA	TTATCTGGAG	1920
CGCAAGTTGA	TTTTCGAATA	CGAAGAAAAA	CGATTGATTA	CGACTAAGTA	TGCCAAGAAA	1980
TTACGACAAA	ATGTAAATAA	CTTAGAGAAC	TATTCCTTGA	AGGAAGCTGC	CAATACCCCTG	2040
CCGTATGATA	TGGTGGAAAT	GGTAAGAAGA	AATTAG			2076

(2) INFORMATION FOR SEQ ID NO:1658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1658:

AGCATGTTAA	GTTTATCGGT	CTTACCCACT	GTGGACGAAT	CTGGGAAGGA	TGGGGTGTTC	60
CAANAGAACG	TATCATCGTT	GTAAACCAG	GTGACCATAT	TGGAATTAAA	AGATATGAAG	120
ATTCATGCAG	TAGAATCATT	TGACCGTACT	TGCTTGGTNA	CTCTCCCAGT	GAACGGTGCT	180
GATGAGACAG	GCGGTGAACT	TGCTGGCTTG	GCTGTTACAG	ATGAAGAAAT	GGCTCAAAAG	240
GCTGTAACT	ATATCTTTGA	AACACCAGGT	GGAACCATCT	ATCATGGTGC	AGATTCTCAC	300
TTCTCAAAC	ATTTTGCAAA	ACATGGTAAA	GACTTTAAAA	TTGATGTTGC	TTTGAATAAC	360
TATGGTGAAA	ATCCGGTAGG	TATCCAAGAC	AAAATGACAT	CTATCGACCT	TCTTCGTATG	420
GCAGAAAATC	TGCGTACCAA	AGTCATTATC	CCAGTTCACT	ATGATATCTG	GTCTAACTTC	480
ATGGCTTCTA	CTAATGAGAT	TCTAGAACCT	TGGAATATGC	GAAAAGATCG	CTTGCAATAC	540
GATTTCCATC	CATTTATCTG	GGAAGTTGGC	GGTAAGTACA	CTTATCCTCA	AGATCAACAC	600
TTAGTAGAAT	ACCATCAT					618

(2) INFORMATION FOR SEQ ID NO:1659:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 873 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...873
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1659:

GAGTATCTAA	GAAATTTGAA	ATTTAAGAGG	AGAAGCATGA	TGAAACAAGA	TGAAAGAAAA	60
GCCCTGATTG	GCAAAATACAT	TCTATTGATT	CTAGGATCGG	TTCTGCTTTT	AGTGCCGCTC	120
CTTGCTACCC	TCTTTAGTTC	CTTCAAACCC	ACTAAGGATA	TTGTAGATAA	TTTCTTTGGC	180
TTTCCAACCA	ACTTCACATG	GGACAACTTT	AGCCGTCTCT	TAGCTGATGG	GATTGGAGGC	240
TATTATTGGA	ACTCTGTCTG	CATCACTGTC	TTGTCTTTAC	TTGCAGTAAT	GATCTTTATC	300
CCTATGGCAG	CCTACTCCAT	CGCTCGCAAT	ATGAGTAAAA	GAAAAGCCTT	TACCATCATG	360
TATACCCCTCT	TAATCCTCGG	AATCTTCGTA	CCTTTCCAAG	TCATCATGAT	TCCGATTACG	420
GTTATGATGA	GTAAACTCGG	TTTGGCTAAT	ACCTTTGGTT	TGATCTTGCT	CTACTTGACC	480
TATGCGATTG	CACAGACCCT	CTTCTCTAT	GTTGGCTATA	TCAAAATCTC	GATTCCAGAA	540
AGTCTGGATG	AAGCAGCAGA	GATCGATGGG	GCTAATCAAT	TTACAACCTA	TTTCCGCATC	600
ATCTTCCCAA	TGATGAAACC	GATGCATGCG	ACAACCATGA	TCATCAATGC	CCTTTGGTTC	660
TGGAATGACT	TCATGTTGCC	ACTCCTTGTC	TTGAACCGGG	ATTCCAAAAT	GTGGACTCTG	720
CCTTTGTTCC	AATACAACCTA	CGCAGGCCAA	TATTTCAACG	ACTACGGACC	AAGCTTTGCC	780
TCTTACGTGG	TCGGCATTAT	CAGTATCACC	ATTGTCTATC	TCTTCTTCCA	ACGCCATATC	840
ATTTACAGGAA	TGAGCAACGG	GGCAGTGAAG	TAA			873

(2) INFORMATION FOR SEQ ID NO:1660:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1660:

GGAAGACTAA	GCATGGCCCA	ATCACTTAAC	AAAACAGTAC	TCCTCAGTAC	GACAGGCACT	60
TCCTACCTCT	CTATCGCTGG	GAAAGTTGGG	AAATTCCTTG	TCGGAGATCA	GGCTTTGGAA	120
TTTTACCCAG	ATGTCAATGT	CGAACAATTT	ATCCAGATTC	CTTGGAGCCA	TATCAATCAG	180
ATTGGAGCCA	ATGTCACTGG	ATGCAAAATC	AGCCGCCACT	TCGAAGTCTT	TACAGACAAA	240
GGAAAATTCC	TCTTTGCTTC	AAAAGACTCA	GGTGCCATTC	TCAAAATTGC	ACGCGACAAA	300
TTGGGCAATG	ACAAGGTCGT	CAAAC'TCCG	ACCTGATTTC	AGACAATTAG	CCAAAAATTT	360
AAAAATCTAT	TTGCAAAAAA	ATAG				384

(2) INFORMATION FOR SEQ ID NO:1661:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 366 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1661:

AAAAGGAGGC	TTGTGATGGA	ACACTTGTTT	AAAATGATAA	TCTTATTACC	CTGTTTTTAC	60
TTTTTCAGCT	GGATTGACAA	GGATAATAGA	GAAAGTAAAT	TTTTCCCAAT	TTTTTACTAT	120
TTTTACTGGA	TTTACATCAC	CCTCTATGCT	CTTTT'TAGCC	TTGCTTGGAC	AGTTTTTTCA	180
GTTCTGTTTT	TCAATATCGT	CTTGAGAAAT	TTGACAGATA	TCAAGTTATG	GGGTATTTGG	240
CTATTATTAC	TACTTATCGC	TTTTGCTAGT	GACTGGTTAG	ACTATATCTG	TTTCAAAAAA	300
ATGCTTGACT	TGAGACGGGA	ACTAGGGAAG	TCTAAAGGTG	TGCATAAAGG	AAGGTGTAGG	360
AACTAA						366

(2) INFORMATION FOR SEQ ID NO:1662:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 765 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1662:

```
ACTAAAATAA GTAGAAGTTT TGAAAGGAAA AAAATGAAAC TAGAACATAA AAATATCTTT      60
ATTACAGGTT CGAGTCGTGG AATTGGTCTT GCCATCGCCC ACAAGTTTGC TCAAGCAGGA      120
GCCAACATTG TCTTAAACAG TCGTGGGGCA ATCTCAGAAG AATTGCTCGC TGAGTTTTCA      180
AACTATGGTA TCAAGGTGGT TCCCATTTC AAGAGATGTAT CAGATTTTGC AGACGCTAAG      240
CGTATGATTG ATCAAGCTAT TGCAGAACTG GGTTCAGTAG ATGTTTTGGT CAACAATGCA      300
GGGATTACCC AAGATACTCT TATGCTCAAG ATGACAGAAG CAGATTTTGA AAAAGTGCTC      360
AAGGTCAATC TGA CTGGTGC CTTTAATATG ACACAATCAG TCTTGAAACC GATGATGAAA      420
GCCAGAGAAG GTGCTATCAT TAATATGTCT AGTGTGTGTTG GTTTGATGGG GAATATTGGT      480
CAAGCTAACT ATGCTGCTTC TAAGGCTGGC TTGATTGGCT TTACCAAGTC TGTGGCACGC      540
GAGGTCGCTA GTCGGAATAT ACGAGTCAAT GTGATTGCTC CAGGAATGAT TGAGTCTGAT      600
ATGACCGCTA TCTTATCAGA TAAGATTAAG GAAGCTACAC TAGCTCAGAT TCCGATGAAA      660
GAATTTGGGC AGGCAGAGCA GGTTCAGAT TTGACAGTAT TTTTAGCAGG CCAAGATTAT      720
CTAACTGGTC AAGTGGTTGC CATTGATGGT GGCTTAAGTA TG TAG      765
```

(2) INFORMATION FOR SEQ ID NO:1663:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 711 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1663:

```
CGAAAAATAA GTAGGTCAGC CATGGGGAAA CGGATTTTAT TACTTGAGAA AGAACGAAAT      60
CTAGCTCATT TTTTAAGTTT GGAAGTCCAG AAAGAGCAGT ATCGGGTTGA TCTGGTAGAG      120
GAGGGGCAAA AAGCCCTTTC CATGGCTCTT CAGACAGACT ATGATTTGAT TTTATTGAAC      180
GTTAATCTGG GAGATATGAT GGCTCAGGAT TTTGCAGAAA AATTGAGTCG AACTAAACCT      240
GCCTCAGTCA TCATGATTTT AGATCATTGG GAAGACTTGC AAGAAGAGCT GGAAGTTGTT      300
CAGCGTTTTC CAGTTTCATA CATCTATAAG CCAGTCTTTA TCGAAAATCT GGTAGCGCGT      360
ATTTCCGGCGA TCTTCCGAGG TCGGGACTTC ATTGATCAAC ACTGCAGTCT GATGAAAGTT      420
CCAAGGACCT ACCGCAATCT TAGGATAGAT GTTGAACATC ACACGGTTTA TCGTGGTGAA      480
GAGATGATTG CTCTGACCCG CCGTGAGTAT GACCTTTTGG CGACACTTAT GGAAGTAAG      540
AAAGTATTGA CTCGTGAGCA ATTGTTGGAA AGTGTGTTGGA AGTATGAAAG TCGGACCGAG      600
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ACAAATATCG TAGATGTCTA TATCCGCTAT CTACGGAGCA AGCTTGATGT TAAAGGCCAA	660
AAAAGCTACA TTAAACCCT GCGTGGTGT GGTACACCA TGCAAGAATA G	711

(2) INFORMATION FOR SEQ ID NO:1664:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3720 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...3720
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1664:

ACAAGAATAA GCAGTTCAC	TAGAAATAGAA AGGGAAGAAA TAGTGGTTGA	TGTAAATCGT	60
TTTAAAAGTA TGCAATCAC	CCTAGCTTCT CCAAGTAAAG TCCGTTTCATG	GTCTTATGGA	120
GAAGTCAAAA AACCTGAAAC	AATCAATTAT CGTACCTTGA AACCAGAACG	TGAAGGACTC	180
TTTGATGAAG TGATCTTTGG	TCCTACAAAA GACTGGGAAT GTGCTTGTGG	TAAGTACAAA	240
CGCATTTCGTT ACAGAGGAAT	TGTTTGTGAC CGCTGTGGGG TTGAAGTAAC	GCGTACGAAA	300
GTTTCGTCGTG AGCGTATGGG	ACATATCGAA TTGAAAGCTC CTGTATCTCA	CATCTGGTAC	360
TTCAAGGGGA TTCCAAGCCG	TATGGGCTTG ACCCTTGATA TGAGCCCTCG	TGCCCTCGAG	420
GAAGTTATCT ACTTTGCGGC	TTATGTGGTG ATTGATCCTA AGGATACACC	ACTTGAGCAC	480
AAGTCTATCA TGACAGAGCG	CGAATACCGA GAGCGCTTGC GCGAATATGG	TTATGGTTCA	540
TTTGTTGCCA AGATGGGTGC	GGAAGCCATC CAAGACCTTT TGAAGCAAGT	AGATCTTGAA	600
AAAGAAATTG CTGAACTCAA	AGAAGAAATTG AAAACAGCTA CTGGACAAAA	ACGTGTCAAA	660
GCCATCCGTC GTTTGATGT	TTTGATGCC TTTTACAAAGT CTGGAAACAA	ACCTGAATGG	720
ATGATTCTTA ACATTCTTCC	GGTTATCCCA CCAGATCTTC GTCCAATGTT	GCAGTTGGAT	780
GGTGGCCGTT TTGCCTCATC	TGACTTGAAT GACCTTTACC GCCGTGTTAT	CAACCGTAAC	840
AACCGTTTGG CTCGTTTGCT	TGAGTTAAAT GCACCAGGTA TCATCGTTCA	AAATGAGAAG	900
CGTATGCTTC AAGAAGCAGT	TGACGCTTTG ATTGACAATG GTCGTCGTGG	TCGTCCAATC	960
ACAGACCAG GTAGCCGTCC	ATTGAAATCA TTGAGCCACA TGCTTAAAGG	TAAACAAGGA	1020
CGCTTCCGTC AAAACTTGCT	CGGTAAACGT GTTGACTTCT CAGGACGTTT	CGTTATCGCC	1080
GTTGGTCCAA CTCTTAAGAT	GTACCAATGT GGTGTGCCGC GTGAAATGGC	GATTGAACTC	1140
TTTAAACCAT TTGTCATGCG	TGAAATCGTT GCGCGTGATA TCGTGCAAAA	CGTCAAAGCA	1200
GCTAAACGCT TGGTGGAACG	CGGAGATGAG CGTATCTGGG ATATCCTTGA	AGAAGTGATT	1260
AAAGAACACC CAGTGCTTTT	GAACCGCGCA CCGACCCTTC ACCGTTTGGG	TATCCAAGCC	1320
TTCGAGCCAG TCTTGATTGA	TGGTAAGGCT CTTTCGCTTGC ACCCACTTGT	CTGTGAAGCC	1380
TACAAATGCTG ACTTTGACGG	GGACCAAATG GCCATCCACG TACCACTTTC	AGAAGAAGCA	1440
CAAGCAGAAG CTCGTATCCT	CATGCTAGCT GCTGAGCACA TCTTGAACCC	GAAAGATGGG	1500
AAACCGGTAG TTAATCCATC	TCAGGACATG GTTTTGGGTA ACTACTACTT	GACCATGGAA	1560
GAAGCTGGTC GCGAAGGTGA	AGGAATGGTC TTCAAAGACC GTGACGAAGC	GGTTATGGCT	1620
TACCGCAATG GTTATGTTCA	CCTCCACTCA CGTGTTGGTA TCGCAACAGA	CAGCCTCAAC	1680
AAGCCTTGGA CAGAAGAGCA	AAGACATAAG GTCTTGCTTA CAACAGTTGG	TAAAATTCTC	1740
TTCAACGATA TCATGCCAGA	GGGGCTACCA TACTTGCAAG AACCACAAAC	TGCCAACTTG	1800

ACAGAAGGTG	TTCCAGCTAA	ATACTTCTTG	CCACTTGGTG	GAGATATCAA	GGAAGCTATC	1860
AGCAATCTTG	AGCTCAACCC	TCCATTCAAG	AAGAAAAACC	TTGGAAATAT	CATCGCTGAA	1920
ATCTTCAAAC	GTTTCCGTAC	GACAGAAACT	TCTGCCCTAC	TTGACCGCAT	GAAGAACCTC	1980
GGTTACCACC	ACTCAACTCT	TGCAGGATTG	ACAGTGGGTA	TTGCCGACAT	CCCAGTCGTT	2040
GATGACAAGG	CTGAAATCAT	TGAAGAATCA	CACAAACGTG	TCGAACAAAT	CACCAAACAA	2100
TTCCGTCGTG	GTATGATCAC	AGACGACGAG	CGTTACAATG	CTGTTACAGC	TGAATGGCGT	2160
GCTGCCCGTG	AAAAACTTGA	GAAACGCTTG	ATTGCTAACC	AAGATCCTAA	GAACCCAATC	2220
GTTATGATGA	TGGACTCTGG	AGCCCGTGGT	AACATCTCAA	ACTTCTCACA	GCTTGCCGGT	2280
ATGCGTGGTC	TGATGGCTGC	TCCGAATGGA	CGTATCATGG	AATTGCCAAT	CCTTTCAAAC	2340
TTCCGCGAAG	GTTTGTCTGGT	ATTGGAAATG	TTCTTCTCAA	CTCACGGTGC	TCGTAAAGGT	2400
ATGACCGATA	CGGCCCTTAA	GACAGCCGAC	TCAGGTTACT	TGACTCGTCG	TTTGGTTCGAC	2460
GTTGCCCAAG	ACGTTATCAT	CCGTGAGGAC	GACTGTGGAA	CTGACCGTGG	TCTCTTGATC	2520
CGTTCTATCG	CAGAAGGAAA	AGAGATGATC	GAGTCTCTCG	AAGAGCGTCT	CAACGGTCGT	2580
TACACTAAGA	AAACTGTTAA	ACATCCAGAA	ACTGGTGCAG	TGATTATTGG	TCCAAATGAA	2640
TTGATTACAG	AAGACAAGGC	GCGTGAAATT	GTCAATGCTG	GTGTGGAAGA	AGTGACTATC	2700
CGTTCTGTAT	TTACATGTAA	CACTCGTCAC	GGTGTCTGCC	GTCACGTGTTA	CGGTATCAAC	2760
TTGGCGACTG	GTGATGCGGT	TGAAGTTGGT	GAAGCAGTTG	GTACAATCGC	TGCCCAATCT	2820
ATCGGGGAAC	CTGGTACACA	GCTTACAATG	CGTACCTTCC	ACACAGGTGG	GGTTGCCTCA	2880
AATACCGATA	TCACTCAGGG	TCTTCCTCGT	GTCCAAGAAA	TCTTTGAAGC	CCGCAATCCT	2940
AAAGGGGAAG	CGGTTATCAC	AGAGGTTAAA	GGACAAGTTA	CTGCTATCGA	AGAGGATGCA	3000
TCAACTCGTA	CCAAGAAAGT	CTTTGTTTAAG	GGTGAAACTG	GCGAAGGTGA	ATATGTCGTT	3060
CCATTTACAG	CTCGTATGCG	TGTCGAAGTT	GGGGGCCAAG	TAGCGCGTGG	TGCTGCTCTG	3120
ACAGAAGGTT	CTATCCAACC	AAAACGTCTC	CTTGCAGTTC	GTGATGTCTT	GTCAGTTGAA	3180
ACGTACCTTC	TCGGTGAAGT	ACAAAAAGTT	TACCGTAGCC	AAGGGGTAGA	AATCGGTGAC	3240
AAACACATCG	AGGTAATGGT	TCGTCAAATG	ATCCGTAAAG	TCCGTGTCAT	GGATCCAGGT	3300
GATACAGATC	TTCTCATGGG	TACCCTCATG	GATATCAATG	ACTTTACAGA	TGCCAACAAA	3360
GATGTCCTTA	TCGCAGGTGG	AGTTCCAGCG	ACAGGTCCGC	CAGTCCTTAT	GGGAATTACC	3420
AAAGCCTCAC	TTGAAACAAA	CAGTTTCTTG	TCAGCGGCTT	CCTTCCAGGA	AACAACTCGT	3480
GTCCTTACTG	ACGCAGCTAT	CCGTGGTAAG	AAAGACCATC	TCCTTGGAAT	TAAAGAAAAT	3540
GTTATCATCG	GTAAGATCAT	CCCAGCTGGT	ACTGGTATGG	CCCGTTACCG	TAACCTTGAA	3600
CCACATGCTG	TCAACGAAGA	AGAATACCTT	AATCCTCCAG	TAGAGGAAGA	AGGAAATGAA	3660
GAAACAACAG	AAGTAGTTGT	GGATACTGCC	GTTGAAACTG	TGGAAGAAAC	AGTAGAATAA	3720

(2) INFORMATION FOR SEQ ID NO:1665:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...261
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1665:

GTCATAGTAA	GGGCTAAACA	TATCCATAGT	AATAATTTTG	ACGCGACATC	GGACGGCTCT	60
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ATCATATTTA AGAAAGTGAT TTCGAATGAT AGCTTGTGTT CTTCCCTCAA GAACAGTGAT	120
GATATTGAGA TTGTTAAAAT CTTGCGCAAT GAAGCTCATC TTTCCCTTTG TAAAAGCATA	180
CTCATCCCAA GACATAATCT CAGGAAGACA AGAAAAATCA TGTTTAAAGT GAAAATCATT	240
GAGCTTACGA ATAACAGTTG A	261

(2) INFORMATION FOR SEQ ID NO:1666:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 252 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...252
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1666:

GTCATAGTAA GGACTAAACA TATCCATAGT AATGATTTTG ACGCGACATC GGACGGCTCT	60
ATCATATTTA AGAAAGTGAT CTCGGATGAC AGCTTGTGTT CTACCTTCAA GAACAGTGAT	120
GATATCGAGC TTTTCAAAT CTTGCGCAAT AAAGCTCATC TCCATCTCCC GATTGAAACA	180
GTCAC TCCCC GGACTGTTTC AACGTCCCAG GACATAATCT CAGGAAGACG CGAAAAATCA	240
TGCTCAAAGT GA	252

(2) INFORMATION FOR SEQ ID NO:1667:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 915 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...915
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1667:

AGAAGAGTAA	GGAGAGACAT	GTCAAATAGT	TTAAAAGGGA	CTTTACTAAC	AGTTGTGGCT	60
GGTATTGCTT	GGGGGGTGTC	AGGAACGAGT	GGCCAATACC	TAATGGCACA	CGGAATTTTCG	120
GCTCTGGTCT	TGACCAACTT	GCGTCTTTTA	ATCGCTGGTG	GAATTCTCAT	GATCTTGGCT	180
TATGCTACTG	CAAAGGATAA	AATACTGGTC	TTTTTAAAGG	ATAGAAAGAG	TTTGCTGTCT	240
CTTCTTATTT	TTGCTCTGAT	TGGTCTTTTT	CTCAACCAAT	TCGCCATATCT	GTCTGCTATT	300
CAGGAGACCA	ATGCGGGAAC	AGCGACGGTG	CTTCAGTATG	TTTGTCCCTGT	CGGAATTTTA	360
ATTTATAGCT	GTATCAAGGA	TAGGGTGGCA	CCGACACTGG	GAGAGATAGT	TTCCATCATA	420
TTCGCCATCG	GAGGAACCTT	CCTGATTGCA	ACACATGGGC	AGTTGGACCA	GTTATCCATG	480
ACACCTGCTG	GCCTGTTCTG	GGGTCTCTTT	TCTGCCTTGA	CTTATGCTCT	ATATATCATT	540
TTACCCATAG	CCTTGATTAA	AAAGTGGGGG	AGCAGCTTGG	TCATTGGTGT	GGGAATGGTT	600
ATAGCAGGTT	TGGTCGCCCT	TCCTTTTACA	GGGGTTCTAC	AGGCCAATAT	CCCGACTAGT	660
CTTGATT TTC	TCCTTGCGTT	TGCAGGTATT	ATCCTTATCG	GGACTGTCTT	TGCCTATACA	720
GCTTTCCTTA	AAGGAGCCAG	TCTGATAGGA	CCGGTCAAGT	CAAGCTTGTT	GGCTTCAATT	780
GAGCCAATAT	CGGCGTTTTT	CTTTGCCTTC	TTAATAATGA	ATGAACAATT	TTATCCCATT	840
GATTTTCTTG	GTATGGCAAT	GATATTGTTT	GCTGTAACCT	TGATTTCTTT	GAAAGATTTA	900
TTCTTAGAAA	AATAA					915

(2) INFORMATION FOR SEQ ID NO:1668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1668:

TGGGAGGTAA	GGATGGAATT	ACGCAGACCA	AGATTAGCGG	ATAAGAAAGC	TGTTTTAGAT	60
ATGATGACAG	AGTTTGAAAA	GAGCCAATCA	GCCCATGATG	GAGGATTTTG	GGATGTTGAG	120
GATTTTTCTT	ACGAGGAGTG	GCTAGAAGGT	AACCGTAATA	AAGAAATGGG	AATATGGCTA	180
CCTGAAAATC	GCGTTCCATC	GATACAGTTC	GTATTGTTTG	GTGAATCAGG	TTGTGCTCTA	240
GGATTTTTGA	ATCTGCGATT	GAGACTGAAT	GAGGGGTTAC	TGAATTATGC	TGGCCACATT	300
GGCTACTCCA	TCCGTCATC	TGAAAGAGGC	AAGGGTTATG	CAAAAGAGAC	TCTCCGTCAG	360
GGCTTGCAAG	TTGCTAAGGA	AAAGAACATC	AAGAAAGCTC	TGGTGACCTG	TAGCGTGAAT	420
AATCTTGCTA	GCAGAGCAGT	CATTCTAGCA	AATGGTGGAA	TATTTGAGGA	TGCTCGCAAT	480
GGAGTCGAGC	GTTATTGGAT	AGAGGTAGCG	AATGAATAA			519

(2) INFORMATION FOR SEQ ID NO:1669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1669:

AAAAATTCAA	GCCTATCATT	CTTAGAAAGG	AAACTATGG	CAAACATTCT	CTTGGCTGTA	60
ACGGGTTCAA	TCGCCTCTTA	TAAGTCGGCA	GATTTAGTCA	GTTCTCTAAA	AAAACAAGGC	120
CATCAAGTCA	CTGTCTTAAT	GA CTCAGGCT	GCTACAGAGT	TTATCCAACC	TTTGACACTA	180
CAGGTACTCT	CACAGAATCC	TGTCCACTTG	GATGTCATGA	AAGAACCCTA	TCCTGATCAG	240
GTCAATCATA	TCGAACTTGG	AAAAAAAAGCA	GATTTATTTA	TCGTGGTACC	TGCAACTGCT	300
AACACTATTG	CAAAACTAGC	TCACGGATTT	GCGGACAACA	TGGTAACCAG	TACAGCTCTA	360
GCCCTACCAA	GTCATATTCC	CAAACTAATA	GCTCCTGCTA	TGAATACAAA	AATGTATGAC	420
CATCCAGTAA	CTCAGAATAA	TCTGAAAACA	TTAGAAACCT	AC		462

(2) INFORMATION FOR SEQ ID NO:1670:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 582 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1670:

AGCTGTTCAA	GAAAAAACCG	GATTGATTTG	ATTATCACAG	ATGTCATGAT	GCCTCGGATG	60
GGATGGTATG	ATCTAATCAG	TGAGGTTCAA	TACTTATCAC	CAGAGCAGCC	TTTCCTATTT	120
ATTACTGCTA	AGACCACTGA	ACAGGACAAG	ATTTACGGCC	TGAGCTTGGG	AGCAGATGAT	180
TTTATTGCTA	AGCCTTTTAG	CCCACGTGAG	CTAGTTTTGC	GTGTCCACAA	TATTTTGCGC	240
CGCCTTCATC	GTGGGGGCGA	AACAGAGCTG	ATTTCCCTTG	GCAATCTAAA	AATGAATCAT	300
AGTAGTCATG	AAGTTCAAAT	AGGAGAAGAA	ATGCTGGATT	TAACTGTTAA	ATCATTGTGAA	360
TTGCTGTGGA	TTTTAGCTAG	CAATCCAGAG	CGAGTTTTCT	CCAAGACAGA	CCTCTATGAA	420
AAGATCTGGA	AAGAAGACTA	CGTGGATGAC	ACCAATACCT	TGAATGTGCA	TATCCATGCT	480
CTTCGACAGG	AGCTGGCAAA	ATATAGTAGT	GACCAAACGC	CCACTATTAA	GACAGTTTGG	540

(2) INFORMATION FOR SEQ ID NO:1671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1671:

CCCGTCTCAA	GCACGCGTCA	ACTCTGGCTC	ATGCTGATTA	TCCTTCCTAC	CTGGATCAAT	60
TTGCTCCTTA	AAGCCTATGC	TTTTATCGGG	ATTTTGGTC	AAAATGGCTC	TATTAACCAA	120
TTCTTGGAAT	TTATCGGAAT	TGGTTCACAA	CAGTTGCTTT	TTACCGATTT	TTCCTTTATC	180
TTTGTCGCAA	GCTACATCGA	GCTCCCCTTT	ATGATTTTGC	CGATTTTCAA	TGTCTTAGAC	240
GACATGGATA	ATAATCTCAT	CAATGCTAGT	TATGACCTTG	GTGCAACTAA	GTGGGAGACC	300
TTCCGTCATG	TCATCTTCCC	TCTATCTATG	AACGGTGTGC	GAAGTGGGGT	TCAGTCGGTC	360
TTTATCCCAA	GTTTGAGTCT	CTTCATGCTG	ACCCGTTTGA	TTGGTGGGAA	CCGCGTTATC	420
ACCTTGGGGA	CGGCTATTGA	GCAGAATTTT	CTAACCAATG	ACAACTATGG	TATGGGTTCA	480
ACTATCGGTG	TGATTCTCAT	CCTGACCATG	TTCATCACCA	TGTGGGTGAC	TAAGGAAAGG	540
AGAGAACGAT	GA					552

(2) INFORMATION FOR SEQ ID NO:1672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1672:

ACTTCATCAA	GACTCAGGCA	GATGCAGACT	ACGATGAGAG	TTTTGATCCA	GGTGAGGTTT	60
CTGAAAATGA	AGGAGAATTT	TCGGATGGAG	ATGCTGGTGG	TGATCCGCTT	TTTGAAGAAG	120
CTAAGTCTTT	GGTTATCGAA	ATACAGAAAG	CAGTTGGAAT	CCATGATTCA	GCGTCGTTTG	180
TCAGTTGGAT	TTAACCGTGC	GACCCGTCTC	ATGGAAGAGC	TTGAGATGGC	AGGTGTCATT	240
GGTCCAGCTG	AAGGTACCAA	GCCAAGAAAA	GTATTGCAGC	AATAA		285

(2) INFORMATION FOR SEQ ID NO:1673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1673:

ACAAAATCAA	GAATTTTCTG	TCTATTTTTT	GAATATTTAT	GGAGAATGAG	ACTGATGAAA	60
ATATGGTATA	ATGAAATAAA	GGAGTTTAT	ATGCAAAAAT	TTATTCAGGC	TTATATTGAA	120
AAGCTAGATG	TGACAACCAT	TATCGAGAAT	ATTCTAACCA	AGGTCATTTT	TCTTTTACTG	180
CTTTTGATTG	TATTTTATAT	TGCTAAAAAA	ATGCTTCATA	CCATGGTGCA	GAGAATTGTC	240
AAACCTTCTC	TAAAAATGTC	TCGTTCATGAT	GTCGGACGCC	AAAAAAACCAT	CTCACGTTTA	300
CTAGAAAATG	TGTTTAATTA	TACGCTATAT	TTCTTTTTTAC	TCTACTGCAT	TTTGTCGATT	360
TTAGGTTTGC	CAGTTTCTAG	TTTGCTGGCT	GGAGCTGGTA	TTGCTGGGGT	ANCGATTGGT	420
ATGGGAACCA	AGGCTTTCTG	TCTGATGTCA	TCAATGGCTT	TTTCATCCTC	TTTGAACGTC	480
AACTGGATGT	GGGAGATGAG	GTCGTTCTGA				510

(2) INFORMATION FOR SEQ ID NO:1674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1674:

GAAAAATCAA	GGAGAAACCT	AATGTTTGTA	AAAAAAGGCG	ACAAAGTTCG	CGTAATCGCT	60
GGTAAAGATA	AGGGAACAGA	AGCTGTTGTC	CTTACTGCCC	TTCCAAAAGT	AAACAAAGTT	120
ATCGTTGAAG	GTGTTAACAT	TGTTAAGAAA	CACCAACGTC	CAACTAACGA	GCTTCCTCAA	180
GGTGGTATCA	TCGAGAAAAG	AGCAGCTATC	CACGTATCAA	ACGTTCAAGT	TTTGGACAAA	240
AATGGTGTAG	CTGGTCGTGT	TGGTTACAAA	TTTGTAGACG	GTAAAAAAGT	TCGCTACAAC	300
AAAAAATCAG	GCGAAGTGCT	TGATTAA				327

(2) INFORMATION FOR SEQ ID NO:1675:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 909 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1675:

CGGAATGGGC	TTGGCCAAAT	GAAACAAGAT	CAACTAAAGG	CTTGGCAACC	AGCTCAGTTT	60
GACCGTTTTG	TCCGTATCTT	AGAACAAGAC	CAGCTCAATC	ACGCCTATCT	CTTTTCAGGT	120
TTCTTTGGAA	GCTTGGAAT	GGCGCAATTT	TTAGCTAAGA	GCCTCTTTTG	TACGGATAAA	180
GTTGGCGTCT	TACCATGTGA	GAAATGCCGA	AGTTGCAAGC	TGATTGAACA	GGAAGAGTTT	240
CCAGATGTCA	CCTTGATTAA	GCCAGTCAAT	CAGGTCATCA	AGACAGAACG	CATTTCGGGAA	300
TTGGTGGGAC	AGTTTTCTCA	AGCAGGGATT	GAAAGCCAGC	AACAGGTCTT	TATTATCGAG	360
CAAGCGGATA	AAATGCATCC	CAACGCAGCC	AATTCTCTGC	TCAAGGTCAT	CGAAGAACCC	420
CAGAGTGAAAG	TTTATATTTT	CTTCTTGACT	AGCGATGAGG	AAAAGATGTT	ACCGACAATC	480
CGAAGTCGGA	CTCAGATCTT	CCACTTTAAA	AAGCAAGAAG	AAAAACTTAT	CTTACTCTTA	540
GAACAAATGG	GACTTGTTAA	GAAAAAAGCG	ACTCTTTTAG	CTAAGTTTAG	TCAATCGCGA	600
GCTGAAGCAG	AAAAGTTGGC	TAATCAGGCA	AGTTTTTTGA	CCTTGGTCGA	TGAAAGTGAA	660
CGCCTGCTGA	CTTGTTAGT	AGCTAAGAAA	AAAGAAAGTT	ATCTACAGGT	TGCCAAATTA	720
GCCAACTTGG	CAGATGATAA	GGAAAAACAG	GATCAGGTTT	TACGGATTCT	TGAAGTTCTC	780
TGTGGGCAGG	ACCTCTTGCA	GGTAAGAGTA	AGAGTGATTCT	TACAAGATTT	ACTAGAAGCT	840
AGAAAAATGT	GGCAAGCTAA	TGTCAGCTTT	CAAAATGCCA	TGGAATATCT	GGTCTTGAAA	900
GAAATATAA						909

(2) INFORMATION FOR SEQ ID NO:1676:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 186 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1676:

ATGCCTCCAA GAAAGAGAAT AACAGCCATC AGAGAGGTCC AACCAGATGT CGGATTGCCC	60
AAAATGAGGG TCCGAACCAC AACAAAAAAG GTCATCAGCA GAGAAAGAAA ACAAGATAGG	120
AGACCAGCTA CAAAGGCTAT AGTCAAAGGG AAATCTGAAA AATTAACAAT CCCTTCAATG	180
GAGTAA	186

(2) INFORMATION FOR SEQ ID NO:1677:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 477 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1677:

AAAAAGCCAA GACACTCTCT GCCTCAGCTA ATAGTTCTCG CAAAGACTAT TATATCACAA	60
AGGAGACAGA GAGTGAACAA GGCTAAAGAG CTCTTGAAAG AGTTGCAGGA TCTGGACATG	120
GACATCCAAA GCCGTATAGA CGAAATTAAC GAGCTTGAGG CAGGTTTGCT CTCAAGCCCT	180
AAATGGTCCG AGGTAAAGT CCAAGGTGGA CAGACTAGAA AAGTTGATGA TGTCTATACT	240
CAGTTGGTAG TGATGAAAGA GGCTATAGAG CAGGATACTA AAGAGGTCAT TAACAGAAAA	300
CTTGAATTAG GTAGAATGAT CAATAGGCTT AAAAATCCAA AGTACAGGGC AGTATTAAGA	360
ATGACTTACA TCAACAAAGG CACCGCTGAT AGCGTTTGTT ATGATTTGAA TATGAGTCGT	420
ACAACCTACT ACAGGTTAAA AAATGAGGCG GTCTTAGCTT TGGAAGAAGT TATCTAA	477

(2) INFORMATION FOR SEQ ID NO:1678:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1179 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1179
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1678:

AGGTCAACAA	GAAGTCTAAA	TTTCGAATTG	TGCCATCTTG	TACTATTTAT	AATGAATGCG	60
GAGGCTGCGC	AAATCATGCA	CCTGCATTAT	GATAAGCAGC	TGGAGTTCAA	GACGGACTTA	120
CTTCATCAAG	CGCTGAAAAA	ATTTGCTCCT	GCAGGATATG	AAAATTATGA	AATTCGTCCA	180
ACTATTGGAA	TGCAGGAACC	AAAATATTAC	AGAGCTAAGT	TACAATTTCA	GACTCGAAAA	240
TTTAAAAATC	AGGTCAAGGC	GGGCTTATAT	GCACAAAAC	CTCACTATTT	AGTAGAGTTG	300
AAAGACTGCC	TGGTACAAGA	TAAGGAAACC	CAAGTGATTG	CTAATCGCTT	AGCAGAATTA	360
CTTACTTATC	ACCAGATTCC	AATCACGGAT	GAGAGAAAAG	TTCTAGGTGT	CCGTACTATT	420
ATGGTCCGAC	GCGCGAGAAA	GACCGGACAG	GTTCAGATTA	TTATTGTTAC	AAACCGCCAG	480
CTTAATTTAA	CTCAATTGGT	AAAAGAGTTG	GTAAAGATT	TCCCAGAAGT	TGTGACAGTA	540
GCTGTTAATA	CAAATACAGC	TAAAACCAGT	GAGATATATG	GTGAAAAGAC	AGAGATTATC	600
TGGGGGCAAG	AGAGTATTCA	AGAAGGTGTA	CTCAATTATG	AATTTTCACT	ATCCCCTCGA	660
GCTTTTTTATC	AACTAAATCC	TGAGCAAACA	GAAGTCCTCT	ATAGCGAAGC	AGTAAAAGCG	720
CTGGATGTTG	ATAAAGAAGA	CCATTTGATT	GACGCTTATT	GTGGAGTTGG	AACGATTGGA	780
TTTGCCTTTG	CAAAGAAAGT	AAAAACACTC	AGAGGTATGG	ATATTATTCC	AGAAGCTATT	840
GAAGATGCCA	AGCGAAATGC	TAAAAGAATG	GGATTTGACA	ATACTCATTA	TGAAGCTGGA	900
ACGGCAGAAG	AGATTATTCC	TCGTTGGTAC	AAGGAAGGCT	ACCGAGCAGA	TGCTTTGATT	960
GTTGACCCAC	CACGTACAGG	TCTGGATGAT	AAGTTATTAG	ATACTATTCT	TACTTATGTA	1020
CCAGAAAAAA	TGGTTTATAT	TTCTTGTAAT	GTTTCGACCT	TGGCTCGTGA	TTTGGTACGC	1080
TTAGTAGAAG	TCTATGATCT	TCATTATATC	CAGTCGGTCG	ATATGTTCCC	ACATACAGCT	1140
CGAACTGAAG	CTGTTGTAAA	ATTAATAAAA	AAAGTTTAA			1179

(2) INFORMATION FOR SEQ ID NO:1679:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 966 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...966
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1679:

TTACAGACAA	GAAAATTTCC	AACATCCAAG	AAATCTTGCC	ACTTTTGGAA	AGCATTCTCC	60
AAGAGCATTG	TTCCATTTGG	GATTATGCCG	GATGATGTGG	ATGGTGAGGC	TCTTCCAAC	120
CTTGTTTTGA	ACAATATTCG	TGGAACCTTC	AACGTAGTAG	CAGTCAAGGC	ACCTGGTTTT	180
GGTGACCGTC	GCAAAGCCAT	GCTTGAAGAT	ATCGCCATCT	TAACAGGCGG	AACAGTTATC	240
ACAGAAGACC	TTGGTCTTGA	GTTGAAAGAT	GCGACAATTG	AAGCTCTTGG	TCAAGCAGCG	300
AGAGTGACCG	TGGACAAAGA	TAGCACGGTT	ATTGTAGAAG	GTGCAGGAAA	TCCTGAAGCG	360
ATTTCTCACC	GTGTTGCGGT	TATCAAGTCT	CAAAATCGAAA	CTACAACCTC	TGAATTTGAC	420
CGTGAAAAAT	TGCAAGAACG	CTTGGCCAAA	TTGTCAGGTG	GTGTAGCGGT	TATTAAGGTC	480
GGAGCCGCAA	CTGAAACTGA	GTTGAAAGAA	ATGAAACTCC	GCATTGAAGA	TGCCCTCAAC	540
GCTACTCGTG	CAGCTGTTGA	AGAAGGTATT	GTTGCAGGTG	GTGGAACAGC	TCTTGCCAAT	600
GTGATTCCAG	CTGTTGCTAC	CTTGGAATTG	ACAGGAGATG	AAGCAACAGG	ACGTAATATT	660
GTTCTCCGTG	CTTTGGAAGA	ACCCGTTTCG	CAAAATGCTC	ACAATGCAGG	ATTTGAAGGA	720
TCTATCGTTA	TCGATCGTTT	GAAAAATGCT	GAGCTTGCTA	TAGGATTCAA	CGCAGCAACT	780
GGCGAGTGGG	TTAACATGAT	TGATCAAGGT	ATCATTGATC	CAGTTAAAGT	GAGTCGTTCA	840
GCCCTACAAA	ATGCAGCATC	TGTAGCCAGC	TTGATTTTGA	CAACAGAAGC	AGTCGTAGCC	900
AATAAACCCAG	AACCAGTAGC	CCCAGCTCCA	GCAATGGATC	CAAGTATGAT	GGGCGGGATG	960
ATGTAA						966

(2) INFORMATION FOR SEQ ID NO:1680:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 414 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...414
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1680:

AAATTTGCAA	GGTCTAATAT	TACAGGCATT	TTCGAAGAAA	GAGCTGAAAA	AATTGCTTCA	60
GATATTGACA	GAGCTGAAGA	AGCCCGTCAA	AAAGCAGAAG	TATTGGGCTCA	AAAACGCGAA	120
GATGAATTGG	CTGGTAGCCG	TAAAGAAGCT	AAGACAATCA	TTGAAAAATGC	AAAGGAAACA	180
GCTGAGCAAA	GTAAGGCTAA	TATCTTAGCA	GATGCTAAAC	TAGAAGCAGG	ACACTTAAAA	240
GAAAAAGCCA	ATCAAGAAAT	TGCTCAAAAT	AAAGTAGAAG	CTTTACAGAG	TGTTAAGGGT	300

GAGGTCGCAG ATTTGACCAT CAGCTTAGCT GGTAAAATCA TCTCACAAAA CCTTGACAGT	360
CATGCCCATA AAGCACTCAT TGATCAGTAT ATCGATCAGC TAGGAGAAGC TTAA	414

(2) INFORMATION FOR SEQ ID NO:1681:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 822 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...822
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1681:

CTTATCGCAA GGAATATTGA TTCCCTAAAC GCTGCCCTAA CTAGTGA	60
CTAGTGAAGT AGCTCGTGCC AAATTGTCCC AAGAAGTCCT	120
ACAAACCTTG GTCGCTGAAA ATGCTGATAT CATTGCTATC	180
CAAGAAACCA AGCTTTCTGC CAAAGGACCT ACAAAGAAAC	240
ACGTGGAAAT TTTAGAAGAA CTCTTCCCAG GCTACGAAAA	300
CACATGGCGC TCTTCCCAAG AGCCTGCCCC TAAAGGCTAT	360
GCTGGAACCA TGTTCCCTTA TAAGAAAGAA CTTACGCCTA	420
CGATCAGTTT TCCAGAAATC GGTGCCCCTT CTACCATGGA	480
CTTGGAAGGC CGTATCATCA CTCTAGAATT TGATGCATTT	540
TTCGTAACCC AAGTTTACAC TCCAAACGCT GGTGACGGTC	600
TCAAACGCTT GGAAAAACGC CAAGTCTGGG ATGTTAAATA	660
TGCTGAGTAT TTGGCTGAAC TAGACAAAGA AAAACCAGTC	720
CTTGCGACCG GTGACTACAA CGTAGCCCAC AATGAAATCG	780
ACCTTGCAAA TCCTGCTAGC AACC GCCGTT CACCTGGATT	822
TACTGACGAG GAACGTGCTG GATTTACCAA CCTTTTGGCA	
ACTGGATTTA CAGACACCTT CCGCCATGTT CATGGCGATG	
TTCTGAAACG CTACACTTGG TGGGCACAAC GCAGCAAAAC	
TTCTAAAATC AACAAATACAG GCTGGAGAAT CGACTACTGG	
CTCACAAGTA ACCGTATCGC TGACAAGGTC ACTAAATCTG	
ATATGATTGA CTCAGGTGCT CGCCAAGACC ATACACCGAT	
TGTCTTGGAA ATTGACTTGT AA	

(2) INFORMATION FOR SEQ ID NO:1682:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1682:

GCAACCGCAA	GTAGTCATAG	ATTAAGGAGA	AAACTTATGC	CAATCACAGC	TGCAGATATT	60
CGTCGTGAAG	TCAAGGAAAA	AAATGTTACC	TTTATTTCGTC	TTATGTTCTC	AGATATTTTG	120
GGAACCATGA	AAAACGTCGA	AATTCCTGCT	ACAGATGAAC	AGTTAGATAA	GGTCTTGTCG	180
AACAAGGTTA	TGTTTGATGG	ATCTTCTATT	GAAGGTTTTG	TACGTATCAA	TGAGTCGGAT	240
ATGTACTTGT	ACCCGGACTT	GGATACATGG	ACAGTCTTCC	CTTGGGGAAG	ATGA	294

(2) INFORMATION FOR SEQ ID NO:1683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1683:

AATCAAGCAA	GACCAGTTTG	GGACAGAGTT	GATTTAGGGA	GGCTTATGAG	AAAATCATTT	60
TACACTTGGC	TCATGACCGA	GCGCAATCCT	AAAAGTAACA	GTCCCAAAGC	AATTTTGGCA	120
GACCTCGCTT	TTGAAGAGTC	AGCCTTTCCA	AAACATACAG	ATGATTTTGA	TGAGGTCAGT	180
CGCTTTTGG	AGGAGCATGC	CAGTTTCTCT	TTTAACCTAG	GAGATTTTGA	CAGCTCTTGG	240
CAGGAGTCT						249

(2) INFORMATION FOR SEQ ID NO:1684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...858

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1684:

```
AATTATCAAAA GATTTACCAG GAAGGAAATG GGAGTGAAAA AGAAACTAAA GTTGACTAGT      60
TTGCTAGGAC TGCTCTGTT AATCATGACA GCCTGTGCGA CTAATGGGGT AACTAGCGAT      120
ATTACAGCCG AATCGGCTGA TTTTGGAGT AAATTGGTTT ACTTCTTTGC GGAAATCATT      180
CGCTTTTAT CGTTTGATAT TAGTATCGGA GTGGGGATTA TTCTCTTTAC GGTCTTGATT      240
CGTACAGTCC TCTTGCCAGT CTTTCAGGTG CAAATGGTGG CTTCTAGGAA AATGCAGGAA      300
GCTCAGCCAC GCATTAAGGC GCTTCGAGAA CAATATCCAG GTCGAGATAT GGAAAGCAGA      360
ACCAAAC TAGCAGGAAAT GCGTAAAGTA TTTAAAGAAA TGGGTGTCAG ACAGTCAGAC      420
TCTCTTTGGC CGATTTTGAT TCAGATGCCG GTTATTTTGG CCCTGTTCCA AGCCCTATCA      480
AGAGTTGACT TTTTAAAGAC AGGTCATTTT TTATGGATTA ACCTTGGTAG TGTGGATACA      540
ACCTTGTTT TTCCGATTTT AGCAGCAGTA TTCACCTTTT TAAGTACTTG GTTGTCCAAC      600
AAAGCTTTGT CTGAGCGAAA TGGCGCTACG ACTGCGATGA TGTATGGGAT TCCAGTCTTG      660
ATTTTATCT TTGCAGTTTA TGCGCCAGGT GGAGTCGCCC TATACTGGAC AGTGTCTAAT      720
GCTTATCAAG TCTTGCAAAC CTATTTCTTG AATAATCCAT TCAAGATTAT CGCAGAGCGC      780
GAGGCCGTAG TACAGGCACA AAAAGATTTG GAAAATAGAA AAAGAAAAGC CAAGAAAAAG      840
GCTCAGAAAA CGAAATAA                                     858
```

(2) INFORMATION FOR SEQ ID NO:1685:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1685:

```
ACTTGTCAAAA GTTGCAACAA GACAAAAATT AAAAAATAAAA AAGGAGTATT TGTCATGAAT      60
ACAAAAATGA TGGAACAATT TTCTGTTATG GATAATGAAA TGCTTGATAG GATAGAGGGA      120
GGAATATTTG GAGTTGACGA TGCTTTGTTT TGGGCAGGGT TAGGCTATGT TGCAGGTAGC      180
ATTGTTGATA CAGCAATTGA TGATTTTACG AATCAATGCC GGAAAAATCC TCATCAGTGG      240
TTCTGTGTTT GTGTATAG                                     258
```

(2) INFORMATION FOR SEQ ID NO:1686:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1686:

TGGGGCCAAA GGTTCACTC ATCGATAGTG GGGCAGAGTG CGTACGGGAT ATCTCAGTTC	60
TTACTCAATT ATTTTGAAAT CAATCGTGGT CGCGATGCTG GACCACTCCA TCACCGTTTT	120
TACACAACAG CCAGTAGCCA AATTTTGCCC CAATTGGTGA AGAATGGCTG GGAAAAAGAG	180
ATTCATGTGG AGCATGTAGA ATTATGA	207

(2) INFORMATION FOR SEQ ID NO:1687:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1158 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1687:

GGATTCAAAA GTGAAGAAAA CATGAGTAAA GAAATGCTAG AGGCCTTCCG CATTTTGGAA	60
GAAGACAAGG GAATCAAAAA AGAAGATATC ATCGACGCAG TAGTAGAGTC GCTTCGTTCC	120
GCTTATCGCA GACGCTATGG TCAGTCAGAC AGCGTAGCTA TTGACTTCAA CGAAAAAACA	180
GGTGACTTTA CAGTTTATAC TGTCCGTGAA GTTGTTGATG AAGTATTTGA TAGCCGTTTG	240
GAAATCAGCT TGAAAGATGC TCTTGCCATT AATTCAGCTT ATGAACTTGG AGACAAAATC	300
AAGTTTGAAG AAGCACCAGC TGAGTTTGGT CGTGTAGCAG CCCAATCTGC CAAACAAACC	360
ATCATGGAAA AAATGCGCAA GCAAAACAGT GCCATCACTT ACAATACTTA CAAAGAACAT	420
GAGCAAGAAA TCATGTCTGG TACAGTAGAA CGCTTTGACA ACCGCTTTAT CTATGTCAAC	480

CTTGGTAGCA	TCGAAGCCCA	ATTGTCAAAA	CAAGACCAAA	TTCCTGGAGA	AGTTTTTGCT	540
TCTCATGATC	GTATCGAAGT	TTATGTTTAC	AAGGTTGAAG	ACAACCCTCG	TGGTGTGAAC	600
GTCTTTGTTA	GCCGTAGCCA	TCCAGAAATG	ATCAAACGTT	TGATGGAGCA	AGAAATTCCA	660
GAAGTTTATG	ATGGAAGTGT	TGAAATCATG	AGCGTGGCTC	GTGAAGCAGG	TGACCGTACG	720
AAGGTTGCTG	TTCGTAGCCA	CAATCCAAAC	GTGGATGCTA	TCGGTACAAT	CGTTGGACGT	780
GGTGGTGCTA	ATATCAAGAA	GATTACTAGC	AAATTCCACC	CAGCTCGTTA	CGATGCTAAA	840
AATGACCGCA	TGGTACCAAT	CGAAGAAAAAT	ATCGATGTTA	TCGAGTGGGT	AGCAGATCCA	900
GCTGAATTTA	TCTACAATGC	CATCGCTCCT	GCTGAGGTTG	ACCAAGTTAT	CTTTGATGAA	960
AACGACAGCA	AACGTGCCTT	GGTGGTTGTT	CCAGATAACA	AGCTTTCTCT	TGCCATTGGT	1020
CGTCGTGGAC	AAAACGTGCG	CTTGGCGGCT	CAC TTGACTG	GTTACCGTAT	CGATATCAAG	1080
TCTGCTAGCG	AATTTGAAGC	CATGGAAGAC	GCTGCTTCAG	TAGAGTTGGA	AGTAGAAAAC	1140
GATACTGTAG	AAGAATAA					1158

(2) INFORMATION FOR SEQ ID NO:1688:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...216
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1688:

CGAACAAAAA	GTGATGTAAT	TTCTGAAATT	AACACAGGAT	TACCTTTGAA	AAAATGGACT	60
TTTTCAAGGG	CTTTTGGCCG	TGCTCTAAAA	TCATCGCCAA	ATCATCAAAT	TGAAATAAGA	120
AATAGTTTAG	ATAAACTAT	TGACTTTTCT	TATAGTTTGT	CTTTCTTCTA	TCTTCCATTA	180
TATCATACTT	TTTCAGTCTA	TGGTAGCTCT	CTTTAA			216

(2) INFORMATION FOR SEQ ID NO:1689:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1689:

CGAACAAAAA	GTGATGTAAT	TTCTGAAATT	AACACAGGAT	TACCTTTGAA	AAAATGGACT	60
TTTTCAAGGG	CTTTTTGCCG	TGCTCTAAAA	TCATCGCCAA	ATCATCAAAT	TGAAATAAGA	120
AATAATTTAG	ATAAACTAT	TGACTTTTCT	TATAGTTTGT	CTTTCATTTC	TGTGTTTCAT	180
AGATTTACAG	GTAAACGGCA	TTGTTGGCAA	CCAAGTCTGC	ATGCGTGCCT	TGACCAATCA	240
ATCGTCCTTG	ATTTAGAACC	AAGATCTTGT	CTGCATGGAC	AACCGAGCTA	A	291

(2) INFORMATION FOR SEQ ID NO:1690:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 579 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1690:

TGGCAAAAAA	GAAAGAATTT	ATTGAAAGTT	CAAGAAAAAT	TGAAATTATT	AAAAGAGTTT	60
ATAAAAAATAT	GTTCTAAAAA	TAAAAATGAAG	TATTTTGCTT	CTGGAGGTAG	TCTATTGGAA	120
GCTGCAAGAT	ACAAAGGTTT	TATTCCTTGG	AATGATGATA	TGGCTCTAGG	TTTACCAAGA	180
AAGCATTTTG	AAAAGTTTAT	AAATGAAATA	GATTTTGAAA	AATATAATAA	AAATTATATT	240
TTAGAAAGTT	CGGAAATGAA	TTTAGGTATT	TTTCAATATA	AATTAAAATC	TGCTATTTTA	300
ATTTTAGGGA	AATCGTATGA	CGTATGTTTG	AATTTATTTT	TGTTAGACAG	GATGTCAGAA	360
TTGGTTATTG	ATGGTGAGTC	AGGTTTTTAA	GTCCCCTAT	ATAATTTAGA	AGTGGCTGTA	420
GATAGAAAGTA	GAAGTATTAT	TGAGAATAGA	GAAGTAGCCA	ATGAGTTAGG	TAGTGTGCT	480
TTCCAAAGAG	TTCAATCTAT	ATTTGAAATA	AAAGAAAAAG	TGTCAGAGCT	AGAGAATATA	540
TTCATGAGTT	TAGGAGAAGA	TGATAATGTC	AATATATAA			579

(2) INFORMATION FOR SEQ ID NO:1691:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 951 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1691:

TTGAAAAAAA	GGAGTTTGTT	TATGGCACAA	AAAATTATGA	GCCTACAAAA	TAGGAAGAAT	60
CAAAAAAGAC	GATTATCTT	TTTATTTCTT	TTGCCAACGT	TGATTTGTTT	CTTCTATTTT	120
TATTTTATT	CTGTAGTAAC	AATCTTTTAA	ACTTCATTTG	CTAAATGGGA	TTATACAAAT	180
TTAAACACCC	CTGAGTTTCT	TGGATTTGAT	AAATTATTTG	AAAATTATAG	GTATGTTTTT	240
AAAGAATACC	CATTTTTTAC	AGAAGCTCTA	ATTAATTCTG	TTCGTTGGGC	TGTAATTGGT	300
GTTATTATTC	AAGTTCCTTT	AGCTGTATCT	GTTGCAATTA	CATTATCTAA	GAAATTAAAA	360
GGCTGGAAGA	TATCTAGGAA	TCTTTATATT	GTACCAAGTA	TCATTTCTAG	TGCTGCTATG	420
GGCTTGATTT	TTCTTCAAAT	CTATAATCCA	AACTATGGTG	TTGTAAACCA	AATTATTCAT	480
CTATTTAATC	CATCGTTTAA	AGATTCAGTA	CTGTTGACTC	CAGGATTAAA	TATAGTAGCT	540
ATGACTGGCG	CTTATATCTT	CTTTCAGGA	GCATCAACCA	TTATGATTCT	TGGGCAAATT	600
TTTGCTATTC	CAGAAGAAGT	TCAAGAAGCT	GCTATTTTAG	ACAATATTAC	TGGTTGGAGG	660
AAAGAGTGGT	ATATTACGAT	TCCGATGATT	AAGGGGACAA	TTAAAACTGT	TTCAATTATG	720
GCAGCAACTT	CAGGGTTTTT	GCTCTATAAC	GAAGTATTCT	TTTTGACAAA	TGGTGCTGCA	780
GGAACAAAAA	GTATCAGTTT	TGTTATTTCGA	GAATTAGCAG	TGGCTAGCTC	ACGAACCTCAG	840
TATGCTCGTG	CAAATACAAT	TGGAGTTATA	CAAATTTTAG	GTGGAATGTT	GATTATCGTT	900
TGTATTAATA	TTTTATTTCAG	AGAAAGAAAA	AGACTGAAAG	GTGGGAAATG	A	951

(2) INFORMATION FOR SEQ ID NO:1692:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 828 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1692:

GAGGAAAAAA	GGATGAAAGT	GATTAATCAA	ACCTTATTAG	AAAAAGTTAT	TATTGAACGT	60
TCTCGTTCAA	GTCATAAAGG	AGATTATGGT	CGTCTGCTGC	TGCTTGGTGG	TACTTATCCT	120
TATGGTGGTG	CTATCATCGT	GGCTGCTTTG	GCAGCTGTGA	AAAGTGGGGC	AGGATTGGTG	180

ACTGTTGGAA	CGGATAGGGA	AAATATCCCCT	GCTCTGCACA	GTCATTTACC	TGAGGCTATG	240
GCCTTTGCTC	TTCAAGACAA	GCAATTGTTA	AAAGAGCAGT	TGGAGAAGGC	AGAAGTTGTT	300
TTGCTGGGAC	CTGGTTTAGG	AGACGATGCT	TCTGGAGAAG	ATTTAGTTAA	ACAGGTCTTT	360
GCTGGCTTAA	AACAGAAATCA	GATTTTGATT	GTAGACGGAG	GTGCCTTGAC	TATTTCTTGCT	420
AGGACAAAGTC	TGTCATTTCC	TTCTAGCCAG	CTTATCCTAA	CTCCCCACCA	AAAGGAGTGG	480
GAAAACTGT	CTGGAATTAC	GATTGAAAAG	CAAAAGGAAG	ATACAACGGT	TAGTGCCCTG	540
ACTTCTTTCC	CTAAAGGAAC	AATTTTGGTG	GAGAAAGGTC	CGGCTACTCG	TGTTTGGCAA	600
GCTGGCCAGT	CTGATTATTA	CCAGTTACAG	GTTGGCGGTC	CCTATCAGGC	AACTGGGGGA	660
ATGGGAGATA	CTCTGGCTGG	GATGATCGCA	GGATTTGTAG	GCCAATTCCG	ACAGGCCAGT	720
CTCTACGAGC	GTGTAGCAGT	AGCGACCCAT	CTTCATTTCAG	CCATAGCCCA	AGAACTATCT	780
CAAGAAAATT	ATGTGGTCTT	ACCGACGGAA	TCAGCAGTGC	TTCTCACA		828

(2) INFORMATION FOR SEQ ID NO:1693:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...258
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1693:

AATAGAAAAA	GTGAAGAGAG	GTATGAAATG	AGCAAGAAAAG	ATAAAAAAAT	CGAAATTCAA	60
GTAGCGGATG	CCAAAGTTAA	TGTTGGTAAA	GACAGTTTTG	AAGGTTATAC	ATTGACTATC	120
GGTAAAAAAG	TTATCGGAGA	AATTGCCGAA	TTAGACGGAC	AATTTGCCAT	TATAAAGAAT	180
GGGAATGTCG	ATAGTTTTTA	TAAAAAATTG	GAAAAAGCTG	TGGAAATTTT	GATTGAAAAAT	240
TATAATTTAG	CAAAATAA					258

(2) INFORMATION FOR SEQ ID NO:1694:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1694:

AATAAGAAAA	GAACGATCCT	AAAGTCAGGA	ATTTTAAAGG	AATTTCTGGC	TTTTTATGAT	60
AAAATAGGTA	AAAGTATTGC	AAGTATGAGG	TCCAGTATGA	AACTAAAAAC	AAACATTTCGC	120
CATTTACATG	GTAGTATCCG	CGTCCCAGGT	GACAAGTCTA	TCAGCCACCG	TTCCATTATC	180
TTTGGAAGTT	TGGCTGAGGG	TGAGACCAAG	GTTTATGATA	TTCTGCGAGG	CGAAGACGTT	240
CTTTCGACCA	TGCAGGTTTT	TCGTGACCTT	GGTGTTGAAA	TTGAGGATAA	AGATGGGGTT	300
ATTACCATTG	AAGGTGTAGG	CATGGCTGGC	TTAAAAAGCGC	CGCAAAATGC	CCTTAATATG	360
GGAAATTCTG	GCACCTCGAT	TCGCCTGATT	TCAGGTGTCC	TTGCTGGTGC	AGATTTTCGAA	420
GTAGAGATGT	TTGGAGATGA	TAGTCTTTCC	AAACGTCCTA	TGGACCGTGT	GACCTTCCA	480
CTGAAAAAAA	TGGGCGTCAG	CATTTTCAGG	CAAACGTAAC	GAGACTTGCC	TCCCTTCGC	540
TTAAAAGGGA	CGAAAAACCT	AAGACCTATT	CATTATGAGT	TGCCAATTGC	CTCTGCCCAA	600
GTCAGTCAG	CCTTGATGTT	TGCAGCCTTA	CAAGCTAAGG	GGGAGTCAGT	TATTATCGAA	660
AAAGAGTGCA	CTCGTAATCA	TACTGAAGAT	ATGTTGAAAC	AATTTGGTGG	TCATTTAAGT	720
GTGGACGGTA	AGAAAAATCAT	AGTCCAAGGG	CCACAAAAAT	TGACAGGACA	GAAGGTGGTC	780
GTACCAGGAG	ATATTTCCAG	TGCAGCCTTT	TGGTTAGTCG	CAGGTTTGAT	TGTTCCAAAT	840
TCTCGTCTAG	TGCTGCAGAA	TGTGGGGATC	AACGAAACTC	GCACCGGTAT	TATTGATGTC	900
ATTCGTGCCA	TGGGTGAAAA	ATTGGAAATA	ACTGAAATCG	ATCCAGTCGC	TAAATCTGCA	960
ACCTTGATTG	TTGAGTCTTC	TGACTTGAAA	GGAACAGAGA	TTTGTGGCGC	TTTGATTCCA	1020
CGTTTGATTG	ATGAATTGCC	TATTATTGCC	CTACTTGCGA	CCCAAGCCCA	AGGTGTAACA	1080
GTTATCAAGG	ATGCTGAGGA	GCTCAAGGTC	AAGGAAACAG	ACCGTATTCA	GGTTGTGGCA	1140
GACGCCTTAA	ATAGTATGGG	AGCAGATATT	ACTCCTACGG	CAGATGGGAT	GATTATCAAA	1200
GGAAAATCAG	CTCTTCACGG	TGCTAGAGTC	AATACGTTTG	GTGACCACCG	TATCGGCATG	1260
ATGACAGCTA	TCGCAGCCCT	CTTGGTTGCA	GATGGAGAGG	TGGAGCTTGA	CCGTGCAGAA	1320
GCCATCAATA	CCAGCTATCC	TAGTTTCTTT	GATGATTTGG	AGAGCTTGAT	TCATGGCTAA	1380

(2) INFORMATION FOR SEQ ID NO:1695:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1695:

GGGAATGAAA	GTGTGAAAAA	TTACGGAGAA	GCTTTTTCGAT	ATTTTAGAAA	ATTAAACGGA	60
TATTCTTTAG	AGTATGCTGC	AGCTGATTTT	ATATCAAAAT	CTCAACTTTC	TAGATTTGAA	120
AGGGGAGAAA	ATGAAATTTT	TCTTTCAACA	TTTTTTGAAT	TATTATCAAA	TATCAATGTT	180

TCGATAGAGA	ATTTTTGTAA	TCACCTTAGAA	TATTATAAAA	GATCGGAGCG	TGATGATTTT	240
TTGGTTAATT	TATCTCCAAA	TTTTTATAGT	TTGAATATTA	AAGGATTGGA	GGTAATAAAA	300
AATAAGCAAC	AAAAACTTTT	TGAGAAGAGT	GGGAAAAAAC	TCATAAAATA	A	351

(2) INFORMATION FOR SEQ ID NO:1696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1696:

GCTTGTGAAA	GCTTGGCTGA	CAGTGGTTAT	CAAGGGCTCA	TGAAGATATA	TCTTCAAGCA	60
CAAACCTCCAC	GTAAATCCAG	CAAACCTCAAG	CCGCTAACAG	CTGAAGATAA	AGCCTATAAC	120
CATGCGCTAT	CTAAGGGGAG	AAGCAAGGTT	GAGAATATTT	TTGCCAAAGT	AAAAACGTTT	180
AAAATGTTTT	CAACAACCTA	TCGAAATCAT	CGTAAACGCT	TCGGATTACG	AATGAATTTG	240
ATTGCTGATA	TTATCAATCA	TGAACTAGGA	TTCTAG			276

(2) INFORMATION FOR SEQ ID NO:1697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1697:

AAGTGTGAAA	GAATGAGAGC	AGTTGATTTA	ATACAAAAAA	AACGAGACGG	TCAAGAACTG	60
ACTTCAAGTG	AAATTGAATG	GCTGGTAGAA	GGCTATGTGT	CAGGAACTGT	TCCTGATTAT	120
CAGATGTCTG	CCTTTGCTAT	GGCTGTTTAT	TTTAAAGGAA	TGACGACTCG	AGAAATCTCT	180
GATTTAACGA	TGAATATGGT	TAAGACTGGG	CAAGAGTTTG	ACCTGTCAGC	CATTGATGGT	240
GTGAAAGTTG	ACAAGCATTC	TACTGGTGGT	GTCGGCGATA	AGGTAACCTT	GATTTTAGCT	300
CCTCTTGTG	CTAGCTTCGG	TGTGCCCTGA	GCAAAAATGA	GTGGTCGTGG	TCTTGGCCAT	360
ACAGGCGGAA	CAATTGATAA	ATTGGAGTCC	ATTAAGGGCT	ATCAAGTAGA	ACGTAGTCAA	420
GAGGATTTTA	TTTCGTAGGT	TCAGGATATT	GGAGTATCTG	TCATTGGGCA	ATCAGACCAG	480
CTGGTCAAAG	CAGATAAGCT	TCTCTATGCC	CTTCGTGATG	TGACCGCAAC	TGTCGACACG	540
ATTCCTTTGA	TTGCGAGTTC	GGTGATGAGC	AAGAAAATTG	CGGCAGGGGC	GGATGCTATT	600
TTGCTAGACG	TGACTGTCGG	TGAGGGTGCC	TTCATGAAGA	CGGTTGATGA	GGCGCGTGAG	660
TTGGCTCAAA	CTATGGTAGA	TCTTGGTAAG	GTTGTTGGAC	GGAAGACAGT	AGCAGTGATT	720
ACGGATATGA	GCCAGCCTTT	GGGACGAGCG	ATTGGAAATC	GTCTGGAAAT	CCTTGAAGCA	780
TTGGAGATTT	TGCAAGGTCA	AGGACGTCAG	GATATTACCC	ACTTTATTTG	TGAATTGGCT	840
CAAATTATGC	TTGGTTTGGC	AAATGTTAAC	AAGACTGTTG	AAGAAGTTCA	CCAACATCTT	900
GAAAATGGTC	AAGCACTGGC	TAAGTTTGAG	GAAATGGTGC	AAGCCCAAGG	TGGAGACTTG	960
GAAGACCTCT	ATCGTCCTGT	AAATGTAGCT	CATGTGGTGG	AAATCCCTGC	TCAGGAAACG	1020
GGTGTCATTT	CAGCTCTTCC	AGCTATGGAC	TTTGGTCTTT	ATGCCATGAG	GC'TGGGTGCT	1080
GGTCGTGCAG	TTAAGTCTGA	TGTCTTGGAC	TATGAAACAG	GAATTGTTTT	TGAAAAGAAG	1140
ATTGGAGACT	CCGTTCAAAA	GGGTGAAATT	GTTGCAAAAG	TATACACAAA	TGAAAAAATT	1200
CCACCTCAAC	TAGTTACAGA	TTTCCAAAAA	TGTGTTAAAA	TAAGTGATGA	AGTGAAAAAA	1260
ATCCGTGAAA	TTGTAGAAAT	CATCTCCTAA				1290

(2) INFORMATION FOR SEQ ID NO:1698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1698:

GAGACCGAAA	GAATGAAATT	TGTTGGACTT	GTTGGATCAA	ACTACGATCA	ATCATATAAC	60
CGCAAACCTCT	TGGAATTTAT	CCGTGCAAT	TTCAAATTCA	AATTTGAATT	AGAAGTACTT	120
GAAATCGACG	AAGTTCCAAT	GTTTAACCAA	GACGAAAAAT	GGGACGAAAG	CTTCCAATTG	180
CGTTTCTTGT	ATAACAAGAT	TACACGTGCT	GATGGTGTCA	TTATCGCCAC	TCCTGAGCAC	240
AACCACACTA	TCTCAGCTTC	ACTCAAATCT	GTACTTGAAT	GGCTTTCATA	CGAAGTTCAT	300
CCATTTGAAA	ACAAGCCTGT	TATGATTGTG	GGTGATCAT	ACTATGACCA	AGGAACATCA	360
CGTGCTCAAG	TTCACCTTCG	TAAAATCCTT	GATGCTCCAG	GTGTTAATGC	CTACACGCTT	420
CCAGGTAACG	AATTCCTTCT	TGGTAAAGCT	AAGGAAGCTT	TTGATAACAA	CGGAAATATC	480
ACCAACGAAG	GCACTGTTAA	ATTCCTTGAA	ACTTGCTTAG	ATAACTTTGT	TAAATACGTA	540
GGAGTCGTTT	CGAAATTGAA	AAAACCAAAA	CCAATCGAAT	CAGAAGACTT	GGATTGTGGA	600
AAACCAATCG	CTACAACCAT	CACAGAAGTT	GACCCTGACG	ATCCAGAATG	GGTAGAAAAA	660

GTTGCAGCAA	TCACTGGTGC	TGTTTCTGGT	GATACCTATG	TCAAATTGGA	CCACGGTATC	720
CTAACAGTTA	ACCAAATTGA	TATGTTCTTG	AAAGCTATGC	CATTTGAATT	GACATACGCT	780
GACGACAACA	ACCAATTCCT	CTACTACAAAC	AACGCTCACC	AAGATCCAGA	CACTATGTTC	840
GCTAAACGTG	TACCACCTCA	ATCAGGTAGC	CGTATGTCGA	CTGTTTCATGG	TTCTCTTCCA	900
CCAGCACGTA	TGAAGAACGT	AGAGTGGGTT	ATCGGAACAC	TTCGCAACGG	AAACCAAGAA	960
TACGTCCGTA	CGATCGTTCC	AGGTTCTCCT	GCAGGTGTTA	TCAACACTCA	CAACTACCAA	1020
GCAATGTACT	ATCCTGATGG	ATCATACGCT	GGTATCAATG	AAATCGTCTT	TAACTTCCAA	1080
CCATGGCTTG	ACTGGTACCT	AAAAGAGACT	GGTCAACGTT	TGGTGGGTGG	TAGCGGACCA	1140
TTTGCTCCTG	CTGCCGAGG	TCATGGAGAC	GCCGATGCTA	CTTCTGGCGC	TTCTGATTCA	1200
GGGGATGTTG	GAGGCCACGG	TGGTGACGCA	GACGCTACAG	CCGGTGCAAG	TTACTAA	1257

(2) INFORMATION FOR SEQ ID NO:1699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1053 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1699:

AACTTAGAAA	GAATGAACAA	ATATATGAAT	ACAGCTGATT	TTGATTTCCA	CTTGCCAGAG	60
GAATTGATTG	CCCAAACGCC	CCTTGAAAAA	CGTGATGCCT	CCAAACTCCT	CATCGTCAAC	120
CGTGAGACAG	GAGAAATGCA	AGATAAACAT	TTCCACTCTA	TTATTGATAT	GCTGGAACCT	180
GGTGATGCCC	TTGTCATGAA	CGACACCCGA	GTTCTCCCTG	CCCGCCTCTA	TGGTCAAAAA	240
GTGGAGACAG	GAGGTCATGT	GGAACTTCTC	CTCCTTAAGA	ACACTAGTGG	AGACGAGTGG	300
GAAGTTCTGG	CTAAACCTGC	CAAACGCCTC	AAGGTCGGTA	CTCGTATCAG	CTTTGGTGAT	360
GGCCGCCTCA	GCGCTGTCGT	TACAGAAGAA	TTGACCCACG	GGGGACGCAT	TGTCCGCTTT	420
GAATACCAAG	GAATTTTCCT	AGAAGTCTTG	GAAAGTCTGG	GAGAAATGCC	TCTGCCACCT	480
TATATCCACG	AAAAATTAGA	TGACCGTGAA	CGTTATCAAA	CCGTCTACGC	CAAGGAAAGC	540
GGCTCTGCTG	CAGCACCGAC	TGCTGGTCTT	CAC TTCACCA	AAGAACTGCT	GGCAGAAATC	600
CAAGCTAAGG	GTGTTTCATCT	AGTCTATCTG	ACTCTCCATG	TCGGACTCGG	AACCTTTAGA	660
CCTGTTTCTG	TGGATAATCT	GGACGAACAC	GAAATGCACT	CAGAGTTCTA	TCAACTTTCT	720
GAGGAAGCTG	CTGCCACCCT	TCGCTCTGTC	AAAGAAAATG	GTGGTTCGTG	CATCGCTGTC	780
GGAACCACTT	CTATCCGTAC	CTTGGAACCT	ATTGGTTCCA	AGTTTGATGG	GCAAATCCAA	840
GCAGATTCTG	GTTGGACCAA	TATCTTTATC	AAACCTGGGT	ATGAGTGGAA	GGTTGTGGAT	900
GCCTTCTCAA	CCAACTTCCA	TCTGCCAAAA	TCAACTCTGG	TCATGTTGGT	TTCTGCCTTT	960
GCAGGCCGTG	AATTAGTCTT	AGATGCCTAC	CACCATGCCA	TCCAAGAACA	CTACCGCTTC	1020
TTCAGTTTTG	GTGACGCCAT	GTTTATTTAT	TGA			1053

(2) INFORMATION FOR SEQ ID NO:1700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1700:

TCTCTAGAAA	GAGGTCATTC	TATGGGAATT	GAAGAACAAC	TTGGCGAAAT	CGTTATCGCC	60
CCACGTGTAC	TTGAAAAAAT	CATTGCTATC	GCTACTGCAA	AGGTAGAGGG	TGTTCACTCT	120
TTTTCAAACA	GATCAGTGTC	TGATACCCTT	TCAAAACTTT	CACTCGGCCG	TGGCATTAT	180
CTTAAAAACG	TGGACGAAGA	ACTCACAGCA	GATATCTATC	TCTACCTTGA	GTACGGAGTA	240
AAAGTTCCTA	AGGTAGCGGT	TGCTATCCAG	AAAGCTGTCA	AAGATGCCGT	CCGTAATATG	300
GCTGATGTAG	AACTCGCTGC	TATCAATATT	CACGTTGCAG	GTATCGTCCC	AGATAAAACA	360
CCAAAACCAG	AATTGAAAGA	TCTATTTGAC	GAGGACTTCC	TCAATGACTA	G	411

(2) INFORMATION FOR SEQ ID NO:1701:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1701:

TCGCTAGAAA	GATATCTCTT	GTCCCAGTAC	AAAGGGATTG	AGGTTCAAAA	GATTCATATC	60
AAGGATTTGG	TCAAGGAAGG	CAAAAATTTT	TATGAAATGG	ACCATCCCTA	TGTCGCTTTT	120
TTGCCGACCT	ATCTCGAAGG	TGGGAATGGC	GTGGATAACG	GAGATGTTGA	GATTTTGTACG	180
ACACCGGTGG	GAGATTTTAT	TGCCTATGGT	AACAATGCTA	GTAAGTGTTT	TGGTGTGGTT	240
GGGTCAGGAA	ATCGTAACTT	TAATAACCAA	TACTGCCATA	CAGCCAAGCA	ATACAGTCAA	300
CGCTTTGGCT	TCCCTGTATT	GGCTGACTTT	GAAATGCGAG	GCATGCTGGA	AGATATCAAA	360
CATGTCGCAG	CTATTATCGC	AGATTTGTAT	GAGTTGGAAA	AGGAGAATTA	A	411

(2) INFORMATION FOR SEQ ID NO:1702:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1041 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1041
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1702:

AAAATAGAAA	GAGGAAATAA	TAAAATGACA	AATTCAGTAT	TCCAAGGACG	CAGCTTCTTA	60
GCAGAAAAAG	ACTTTACCCG	TGCAGAGTTA	GAATACCTTA	TTGGTCTTTC	AGCTCACTTG	120
AAAGATTTGA	AAAAACGCAA	TATTCAACAC	CACTACCTTG	CTGGCAAGAA	TATCGCTCTC	180
CTATTTGAAA	AAACATCTAC	TCGTACTCGT	GCAGCCTTTA	CAACTGCGGC	TATCGACCTT	240
GGTGCTCACC	CAGAATACCT	CGGAGCAAAT	GATATTCAGT	TGGGTAAAAA	AGAATCTACT	300
GAAGATACTG	CTAAAGTATT	GGGACGTATG	TTTGACGGGA	TTGAATTCCG	CGGATTCAGC	360
CAACGTATGG	TTGAAGAATT	GGCAGAAATC	TCAGGCGTTC	CAGTATGGAA	CGGTCTAACT	420
GACGAATGGC	ACCCAACTCA	AATGCTCGCT	GACTACTTGA	CTGTTCAAGA	AAACTTCGGT	480
CGCTTGGAAG	GCTTGACATT	GGTATACTGT	GGTGATGGAC	GTAACAACGT	TGCCAACAGC	540
TTGCTCGTAA	CAGGTGCTAT	CCTTGGTGTC	AATGTTTACA	TCTTCTCACC	AAAAGAACTC	600
TTCCCAGAAA	AAGAAATCGT	TGAATTGGCA	GAAGGATTTG	CTAAAGAAAAG	TGGCGCACAT	660
GTTCTCATCA	CTGAAGATGC	TGATGAAGCA	GTTAAAGATG	CAGACGTTCT	TTACACAGAC	720
GTTTGGGTAT	CAATGGGTGA	AGAAGACAAA	TTCGCAGAAC	GTGTAGCTCT	TCTTAAACCT	780
TACCAAGTCA	ATATGGACTT	AGTTAAAAAA	GCAGGCAATG	AAAACTTGAT	CTTCCTACAC	840
TGCTTGCCAG	CATTCCACGA	TACTCACACT	GTTTATGGTA	AAGACGTTGC	TGAAAAATTT	900
GGTGTAGAAG	AAATGGAAGT	AACAGACGAA	GTCTTCCGCA	GCAAGTACGC	TCGCCACTTC	960
GATCAAGCAG	AAAACCGTAT	GCACACTATC	AAAGCTGTTA	TGGCTGCGAC	ACTTGGTAAAC	1020
CTTTATATTC	CTAAAGTATA	A				1041

(2) INFORMATION FOR SEQ ID NO:1703:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 555 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1703:

ATTGTAGAAA	GTTGGTTAGT	TATGAAGCTT	CCAAAAGAAG	GCGACTTTAT	TACAATTCAA	60
AGTTATAAGC	ATGATGGGAG	TCTCCACCGA	ACTTGGCGGG	ACACCATGGT	ACTAAAAACA	120
ACAGAAAACG	CCATTATTGG	TGTCAACGAT	CATACACTTG	TTACCGAAAAG	TGATGGTCGT	180
CGTTGGGTCA	CTCGAGAACC	GGCTATTGTT	TACTTTCACA	AGAAATATTG	GTTTAATATC	240
ATTGCCATGA	TTCGTGATAA	TGGAACCTCT	TACTATTGCA	ATATGGCTAG	CCCCTACTAT	300
CTGGATGAAG	AAGCACTGAA	GTATATTGAT	TACGATTTGG	ATGTTAAAAT	TTTTACAGAT	360
GGGGAAAAAC	GTCTCTTGGA	CGTTGAAGAG	TACGAGCGTC	ACAAACGCAA	AATGAATTAT	420
TCTGATGACT	TGGACTATAT	TTTAAAAGAA	CATGTCAAAA	TTCTTGTTGA	TTGGATTAAAC	480
AATGGACGTG	GTCCTTTCTC	AGAAGCCTAT	GTAAACATTT	GGTACAAGCG	CTATGTAGAA	540
CTAAAGAATC	GGTAA					555

(2) INFORMATION FOR SEQ ID NO:1704:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 717 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1704:

ATGGAAGAAA	GTATTAATCC	AATCATCTCT	ATTGGTCCTG	TTATCTTCAA	TCTGACTATG	60
TTAGCCATGA	CTTTGTTGAT	TGTGGGAGTT	ATTTTTGTCT	TTATTTATTG	GGCAAGCCGC	120
AATATGACCT	TGAAACCCAA	AGGAAAGCAA	AATGTACTTG	AGTATGTCTA	TGACTTTGTT	180
ATTGGATTTA	CAGAACCTAA	CATTGGTTTCG	CGCTACATGA	AAGATTACTC	ACTCTTTTTTC	240
CTTTGTTTAT	TCCTTTTCAT	GGTGATTGCC	AATAACCTTG	GCTTAATGAC	AAAGCTTCAA	300
ACGATCGATG	GGACTAACTG	GTGGAGTTCG	CCAACCGCTA	ATTTACCGTA	TGACTTAACC	360
TTATCTTTTC	TTGTCATTTT	GTTGACACAT	ATAGAAAGCG	TTCGTCGTCG	TGGATTTAAA	420
AAAAGTATAA	AATCTTTTAT	GAGTCCTGTT	TTTGTCCATC	CGATGAATAT	CTTGGAAGAA	480
TTTACAAACT	TCTTATCTTT	GGCTTTGCGG	ATTTTTGGGA	ATATCTTTGC	AGGAGAGGTC	540
ATGACGAGTT	TGTTACTTCT	TCTTTCCAC	CAAGCTATTT	ATTGGTATCC	AGTAGCCTTT	600
GGAGCTAATT	TGGCTTGGAC	TGCATTTTCT	GTCCTTTATTT	CCTGCATCCA	AGCTTATGTT	660
TTTACTCTTT	TGACATCTGT	GTATTTAGGG	AATAAGATTA	ATATTGAAGA	AGAATAG	717

(2) INFORMATION FOR SEQ ID NO:1705:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 672 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...672
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1705:

CAAAGAGAAA	GAAC	TTTTGG	AAGT	CTAAAA	ATAAAC	CAGAA	AAACT	CAGTT	GGCATT	TGCTG	60
GCTGAGTTTT	ATTC	GAAAGA	AGGA	AATATG	AATACA	AAATC	TTGCA	AGTTT	TATCGT	TGGA	120
CTGATCATCG	ATGA	AAATGA	CCGT	TTTTAC	TTTGTG	CAAA	AGGAT	GGTCA	AACCTA	TGCT	180
CTTGCTAAGG	AAGAG	GGCCA	ACATA	CAGTA	GGGGAT	ACGG	TCAA	AGGTTT	TGCATA	CACG	240
GATATGAAGC	AAAA	ACTCCG	CCTG	ACAACC	TTAGA	AAGTGA	CTGCC	ACTCA	GGACCA	ATTT	300
GGTTGGGGAC	GTGT	CACAGA	GGTT	CGTAAG	GACTT	GGGTG	TCTTT	TGTGA	TACAGG	CCCTT	360
CCTGACAAGG	AAAT	CGTTGT	GTCAC	TGAT	ATTCT	CCCTG	AGCTC	AAGGA	ACTCT	GTCTT	420
AAGAAGGGCG	ACCA	ATCTAC	ATCCG	TCTTG	AAGTG	GATAA	GAAAG	ACCGT	ATTTG	GGGCC	480
TCTTGCTTA	TCAAG	AAGAC	TTCCA	ACGTC	TTGCT	CGTCC	TGCTT	TACAAC	AACAT	GCAGA	540
ACCAAACTG	GCCAG	CCATT	GTTTA	CCGTC	TCAAG	CTGTC	AGGAA	CTTTT	GTTTAC	CTAC	600
CAGAAAATAA	TATG	CTTGGT	TTTAT	TTCATC	CTAGC	GAGCG	TTACG	CAGAG	CCACG	TTTGG	660
GGCAAGTATT	AG										672

(2) INFORMATION FOR SEQ ID NO:1706:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2493 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2493
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1706:

AGTGAGGAAA	GAATGAAAAT	CAATAAAAAA	TATCTAGCAG	G TTCAGTGGC	AGTCCTTGCC	60
CTAAGTGTTT	GTTCCATATGA	ACTTGGTCGT	CACCAAGCTG	GTCAGGTTAA	GAAAGAGTCT	120
AATCGAGTTT	CTTATATAGA	TGGTGATCAG	GCTGGTCAAA	AGGCAGAAAA	TTTGACACCA	180
GATGAAGTCA	GTAAGAGAGA	GGGGATCAAC	GCCGAACAAA	TTGTTATCAA	GATTACGGAT	240
CAAGGTTATG	TGACCTCTCA	TGGAGACCAT	TATCATTA CT	ATAATGGCAA	GGTTCCTTAT	300
GATGCCATCA	TCAGTGAAGA	ACTTCTCATG	AAAGATCCGA	ATTATCAGTT	GAAGGATTCA	360
GACATTGTCA	ATGAAATCAA	GGGTGGCTAT	GTGATTAAGG	TAGACGGA AA	ATACTATGTT	420
TACCTTAAAG	ATGCGGCCCA	TGCGGACAAT	ATTTCGGACAA	AAGAAGAGAT	TAAACGTCAG	480
AAGCAGGAAC	ACAGTCATAA	TCATAACTCA	AGAGCAGATA	ATGCTGTTGC	TGCAGCCAGA	540
GCCCAAGGAC	GTTATACAAC	GGATGATGGG	TATATCTTCA	ATGCATCTGA	TATCATTGAG	600
GACACGGGTG	ATGCTTATAT	CGTTCCCTCAC	GGCGACCATT	ACCATTACAT	TCCTAAGAAT	660
GAGTTATCAG	CTAGCGAGTT	AGCTGCTGCA	GAAGCCTATT	GGAATGGGAA	GCAGGGATCT	720
CGTCCTTCTT	CAAGTTCTAG	TTATAATGCA	AATCCAGTTC	AACCAAGATT	GTCAGAGAAC	780
CACAATCTGA	CTGTCACTCC	AACTTATCAT	CAAAATCAAG	GGGAAAACAT	TTCAAGCCTT	840
TTACGTGAAT	TGTATGCTAA	ACCCTTATCA	GAACGCCATG	TAGAATCTGA	TGGCCTTATT	900
TTCGACCCAG	CGCAAATCAC	AAGTCGAACC	GCCAGAGGTG	TAGCTGTCCC	TCATGGTAAC	960
CATTACCAC T	TTATCCCTTA	TGAACAAATG	TCTGAATTGG	AAAAACGAAT	TGCTCGTATT	1020
ATTCCCCTTC	GTTATCGTTC	AAACCATTGG	GTACCAGATT	CAAGACCAGA	ACAACCAAGT	1080
CCACAATCGA	CTCCGGAACC	TAGTCCAAGT	CTGCAACCTG	CACCAAATCC	TCAACCAGCT	1140
CCAAGCAATC	CAATTGATGA	GAAATTGGTC	AAAGAAGCTG	TTCGAAAAGT	AGGCGATGGT	1200
TATGTCTTTT	AGGAGAATGG	AGTTTCTCGT	TATATCCCAG	CCAAGGATCT	TTCAGCAGAA	1260
ACAGCAGCAG	GCATTGATAG	CAAACTGGCC	AAGCAGGAAA	GTTTATCTCA	TAAGCTAGGA	1320
GCTAAGAAAA	CTGACCTCCC	ATCTAGTGAT	CGAGAAATTT	ACAATAAGGC	TTATGACTTA	1380
CTAGCAAGAA	TTCACCAAGA	TTTACTTGAT	AATAAAGGTC	GACAAAGTTG	TTTTGAGGTT	1440
TTGGATAACC	TGTTGGAACG	ACTCAAGGAT	GTCTCAAGTG	ATAAAGTCAA	GTTAGTGGAT	1500
GATATTCTTG	CCTTCTTAGC	TCCGATTCTG	CATCCAGAAC	GTTTAGGAAA	ACCAAATGCG	1560
CAAATTACCT	ACACTGATGA	TGAGATTCAA	G TAGCCAAGT	TGGCAGGCAA	GTACACAACA	1620
GAAGACGGTT	ATATCTTTGA	TCCTCGTGAT	ATAACCAGTG	ATGAGGGGGA	TGCCTATGTA	1680
ACTCCACATA	TGACCCATAG	CCACTGGATT	AAAAAAGATA	GTTTGTCTGA	AGCTGAGAGA	1740
GCGGCAGCCC	AGGCTTATGC	TAAAGAGAAA	GGTTTGACCC	CTCCTTCGAC	AGACCATCAG	1800
GATTTCAGGAA	ATACTGAGGC	AAAAGGAGCA	GAAGCTATCT	ACAACCGCGT	GAAAGCAGCT	1860
AAGAAGGTGC	CACTTGATCG	TATGCCTTAC	AATCTTCAAT	ATACTGTAGA	AGTCAAAAAC	1920
GGTAGTTTAA	TCATACCTCA	TTATGACCAT	TACCATAACA	TCAAATTTGA	GTGGTTTGAC	1980
GAAGGCCTTT	ATGAGGCACC	TAAGGGGTAT	ACTCTTGAGG	ATCTTTTGGC	GACTGTCAAG	2040
TACTATGTCT	AACATCCAAA	CGAACGTCCG	CATTTCAGATA	ATGGTTTTTG	TAACGCTAGC	2100
GACCATGTTT	AAAGAAAACAA	AAATGGTCAA	GCTGATACCA	ATCAAACGGA	AAAACCAAGC	2160
GAGGAGAAAAC	CTCAGACAGA	AAAACCTGAG	GAAGAAACCC	CTCGAGAAGA	GAAACCACAA	2220
AGCGAGAAAAC	CAGAGTCTCC	AAAACCAACA	GAGGAACCAG	AAGAAGAATC	ACCAGAGGAA	2280
TCAGAAGAAC	CTCAGGTCTGA	GA CTGAAAAG	GTTGAAGAAA	AACTGAGAGA	GGCTGAAGAT	2340
TTACTTGGAA	AAATCCAGGA	TCCAATTATC	AAGTCCAATG	CCAAAGAGAC	TCTCACAGGA	2400
TTAAAAAATA	ATTTACTATT	TGGCACCCAG	GACAACAATA	CTATTATGGC	AGAAGCTGAA	2460
AAACTATTGG	CTTTATTAAA	GGAGAGTAAG	TAA			2493

(2) INFORMATION FOR SEQ ID NO:1707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 744 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1707:

AATCTTAGAA	GATGGGTTCA	CACTGTTGTC	TTGACTGGGG	ATATTCCTGC	CATGTGGCTT	60
CGGGATTCTGA	CAGCCCAACT	CAGACCCTAC	CTTCATGTAG	CTAAAAGAGA	TGCCCTCCTG	120
CGTCAGACCA	TTGCAGGTTT	GGTCAAACGT	CAGATGACCT	TGGTACTCAA	GGATCCCCTAT	180
GCTAACTCCT	TCAACATTGA	GGAGAACTGG	AAAGGGCACC	ACGAGACTGA	TCACACAGAC	240
CTTAACGGCT	GGATCTGGGA	GCGCAAGTAT	GAGGTGGATT	CACTTTGCTA	TCCTTTGCAG	300
TTGGCTTATC	TCCTCTGGAA	AGAGACTGGC	GAGACTAGTC	AGTTTGATGA	GATTTTTGTC	360
GTAGCGACTA	AGGAAATTCT	CCATCTATGG	ACAGTTGAAC	AAGACCACAA	GAACTCTCCT	420
TATCGTTTTG	TCCGAGATAC	GGACCGTAAG	GAAGACACCT	TGGTAAATGA	TGGCTTTGGA	480
CCTGACTTTG	CAGTGACAGG	TATGACTTGG	TCAGCCTTTC	GTCCGAGTGA	TGACTGTTGC	540
CAGTATAGTT	ACTTGATTCC	GTCAAATATG	TTTGCTGTAG	TAGTCTTGGG	TTATGTGCAA	600
GAAATCTTCG	CAGCATTAAG	CCTAGCTGAT	AGCCAGAGTG	TTATTGCTGA	TGCCAAGCGT	660
CTTCAGGATG	AAATCAAGAA	GGAATCGAAA	ACTACGCTTA	CACCACCAAC	AGCAAGGGCG	720
AAAAGATTTA	CGCTTTTGAA	GTAG				744

(2) INFORMATION FOR SEQ ID NO:1708:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 855 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1708:

ATTATCAGAA	GACCAAGTTG	TCGGAACACC	GTTTCGACCCA	GCGAAACACT	GGACTGCCTA	60
GGAACCTGTC	AGCATCTGAT	AGAAGGAAAT	AAGATGGCAA	AAAATGTAGT	GATTACGGGA	120
GCAACCTCAG	GAATCGGTGA	AGCGATTGCG	CGTGCTTATC	TGGAGCAGGG	TGAGGATGTC	180
GTTCTAACAG	GACGACGGAT	AGACAGATTA	GAAATCCTCA	AGTCGGAGTT	TGCAGTAAGC	240
TTTCCAAATC	AAACCGTCTG	GACTTTTCCA	CTAGATGTGA	CGGATATGGT	CATGGTGAAG	300
ACTGTTTGCT	CTGATATTCT	AGAAACGATA	GGGAGGATTG	ATATCTTGGT	CAACAACGCC	360
GGACTGGCTC	TTGACTTGGC	TCCCTATCAA	GACTATGAGG	AGTTGGATAT	GTTGACCATG	420
TTGGATACCA	ATGTTAAAGG	TCTGATGGCG	GTTACTCGCT	GTTTCTTGCC	AGCAATGATA	480
AAAGTCAATC	AAGGTCACGT	TATCAATATG	GGGTCAACCG	CAGGAATCTA	CGCCTATGCT	540
GGTGCCGCTG	TTTACTCAGC	TACCAAGGCA	GCGGTAAAGA	CCTTTTCGGA	TGGAATGCGA	600

ATTGATACCA	TCGCAACGGA	TATCAAGGTG	ACAACCATTC	AGCCTGGGAT	TGTCGAAACA	660
GATTTCTCAA	CTGTTCGTTT	TCATGGTGAT	AAAGAGCGGG	CTGCGTCCGT	TTACCAAGGA	720
ATAGAAGCCT	TGCAAGCTCA	GGATATTGCA	GACACAGTAG	TCTATGTGAC	CAGTCAGCCT	780
CGCCGTGTTT	AGATTACAGA	TATGACCATT	ATGGCCAATC	AACAGGCGAC	AGGTTTCATG	840
ATTCATAAAA	AATAA					855

(2) INFORMATION FOR SEQ ID NO:1709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1709:

TATAACAGAA	GAATAAACCA	TCACCATCTC	CGGACGGACT	ATGTATCTGG	GGATGGTGAT	60
TTTTATCTGG	AATCTAGTCT	TTGTGGTATA	ATAATTACTA	TGCAGAAAAA	ACCAACGTCA	120
GCCTATGTGC	ACATCCCATT	TTGTACCCAG	ATTTGTTATT	ATTGTGATTT	TTCAAAGGTC	180
TTCATCAAAA	ATCAGCCAGT	CGACAGCTAT	TTAGAGCATC	TGCTGGAAGA	GTTCCGTTCT	240
TATGATATTG	AAAAGTTGTC	AACCCTTTAT	ATCCGTGGTT	GGAACACGAC	AGCCCTGTCTG	300
GCTCCGCAAC	TGGACGTGTT	ACTGAATGGC	TTGACTATTA	ACTTGGATTT	GTCTGTCTTG	360
GAAGAGTTGA	CCATTGAAGC	CAATCCAGGC	GATTTGGATG	CGGATAAGAT	AGCTGTTTTTG	420
AAAAATTCGG	CTGTCAATCG	TGTTTCGCTA	GGTGTCCAGA	CCTTTGATGA	TAAGATGTTG	480
AAAAAGATTG	GGCGCAGTCA	TTTGGAGAAG	GATATTTATG	AAAATATCGA	TCGCCTGAAA	540
CTGGCTGGTT	TTGACAACAT	CTCCATTGAT	TTGATTTATG	CTCTGCCTGG	TCAGACCATG	600
GAGCAAGTAA	AGGAAAATGT	GGCTAAAGCC	ATTGGATTGG	ATATTCCCCA	CATGAGTTTG	660
TATAGTTTGA	TTTTAGAAAA	CCATACGGTC	TTTATGAACC	GGATGCGACG	TGGGAAATTG	720
CCTCTGCCTA	AGGAGGAACT	AGAAGCGGAG	ATGTTTGAGT	ACATCATTGC	AGAGCTGGAG	780
CGAGCGGGTT	TTGAGCATTA	TGAGATTTCT	AATTTCTCCA	AACCCGGCTT	TGAAAGTCGT	840
CATAATCTCA	TGTACTGGGA	CAATGCTGAA	TACTATGGTA	TTGGTGCAGG	GGCATCTGGT	900
TATGTCAATG	GAGTACGCTA	TAAAAATCAT	GGTCCCATTC	GTCATTATCT	CAGTGCGGTT	960
GAGGAAGGCA	ATGCTTGAT	TACAGAAGAT	CACCTGAGTC	AAAAGGAGCA	AATGGAAGAA	1020
GAAATGTTCT	TGGGACTCCG	CAAGAAATCC	GGGGTTTCCA	TGGCGCGATT	TGAGGAAAAA	1080
TTTGGACAGT	CTTTTGCTGG	ACTTTATGGA	GAAATGTGCA	GAGATTTGGT	TCAACAAGGC	1140
CTCATGCAGA	TTGAGGGTGA	CCACGTTTCG	ATGACAAAGA	GAGGTCTCTT	TTTGGGAGAT	1200
ACTGTAGCAG	AACGATTTAT	TTTGGAGTAG				1230

(2) INFORMATION FOR SEQ ID NO:1710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...507
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1710:

ACAGGCAGAA	GGCTTAATAT	CCCGCTCAAG	TCTATTGACC	AAGTAGACTT	TGTCGATGTG	60
ACGGTTGATG	GCGCGGATGA	AGTGGATAGT	CAGTTTAAATG	GAATCAAAGG	CGGTGGTGGT	120
GCCCTTCTCA	TGGAAAAGGT	GGTCGCAACA	CCATCAAAAG	AATACATTTG	GGTGGTGGAT	180
GAAAGCAAGC	TGGTCGAAAA	ACTAGGTGCT	TTTAAATTGC	CAGTAGAAGT	GGTTCAGTAT	240
GGTGACAGAGC	AAGTCTTTTCG	TCATTTTGAA	CGAGCTGGCT	ACAAACCAAG	TTCCCGTGAA	300
AAAGACGGCC	AACGTTTTGT	GACGGATATG	CAGAAATTTA	TCATTGACCT	CGCCTTGGAT	360
GTTATTGAAA	ATCCAATTGC	TTTTGGACAA	GAATTGGACC	ATGTCGTTGG	TGTTGTGGAG	420
CATGGTTTAT	TCAACCAAAT	GGTGGATAAG	GTAATCGTTG	CTGGACGAGA	TGGAGTTCAG	480
ATTTCAACTT	CAAAAAAAGG	AAAATAG				507

(2) INFORMATION FOR SEQ ID NO:1711:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 645 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...645
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1711:

GGACAAAGAA	GACCGAGTTA	TCACAAGGAA	AACAACATAC	ACCTTGGTAG	CAACTCCTGC	60
AAATGCGTAC	CAGAAGACGG	TGCAACAGTT	GACTATTACT	ACCGTGAGAA	TGTTGAGGAA	120
ACAGTGGTTC	CCAAAACAGC	AACCTCTACT	GAGACGAAGA	CTATAACGCG	TATCATTCAT	180
TACGTTGATA	AAGTTACGAA	CCAAAATGTA	AAAGAAGATG	TTGTTCAACC	TGTAACCTTA	240
AGCCGTACAA	AAACTGAGAA	CAAGGTCACG	GGAGTTGTAA	CCTACGGTGA	ATGGACAACA	300
GGAAACTGGG	ACGAGGTTGT	ATCTGGTAAG	ATTGACAAAGT	ACAAAGATCC	AGATATTCCA	360
ACAGTTGAAT	CACAAGAAAGT	TACGTCAGAC	TCTAGTGATA	AAGAAATAAC	GGTAAGGTAT	420

GACCGTTTAT CAACACCAGA TAAACCAACT CCAGACCCAG GTACTCCAAA AACTGAAACT	480
CCAGTGAAATC CAGACCCAGA AGTTCCGACT TATGAGACAG GTAAGAGAGA GGAATTGCCA	540
AACACAGGTA CAGAAGCTAA TGCTACCTTG GCTAGTGCTG GTATCATGAC CTTGTTAGCT	600
AGTCTAGGAT TAGGATTCTT CAAGAAAAAA GAAGATGAAA AATAA	645

(2) INFORMATION FOR SEQ ID NO:1712:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 204 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...204
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1712:

GTCAAAAGAA GTTGTAAGAA ATCTTTAAAA TTAAAAAAC GCATAGTATC AGGTGTTGAA	60
TGTACTGACC CCCAAAAGTT AGATTTTTTC TGTCTAACTT TTGGGGTGCA GTTCATAAGA	120
ACCTTGGTAA TATGCGTTTT ATTATGTAGA GACTTATACT CTTCGAAAAT CTCTTCAAAC	180
CACGTCAGCT TCACCTTGCC GTAG	204

(2) INFORMATION FOR SEQ ID NO:1713:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...318
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1713:

AATCGAAGAA	GTACTTGCAT	AATGAATGTG	TATGATGTTA	TCAAAAAACC	TGTCATCACT	60
GACAGCTCAA	TGGCTCAACT	TGAAGCAGGG	AAATATGTAT	TTGAAGTTGA	CACTCGTGCA	120
AACAACTTT	TGATCAAGCA	AGCTGTTGAA	GCTGCTATCG	AAGGTGTTAA	AGTTGCCAAT	180
GTTAACACAA	TCAACGTAAA	ACCAAAAGCT	AAACGTGTTG	GACGTTACAC	TGGTTTTACT	240
AACAAACTA	AAAAAGCTAT	CATCACACTT	ACAGCTGATT	CTAAAGCAAT	CGAGTTGTTT	300
GCTGCTGAAG	CTGAATAA					318

(2) INFORMATION FOR SEQ ID NO:1714:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 837 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1714:

AGGAGAAGAA	GAATGAGTTT	GCAAGAAACG	ATTATCCAAG	AGCTGGGTGT	CAAACCAGTG	60
ATTGATGCCC	AGGAAGAAAT	CCGTCGTTCT	ATTGATTTCT	TAAAAAGATA	TCTGAAAAAA	120
CATCCCTTCC	TAAAAACCTT	TGTACTAGGG	ATTTCTGGGG	GACAAGACTC	AACCTTGGCA	180
GGGCGTTTGG	CGCAATTAGC	TATGGAAGAA	CTGCGAGCTG	AAACGGGAGA	CGATAGCTAC	240
AAATTTATCG	CTGTCCGCCT	GCCATACGGA	GTGCAAGCTG	ATGAAGCAGA	TGCTCAAAAA	300
GCCCTAGCCT	TCATCCAGCC	AGATGTCAGC	TTGGTTGTGA	ATATCAAGGA	ATCAGCTGAT	360
GCCATGACAG	CTGCAGTTGA	AGCGACAGGT	AGTCCTGTTT	CAGACTTCAA	CAAGGGGAAT	420
ATCAAGGCAC	GTTGCCGTAT	GATTGCTCAG	TATGCCCTTG	CTGGTTCCCA	TAGCGGAGCG	480
GTCATTGGAA	CAGACCACGC	CGCGGAAAAT	ATCACAGGTT	TCTTTACCAA	GTTTGGTGAC	540
GGCGGTGCGG	ATATTCTCCC	TCTTTACCGC	CTCAATAAAC	GCCAAGGAAA	ACAGCTCTTG	600
CAGAAACTTG	GCGCAGAGCC	AGCCCTTTAT	GAAAAAATCC	CAACGGCAGA	CCTAGAAGAA	660
GATAAACCAG	GCCTAGCTGA	CGAAGTCGCA	CTTGGAGTCA	CCTACGCAGA	GATTGACGAC	720
TACCTAGAAG	GCAAAACAAT	CAGCCCAGAA	ACTCAAGCGA	CCATTGAAAA	CTGGTGGCAC	780
AAAGGCCAAC	ACAAACGCCA	CTTACCCATC	ACCGTATTTG	ATGACTTTTG	GGAGTAA	837

(2) INFORMATION FOR SEQ ID NO:1715:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 672 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1715:

AAAAGGAGAA	GTCTCATGGC	AGTTAAAGAT	TTTATGACCC	GCAAGGTAGT	TTATATTAGT	60
CCAGATACAA	CAGTATCTCA	TGCAGCAGAT	TTGATGAGAG	AGCAAGGTTT	GCACCGTCTG	120
CCTGTTATCG	AAAATGATCA	ATTAGTTGGT	TTGGTGACTG	AGGGAACCAT	TGCACAAGCA	180
AGTCCATCTA	AAGCAACAAG	TCTTTCTATA	TATGAGATGA	ATTATCTTCT	GAATAAGACA	240
AAAGTAAAAG	ATGTCATGAT	TCGCGATGTT	GTCACGTGCT	CAGGCTATGC	TAGTCTAGAA	300
GATGCAACTT	ATCTGATGTT	GAAAAATAAG	ATTGGTATTC	TCCCTGTCGT	AGATAACCAT	360
CAAGTATACG	GAGTTATTAC	TGACCGTGAT	GTTTTCCAAG	CCTTCTTGA	AATTGCAGGT	420
TATGGCGAAG	AAGGGATTCTG	TGTACGCTTT	GTTACAGAAG	ATGAAGTTGG	TGTTCTTGGA	480
AAAATTGTTT	CTTTGATTGT	AGAAGAAAAT	TTGAATATCT	CCCATACAGT	CAATATTCCG	540
CGTAAGGATG	GTAAGGTGAT	TATCGAAGTG	CAAATCGATG	AATCAATTGA	TTTACCAGCC	600
TTGAAAGAAA	AATTTGAAGC	AAATGGTATT	CAAGTGGAAG	AAATCGCTCG	CACTTCAGCA	660
AAAGTCTTGT	AA					672

(2) INFORMATION FOR SEQ ID NO:1716:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 573 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1716:

GAAGGGAGAA	GACCGATGAA	GCGTTCTTCT	CTTTTAGTTA	GAATGGTTAT	TTCCATCTTT	60
CTGGTCTTTC	TCATTCTCCT	AGCTCTGGTT	GGAACTTTCT	ACTATCAATC	AAGTTCTTCA	120
GCCATTGAGG	CCACCATTTGA	GGGCAACAGC	CAAACGACCA	TCAGCCAGAC	TAGCCACTTT	180
ATTCAGTCTT	ATATCAAAAA	ACTAGAAACC	ACTTCGACCG	GTTTGACCCA	GCAGACGGAT	240
GTTCTGGCCT	ATGCTGAGAA	TCCCAGTCAA	GACAAGGTCG	AGGGAATCCG	AGATTTGTTT	300
TTGACCATCT	TGAAGTCAGA	TAAGGACTTG	AAAAGTGTG	TGCTGGTGAC	CAAATCTGGT	360
CAGGTCAATTT	CTACAGATGA	CAGTGTGCAG	ATGAAAACCT	CCTCTGATAT	GATGGCTGAG	420
GATTGGTACC	AAAAGGCCAT	TCATCAGGGA	GCTATGCCCTG	TTTGTACTCC	AGCTCGTAAA	480
TCAGATAGTC	AGTGGGTGTC	TTCTGTCACT	CAAGAACTTG	TTGATGCAAA	GGGAGCCAAT	540
CTTGGTGTGC	TTCGTTTGGA	TATTTCTTCA	TGA			573

(2) INFORMATION FOR SEQ ID NO:1717:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1134 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1134
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1717:

AAC	TCT	GGAA	GCCTATCTCA	ATCAACTCCA	GTTGGGGCAG	CAGGCTTTGC	CTTCATTATC	60
AAT	GAAA	AACC	ATGAATTTGT	CTACCATCCT	CAACACACAG	TTTATAGTTC	GTCTAGCAAA	120
ATG	GAGG	GCTA	TGAAACCCCTA	CATCGATACA	GGTCAGGGTT	ATACTCCTGG	TCACAAATCC	180
TAC	GTCAG	TG	AAGAGAAGAT	TGCAGGAACT	GATTGGACGG	TACTTGGCGT	GTCATCATTG	240
GAAA	AGTTAG	ACCAGG	TTTCG	GAGTCAGCTC	TTGTGGACCT	TGCTTGGGGC	CAGTGT CACA	300
TCTCT	TCTTG	TCTGTCTCTG	CTTAGTGTGG	TTCAGTCTTA	AACGCTGGAT	TGCTCCTTTG		360
AAGG	ATTTGA	GAGAAACCAT	GTTGGAAATT	GCTTCTGGTG	CTCAAAATCT	TCGTGCCAAG		420
GAAG	TTGGTG	CCTATGAACT	GAGAGAAGTA	ACTCGCCAAT	TTAATGCCAT	GTTGGATCAG		480
ATTG	ATCAGT	TGATGGTAGC	TATTCGTAGC	CAGGAAGAAA	CGACCCGTCA	GTACCAACTT		540
CAAG	CCCTTT	CGAGCCAGAT	TAATCCACAT	TTCCTCTATA	ACACTTTGGA	CACCATCATC		600
TGGAT	TGGCTG	AATTTTCATGA	TAGTCAGCGA	GTGGTGCAGG	TGACCAAGTC	CTTGGCAACC		660
TATTT	CCGCT	TGGCGCTCAA	TCAAGGCAAG	GACTTGATTT	GTCTCTCTGA	CGAAATCAAT		720
CATGT	CCGCC	AGTATCTCTT	TATCCAGAAA	CAACGCTATG	GAGATAAGCT	GGAATACGAA		780
ATTA	ATGAAA	ATGTTACCTT	TGATAATTTA	GTCTTACCCA	AGCTGGTCCT	ACAACCCCTT		840
GTA	AAAAATG	CTCTTTACCA	TGGCATTAAAG	GAAAAGGAAG	GTCAGGGCCA	TATTAAACTT		900
TCTGT	CCAGA	AACAGGATTC	GGGATTGGTC	ATCCGTATTG	AGGATGATGG	CGTTGGCTTC		960
CAAG	ATGCTG	GTGATAGTAG	TCAAAGTCAA	CTCAAACGTG	GGGGAGTTGG	TCTTCAAAAT		1020
GTCG	ATCAAC	GGCTCAAAC	TCAATTTTGA	GCCAATTACC	AGATGAAGAT	TGATTCTAGA		1080
CCCC	AAAAAG	GGACGAAAGT	TGAAATATAT	ATAAATAGAA	TAGAAACTAG	CTAA		1134

(2) INFORMATION FOR SEQ ID NO:1718:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1718:

CAGTCTGGAA	GAAGTCCGTC	AGGAAGTAAA	AGAGTCTCTG	AGGTAAACTG	CAATCAATCT	60
GTTCTTGATT	TTTTATTAGT	TTGTAATATG	AATTTTAGGAG	AATTTTGGTA	CAATAAAATA	120
AATAAGAACA	GAGGAAGAAG	GTTAATGAAG	AAAGTAAGAT	TTATTTTTTT	AGCTCTGCTA	180
TTTTTCTTAG	CTAGTCCAGA	GGGTGCAATG	GCTAGTGATG	GTACTTGGCA	AGGAAAACAG	240
TATCTGAAAG	AAGATGGCAG	TCAAGCAGCG	AATGAGTGGG	TTTTTGATAC	TCATTATCAA	300
TCTTGGTTCT	ATATAAAAGC	AGATGCTAAC	TATGCTGAAA	ATGAATGGCT	AAAGCAAGGT	360
GACGACTATT	TTTACCTCAA	ATCTGGTGGC	TATATGGCCA	AATCAGAATG	GGTAGAAGAC	420
AAGGGAGCCT	TTTATTATCT	TGACCAAGAT	GGAAAGATGA	AAAGAAATGC	TTGGGTAGGA	480
ACTTCCTATG	TTGGTGCAAC	AGGTGCCAAA	GTAATAGAAG	ACTGGGTCTA	TGATTCTCAA	540
TACGATGCTT	GGTTTTATAT	CAAAGCAGAT	GGACAGCACG	CAGAGAAAGA	ATGGCTCCAA	600
ATTAAAGGGA	AGGACTATTA	TTTCAAATCC	GGTGGTTATC	TACTGACAAG	TCAGTGGATT	660
AATCAAGCTT	ATGTGAATGC	TAGTGGTGCC	AAAGTACAGC	AAGGTGGCT	TTTTGACAAA	720
CAATACCAAT	CTTGGTTTTA	CATCAAAGAA	AATGGAAACT	ATGCTGATAA	AGAATGGATT	780
TTCGAGAATG	GTCACTATTA	TTATCTAAAA	TCCGGTGGCT	ACATGGCAGC	CAATGAATGG	840
ATTTGGGATA	AGGAATCTTG	GTTTTATCTC	AAATTTGATG	GGAAAAATAGC	TGAAAAAGAA	900
TGGGTCTACG	ATTCTCATAG	TCAAGCTTGG	TACTACTTCA	AATCCGGTGG	CTACATGGCA	960
GCCAAATGAAT	GGATTTGGGA	TAAGGAATCT	TGGTTTTACC	TCAAGTTTGA	TGGCAAAATG	1020
GCTGAAAAAG	AATGGGTTTA	CGATTCTCAT	AGTCAAGCCT	GGTACTACTT	CAAATCCGGT	1080
GGTTACATGA	CAGCCAATGA	ATGGATTTGG	GATAAGGAAT	CTTGGTTTTA	CCTCAAATCT	1140
GATGGGAAAA	TAGCTGAAAA	AGAATGGGTC	TACGATTCTC	ATAGTCAAGC	TTGGTACTAC	1200
TTCAAATCCG	GTGGTTACAT	GACAGCCAAT	GAATGGATTT	GGGATAAGGA	ATCTTGGTTT	1260
TACCTCAAGT	CTGATGGCAA	AATGGCTGAA	AAAGAATGGG	TCTACGATTC	TCATAGTCAA	1320
GCCTGGTACT	ACTTCAAATC	TGGTGGCTAC	ATGGCGAAAA	ATGAGACAGT	AGATGGTTAT	1380
CAGCTTGGA	GCGATGGTAA	ATGGCTTGGA	GGAAAAGCTA	CAAATGAAAA	TGCTGCCTTAC	1440
TATCAAGTAG	TGCCGTGTAC	AGCCAATGTT	TATGATTTCAG	ATGGTGAAAA	GCCTTCCTAT	1500
ATATCGCAAG	GTAGTGTCGT	ATGGCTAGAT	AAGGATAGAA	AAAGTGATGA	CAAGCGCTTG	1560
GCTATTACTA	TTTCTGGTTT	GTCAGGCTAT	ATGAAAACAG	AAGATTTACA	AGCGCTAGAT	1620
GCTAGTAAGG	ACTTTATCCC	TTATTATGAG	AGTGATGGCC	ACCGTTTTTA	TCACTATGTG	1680
GCTCAGAATG	CTAGTATCCC	AGTAGCTTCT	CATCTTCTG	ATATGGCAGT	AGGCAAGAAA	1740
TATTATTCGG	CAGATGGCCT	GCATTTTGAT	GGTTTTAAGC	TTGAGAATCC	CTTCCTTTTC	1800
AAAGATTTAA	CAGAGGCTAC	AAACTACAGT	GCTGAAGAAT	TGGATAAGGT	ATTTAGTTTG	1860
CTAAACATTA	ACAATAGCCT	TTTGGAGAAC	AAGGGCGCTA	CTTTTAAGGA	AGCCGAAGAA	1920
CATTACCATA	TCAATGCTCT	TTATCTCCTT	GCCCATAGTG	CCCTAGAAAAG	TAAGTGGGGA	1980
AGAAGTAAAA	TTGCCAAAAG	TAAGAATAAT	TTCTTTGGCA	TTACAGCCTA	TGATACGACC	2040
CCTTACCTTT	CTGCTAAGAC	ATTTGATGAT	GTGGATAAGG	GAATTTTAGG	TGCAACCAAG	2100
TGGATTAAAG	AAAAATTATAT	CGATAGGGGA	AGAACTTTCC	TTGGAAACAA	GGCTTCTGGT	2160
ATGAATGTGG	AATATGCTTC	AGACCTTAT	TGGGGCGAAA	AAATTGCTAG	TGTGATGATG	2220
AAAATCAATG	AGAAGCTAGG	TGGCAAAGAT	TAG			2253

(2) INFORMATION FOR SEQ ID NO:1719:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 648 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1719:

CGTGTAGGAA	GTCTGTTTGT	TGAGGAGGAT	AATTTTATGG	AGTTTTTTGA	TAAATTTTCAT	60
GCCTTGTTT	TTGGATTTT	AGTACTAATA	ATTGTCATTA	CAGTTCCTTA	TACGATTAAC	120
CATGGGGATT	TTTTTCAAAA	TGAATCTGCA	TTGATTATTG	TAAGTCTTCT	TGTAACCTCG	180
CTGAGTGTTG	CTTATGCTAG	AAAGTTTGAA	ATGATTTCCTT	TTGGGATGTT	AAGCAAGAAA	240
CAACTTTTGC	TTTTCATTCG	AATCTTCTCT	CTAAGTGCTAC	TTGAGACGCT	GGTTTATATT	300
CATTTCTTCG	CTGTTTCTTC	TGGCTCAGGG	GTCCAACACT	TGGCGGAAGT	CAGCAGAGGA	360
ATTTCCCTGT	CTTTGATTTT	GACTACCTCA	GTTTTTGGCC	CCATCCAGGA	GGAACCTCATT	420
TTCAGAGGAC	TTCTTCAAGG	TGCGGTTTTT	GACAATTCTT	GGTTAGGGCT	TGTGCTAACT	480
TCCTCTCTCT	TTTCTTTCAT	GCATGGACCT	TCTAATGTCC	CTTCGTTTAT	TTTTTATCTA	540
CTTGGGGGCT	TGTTGCTGGG	CCTTGCTTAT	AAAAAGAGCC	AAAACCTATG	GGTTTCTACT	600
CTAGTCCACA	TGTTTTACAA	CAGTTGGCCA	CTCCTATATT	ATTTATAG		648

(2) INFORMATION FOR SEQ ID NO:1720:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 573 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION 1...573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1720:

TGGAGAGGAA	GAACGAGAAT	GGATACACAA	AAGATTGAAG	CGGCTGTAAA	AATGATTATC	60
GAGGCTGTAG	GAGAGGACGC	TAATCGCGAG	GGCTTGCAGG	AAACACCTGC	TCGTGTAGCC	120
CGTATGTATC	AAGAGATTTT	TTCAGGTCTT	GGTCAAACAG	CAGAGGAACA	TTTGTCAAAA	180
TCCTTTGAAA	TTATTGACGA	TAATATGGTG	GTAGAAAAGG	ATATCTTTTT	CCATACCATG	240
TGTGAACACC	ACTTCTTGCC	ATTTTATGGT	AGAGCGCACA	TTGCCTACAT	TCCAGATGGT	300
CGTGTGGCAG	GCTTGTCTAA	GCTAGCCCGT	ACGGTTGAAG	TTTATTCGAA	AAAACACAAA	360
ATTCAAGAAC	GTTTGAATAT	CGAAGTGGCC	GATGCCTTGA	TGGACTATCT	AGGTGCTAAA	420

GGAGCCTTTG	TTGTCATTGA	GGCGGAACAT	ATGTGTATGA	GTATGCGTGG	TGTTAGAAAA	480
CCAGGCACTG	CAACCTTGAC	GACAGTAGCT	CGTGGTCTAT	TTGAAACAGA	TAAGGACCTC	540
CGCGACCAAG	CTTATCGTTT	AATGGGGCTA	TAA			573

(2) INFORMATION FOR SEQ ID NO:1721:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 888 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...888
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1721:

GATGGAGGAA	GGTTCGATGC	GTGTGGATGC	CAACATCTCC	CTCGTCCTTA	TGGTCAAGAG	60
AAATTCGGTA	CCAAGACTGA	ATTGAAGAAC	CTCAACTCCT	TCTCAAACGT	TCGCAAGGGG	120
CTTGAATACG	AAGTCCAACG	CCAGGCTGAA	ATTCTTCGCT	CAGGTGGTCA	AATCCGCCAA	180
GAAACACGCC	GTTACGATGA	AGCTAACAAA	ACAACCATCC	TCATGCGTGT	CAAGGAAGGG	240
GCTGCTGACT	ACCGCTACTT	CCCAGAACCA	GACCTACCCC	TCTTTGAAAT	TTCTGACGAG	300
TGGATTGAGG	AAATGCGGAC	TGAGTTGCCA	GAGTTTCCAA	AAGAACGTCG	TGCGCGTTAT	360
GTATCTGACC	TTGGTTTATC	AGACTACGAT	GCTAGTCAGT	TGACTGCTAA	TAAAGTCACT	420
TCTGACTTCT	TTGAAAAAGC	TGTTGCCCTA	GGTGGTGATG	CCAAACAAGT	CTCTAACTGG	480
CTCCAAGGGG	AAGTCGCTCA	GTTCTTGAAT	GCTGAAGGTA	AAACACTGGA	ACAAATCGAA	540
TTGACACCAG	AAAACTTGGT	TGAAATGATT	ACCATCATCG	AAGACGGTAC	TATTTTCATCT	600
AAGATTGCCA	AGAAAGTCTT	TGTCCATCTA	GCTAAAAATG	GCGGTGGCGC	GCGTGAATAC	660
GTGGAAAAAG	CAGGTATGGT	TCAAATTTCA	GATCCAGCTA	TCTTGATCCC	AATCATCCAC	720
CAAGTCTTTG	CCGATAACGA	AGCTGCTGTT	GCCGACTTCA	AGTCAGGCAA	ACGTAACGCC	780
GACAAGGCCCT	TTACAGGATT	CCTTATGAAG	GCAACCAAAG	GCCAAGCCAA	CCCACAAGTT	840
CCCCTTAAAC	TACTTGCACA	GGAATTGGCG	AAGTTGAAAG	AAAACTAG		888

(2) INFORMATION FOR SEQ ID NO:1722:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 885 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1722:

ATAGGAGGAA	GCATGTTTTA	TTCTATCAAA	GAATTGGTCG	AGCAAGCAGA	TCTGGACTTT	60
CAAGGAAATG	TCGCAGAACT	CATGATTACA	ACAGAGTTTG	AATTGACCGG	TCGCGAACGT	120
GAAGAAGTCT	TCCTTCTCAT	GGAACGCAAT	CTGGAAGTTA	TGAAAGCCTC	TGTCCAACCT	180
GGCCTCAATG	AAAATAAAATC	TCGTAGTGGC	CTGACAGGTG	GAGATGCTGC	CAAATTGGAT	240
CACTACATCA	AAAACGAAAA	AACTTTATCA	GATTACACGA	TTCTCTCTGC	TGCCCCGAAAT	300
GCTATCGCAG	TCAATGAACA	CAATGCCAAA	ATGGGCTTGG	TCTGTGCCAC	TCCAACCGCT	360
GGAAGTGCTG	GCTGTCTCCC	TTCCGTTCTC	ACTGCTGCTA	TTGAAAAATT	AGACCTCAGC	420
CACGAGCAAC	AATTGGATTT	CCTCTTTGCT	GCTGGTGCCT	TTGGACTAGT	CATCGCAAAC	480
AATGCCTCCA	TCTCAGGTGC	TGAGGGTGGG	TGTCAAGCTG	AAGTTGGTTC	AGCCTCTGCT	540
ATGAGTGCTG	CCGCCTTGAC	TCTGGCTGCA	GGTGAACAC	CTTATCAGGC	CAGTCAAGCT	600
ATTGCCTTTG	TCATTAAAAA	TATGCTAGGC	CTCATCTGTG	ACCCTGTTGC	AGGTTTGGTC	660
GAAGTTCCTT	GTGTCAAACG	TAATGCCATG	GGAGCTAGCT	TTGCTTTTCAT	CGCAGCAGAC	720
ATGGCCTTGG	CAGGTATCGA	ATCTAAAATC	CCTGTGGATG	AAGTGATCGA	TGCCATGTAC	780
CAAGTAGGAG	CAAGCATGCC	AACTGCCTTT	CGTGAAACAG	CTGAAGGTGG	ACTCGCTACC	840
ACCCCTACTG	GTCTGCGCCT	CAAAAAAGAA	ATTTTCGGAG	AATAA		885

(2) INFORMATION FOR SEQ ID NO:1723:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1723:

CCATCTTTGA	GAAAAATCCT	CAGGCTCAGG	TTACTATTTT	CGGTGCCTTG	GGTGGCCGTA	60
TTGACCATAT	GTTGGCCAAT	GTCTTCTGCT	CTAGCAATCC	TAAGTTNNNN	NNNNNNNNNN	120
NNNNNNNNNN	NNNNNNNNNN	NCAAAAAAAN	NNNNNNNNNN	NGNNNNNNNN	NNNNNGNGGN	180
NNNNNGGGNG	NGGGNGNNG	GGGGGGGGGG	GGGGGGGGGG	GNGGGGGGGG	GGGGGGGGGG	240
GGGGGGGGGN	GGGNNGGGGG	GGGGGGGGGG	NGGGGGGGGG	GGGNGGGGNG	GGNGGGGGGG	300
GGGGGGGG						308

(2) INFORMATION FOR SEQ ID NO:1724:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1785 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1785
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1724:

CACGATTTGA	GATACGAGAT	GATTTCTATC	TCGAATGGAA	AATCATTTAA	GATTTTATCT	60
GGTGCCATTC	ATTATTTTAG	GGTTCCCTCCA	GAGGATTGGT	ATCATTCGCT	CTATAACTTG	120
AAGGCTCTTG	GTTTAAATAC	GGTAGAGACT	TATGTTGCTT	GGAATTTACA	CGAGCCTCGT	180
GAAGGTGAGT	TTCATTTTGA	AGGTGATCTG	GATTTAGAGA	AATTTCTCCA	AATAGCGCAG	240
GATTTGGGTC	TCTACGCAAT	TGTGCGTCCG	TCTCCATTTA	TCTGTGCGGA	ATGGGAATTC	300
GGTGGCTTAC	CAGCTTGGCT	CTTGACCAAG	AACATGCGAA	TTCGCTCATC	CGACCCAACA	360
TATATCGAGG	CAGTTGGTCG	CTACTATGAT	CAGTTATTGC	CAAGACTGGT	TCCTCGTTTG	420
TTGGACAATG	GTGGCAATAT	TCTCATGATG	CAGGTTGAAA	ATGAGTATGG	TTCTTACGGA	480
GAAGATAAGG	CTTACCTGAG	AGCGATTTCGA	CAGCTAATGG	AAGAGTGTGG	CGTAACCTGT	540
CCCCCTCTTTA	CATCAGATGG	TCCATGGCGA	GCTACTCTGA	AAGCTGGAAC	CTTAATTGAG	600
GAGGACCTCT	TTGTAACAGG	AACTTTTGGT	TCTAAGGCAC	CTTACAACCT	TTCGCAGAGG	660
CAGGAATTCT	TTGATGAACA	TGGTAAGAAA	TGGCCACTCA	TGTGTATGGA	GTTCTGGGAT	720
GGTTGGTTTA	ATCGCTGGAA	AGAACCATT	ATCACACGGG	ATCCTAAGGA	ATTGGCAGAT	780
GCAGTTCGAG	AGGTTTGGGA	ACAAGGCTCT	ATCAATCTTT	ACATGTTCCA	CGGTGGTACA	840
AACTTTGGTT	TCATGAATGG	TTGCTCAGCT	CGAGGAACTT	TGGACCTGCC	ACAAGTTACG	900
TCTTATGATT	ACGATGCCCT	TCTGGATGAA	AAAAGAAATC	CAACTGCTAA	ATATCTTGCA	960
GTCAAGAAGA	TGATGGCAAC	ACATTTTTC	GAGTATCCGC	AGTTGGAACC	ACTCTACAAA	1020
GAGAGTATGG	AGTTGGATGC	TATTCCTACTA	GTTGAAAAAG	TTTCTTTGTT	TGAAACCTTA	1080
GATAGCTTGT	CAAGTCCGT	AGAAAGTCTC	TATCCTCAAA	AGATGGAGGA	GCTGGGACAA	1140
AGTTATGGCT	ACCTACTTTA	TCGAACAGAA	ACAACTGGG	ATGCAGAAGA	AGAAAGACTT	1200
CGTATCATTG	ATGGTCGAGA	TAGGGCCCAG	CTGTATGTCG	ATGGTCAGTG	GGTTAAAAC	1260
CAATATCAGA	CAGAGATTGG	GGAAGATATT	TTTTATCAAG	GTAAAAAGAA	AGGGCTATCT	1320
AGGTTAGATA	TCTTGATAGA	AAATATGGGG	CGTGTCAACT	ATGGGCATAA	GTTCTTAGCG	1380
GATACGCAAC	GTAAGGGAAT	TCGGACAGGG	GTCTGTAAGG	ATCTGCATTT	CTTACTAAAC	1440
TGGAAACACT	ATCCACTCCC	ACTAGACAAT	CCTGAGAAAA	TTGATTTTTC	AAAAGGATGG	1500
ACTCAAGGAC	AACCAGCCTT	TTACGCTTAT	GACTTTACAG	TCGAAGAGCC	AAAAGATACT	1560
TACCTAGACT	TGTCTGAGTT	TGGTAAGGGG	GTTGCCTTTG	TCAATGGGCA	GAATCTAGGA	1620
CGTTTTTTGGA	ACGTTGGCCC	AACTCTCTCA	CTTTATATCC	CTCATAGCTA	TCTCAAGGAA	1680
GGTGCCAACC	GCATCATTAT	CTTTGAAACA	GAAGGTCAAT	ATAAAGAAGA	GATTCATTTA	1740
ACTCGTAAAC	CTACACTAAA	ACATATAAAG	GGGGAAAAC	TATGA		1785

(2) INFORMATION FOR SEQ ID NO:1725:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...384
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1725:

AGACTCTTGA GGTGTGTTCT TAGTTCAATG ATGGTAAATC ATCTATCTTA TACCTTCATC	60
ACTCATACCA AACATTTGGT GATTAAATTTG CTACAAAATC AGCCTAAACT AAAGGTTTTG	120
GTTATGAGTA ATTTTGATCA GTATCATGCA AAATTCGTTG CAGAGACACT TTCTTATTAC	180
TGTAGCAATA ATTTTGAAC TGAAGTTTGG ACCGAATTAG AATTATCAAA GGAATCTTTA	240
GAAGATTCAC CTTATGATAT CATTATTTCC AATTTTATTA TTCCTCCTAT TGAAAATAAG	300
AGACTCATCT ATTCAAATA TATAAACACG GTCTCACTCA TATATTTGTT AAATGCCATG	360
ATGTTTATTC GATTAGATGA GTAA	384

(2) INFORMATION FOR SEQ ID NO:1726:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...279
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1726:

TTTTCATTGA GTATAAAATG GAGCCTATTA GATAATATCT GGCTGAGACG TGTCGCTATT	60
GACCACCAGT TGTTAAGAAA AGAGAAGACC AATACTCAAT TAATGGAAAA AATTCTACTT	120
CATAACTTGA ACCAAACAGA ATTTTATATC AATAAGCCA TTGGCTGGAC TCTGCGAGCC	180
TACTCCAAAA CGAACCCAC TTGGGTAGCA TGCTTTATTG ATGAAAACAA GGAAAGAATG	240
GCTGAACCTA GTATCAAAGA AGCAAGCAAG TACCTCTAG	279

(2) INFORMATION FOR SEQ ID NO:1727:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2187 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2187
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1727:

TTTTCATTGA	GTATTAGGGA	AAAGGAGATG	AATATGAAAT	TTGGGAAACG	TCACTATCGT	60
CCGCAAGTGG	ATCAGATGGA	CTGCGGTGTA	GCTTCATTAG	CCATGGTTTT	TGGCTACTAT	120
GGTAGTTATT	ATTTTTTGGC	TCACTTGCGA	GAATTGGCTA	AGACGACCAT	GGATGGGACG	180
ACGGCTTTGG	GCTTGGTCAA	GGTGGCAGAG	GAGATTGGTT	TTGAGACGCG	AGCCATTAAG	240
GCGGATATGA	CGCTTTTGA	CTTGCCGGAT	TTGACTTTTC	CTTTTGTTGC	CCATGTGCTT	300
AAGGAAGGGA	AATTGCTCCA	CTACTATGTG	GTGACTGGGC	AGGATAAGGA	TAGCATTCAT	360
ATTGCCGATC	CAGATCCCCG	GGTGAAGTTG	ACTAAACTGC	CACGTGAGCG	TTTTGAGGAA	420
GAATGGACAG	GAGTGACTCT	TTTTATGGCA	CCTAGTCCAG	ACTATAAGCC	TTATAAGGAA	480
CAAAAAAATG	GTCTGCTCTC	TTTTATCCCT	ATATTAGTGA	AGCAGCGTGG	CTTGATTGCC	540
AATATCGTTT	TGGCAACACT	CTTGCTAACC	GTGATTAACA	TTGTGGGTTT	TTATTATCTG	600
CAGTCTATCA	TTGATACCTA	TGTGCCAGAT	CAGATGCGTT	CGACACTAGG	GATTATTTCT	660
ATTGGGCTAG	TCATCGTCTA	CATCCTCCAG	CAAATCCTGT	CTTACGCTCA	GGAGTATCTC	720
TTGCTTGTTT	TGGGGCAACG	CTTGTCGATT	GACGTGATTT	TGTCTTATAT	CAAGCATGTT	780
TTTCACCTCC	CTATGTCCTT	TTTCGCGACA	CGCAGGACAG	GGGAAATTGT	GTCTCGTTTC	840
ACGGATGCTA	ACAGTATTAT	CGATGCGCTG	GCTTCGACCA	TTCTTTTCGAT	TTTCCTAGAT	900
GTGTCAACAG	TTGTCAATTAT	TTCCCTTGTT	TTATTTTCAC	AAAATACCAA	TCTCTTTTTC	960
ATGACTTTAT	TGGCGCTTCC	TATCTACACA	GTGATTATCT	TTGCCTTTAT	GAAGCCGTTT	1020
GAAAAGATGA	ATCGGGACAC	CATGGAAGCC	AATGCGGTTT	TGTCTTCTTC	TATCATTGAG	1080
GACATCAACG	GTATTGAGAC	TATCAAGTCC	TTGACCAGTG	AAAGTCAGCG	TTACCAAAAA	1140
ATTGACAAGG	AATTTGTGGA	TTATCTGAAG	AAATCCTTTA	CCTATAGTCG	AGCAGAGAGT	1200
CAGCAAAAGG	CTCTGAAAAA	GGTTGCCCAT	CTCTTACTTA	ATGTCGGCAT	TCTCTGGATG	1260
GGGGCTGTTC	TGGTCATGGA	TGGCAAGATG	AGTTTGGGGC	AGTTGATTAC	CTATAATACC	1320
TTGCTGGTTT	ACTTTACCAA	TCCTTTGGAA	AATATCATCA	ATCTGCAAAC	CAAGCTTCAG	1380
ACAGCGCAGG	TTGCCAATAA	CCGTCTAAAT	GAAGTGTATC	TAGTAGCTTC	TGAGTTTGAG	1440
GAGAAGAAAA	CAGTTGAGGA	TTTGAGCTTG	ATGAAGGGAG	ATATGACCTT	CAAGCAGGTT	1500
CATTACAAGT	ATGGCTATGG	TCGAGACGTC	TTGTCCGATA	TCAATTTAAT	CGTTCCCCAA	1560
GGGTCTAAGG	TGGCTTTTGT	GGGGATTTCA	GGGTCAAGTA	AGACGACTTT	GGCCAAGATG	1620
ATGGTTAATT	TTTACGACCC	AAGTCAAGGG	GAGATTAGTC	TGGGTGGTGT	CAATCTCAAT	1680
CAGATTGATA	AAAAAGCCCT	GCGCCAGTAC	ATCAACTATC	TGCCTCAACA	GCCCTATGTC	1740
TTTAACGGAA	CGATTTTGGA	GAATCTTCTT	TTGGGAGCCA	AGGAGGGGAC	GACACAGGAA	1800
GATATCTTAC	GGGCGTCTGA	ATTGGCAGAG	ATTGAGAGAG	ATATCGAGCG	CATGCCACTG	1860
AATTACCAGA	CAGAATTGAC	TTCGGATGGG	GCAGGGATTT	CAGGTGGTCA	ACGTCAGAGA	1920
ATCGCTTTGG	CGCGTGCTCT	CTTGACAGAT	GCGCCGGTCT	TGATTTTGGA	TGAGGCGACT	1980
AGCAGTTTGG	ATATTTTGAC	AGAGAAGCGG	ATTGTCGATA	ATCTCATGGC	TTTGGACAAG	2040
ACCTTGATTT	TCATTGCTCA	CCGCTTGACT	ATTGCTGAGC	GGACAGAGAA	GGTAGTTGTC	2100
TTGGATCAGG	GCAAGATTGT	CGAAGAAGGA	AAGCATGCTG	ATTTGCTTGC	ACAGGGTGGC	2160

(2) INFORMATION FOR SEQ ID NO:1728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1728:

ATGGCTATGA	GAAATCAACT	TGCCCTTAGT	GGCGAAAAAA	TTCTTGAAAA	AATTTATCCT	60
CAACTATTTT	ACCACGTCGG	CATGATTCGT	GGGGAATATT	TGTTGAGAGA	GCTTAATCAA	120
AACATCATAT	TAGCAAGTTG	TCAGCAATTT	GTAAGAAGATT	ATCTAGAGAC	TATCTGCTCC	180
CTGTACTCAG	ATGAAGAAAGT	TTGGTATCGT	TTTTCTGAAT	TAACGAATAC	AGAAGCCAAT	240
TGTTTAGTGG	GGACTAGAGA	GTTTTTTGAC	GAAGGGCATC	CCTTGTTTGG	CTATAGAGGA	300
ACCAGGCGTT	TACTGGCGTG	TTTGGATGAA	TTTCAGGCTG	AAGCACATGT	CGTTACAGAA	360
GTTTATCAAA	CCAACCCCAA	TCTATCTGTT	ATCTTTCCTT	TTGTCAATGA	TGACGACCAA	420
TTAAAACAAG	CTATTACAGT	ATTGCGTCAG	CAGGGTTTTA	CTGGGAAAGT	CGGAACGATG	480
ATTGAATTAC	CGTCAGCGTA	TTTTGACTTA	TCTAGTATAC	TGGAAACGGG	CATTTCAAAG	540
ATTGTAGTTG	GAATGAATGA	TTTGACTTCC	TTTGTTTTTG	CGACTATGAG	AAACAGTCAA	600
TGGCATGATA	TGGAAAGTCC	AATAATGTTA	GATATGCTAA	GAGATATGCA	GGATAAAGCA	660
AGAAAGAACA	AGATTGATTT	TGCTGTAGCA	GGCTATCTGA	ATACTTCTTT	CATACAAAAA	720
ATGAATCAGT	TGGGTATCAA	GTGCATTATC	CACTACAGTT	CTATTCCAGA	GATTTTTTGAT	780
TTAGAGATTG	ACCATCCAGA	TCATCTTAAA	CACATAAAAG	AAGAAAGTAA	AAAATTACAA	840
AGGAGTACCC	ATGATACCGC	AAGAAATGTG	GAATAA			876

(2) INFORMATION FOR SEQ ID NO:1729:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1729:

TACACAATGA	GGTATAATCT	TCTTATGGCA	TATTCAATAG	ATTTTCGTAA	AAAAGTTCTC	60
TCTTATTGTG	AGCGAATAGG	TAGTATAACA	GAAGCATCAC	ACGTTTTCCA	AATCTCACGT	120
AATACCATT	ATGGCTGGTT	AAAGCTAAAA	GAGAAAACAG	GAGAGCTAAA	CCACCAAGTA	180
AAAGGAACAA	AACCAAGAAA	AGTTGATAGA	GATAGACTTA	AAAACTATCT	TACTGACAAT	240
CCAGACGCTT	ATTTGACTGA	AATAGCTTCT	GAATTTGGCT	GTCATCCAAC	TACCATCCAC	300
TATGCGCTCA	AAGCGATGGG	TTACACTCGA	AAAAAAGAAC	CACACCTACT	ATGA	354

(2) INFORMATION FOR SEQ ID NO:1730:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 765 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1730:

GTATTGATGA	GAAACTTGAA	AAGTATACTG	AGACGACACA	TTAGTCTATT	GGGCTTTCTC	60
GGAGTATTGT	CAATCTGGCA	GTTAGCAGGT	TTTCTTAAAC	TTCTCCCCAA	GTTTATCCTG	120
CCGACACCTC	TTGAAATTCT	CCAGCCCTTT	GTTCGTGACA	GAGAATTTCT	CTGGCACCAT	180
AGCTGGGCGA	CCTTGAGAGT	GGCTTTACTG	GGGCTGATTT	TGGGAGTTTT	GATTGCCTGT	240
CTTATGGCTG	TGCTCATGGA	TAGTTTGACT	TGGCTCAAATG	ACCTGATTTA	CCCTATGATG	300
GTGGTCATTC	AGACCATTCC	GACCATTGCC	ATAGCTCCTA	TCCTGGTCTT	GTGGCTAGGT	360
TATGGGATTT	TGCCCAAGAT	TGTCTTGATT	ATCTTAACAA	CAACCTTTCC	CATCATCGTT	420
AGTATTTTGG	ACGGTTTTAG	GCATTGTGAC	AAGGATATGC	TGACTTTGTT	TAGTCTGATG	480
CGAGCAAACC	CTTGGCAAAT	CCTGTGGCAT	TTTAAATCC	CGGTTAGCCT	GCCTTACTTT	540
TATGCAGGTC	TGAGGGTCAG	TGTCTCCTAC	GCCTTTATCA	CAACTGTGGT	ATCTGAGTGG	600
TTGGGAGGTT	TTGAAGGTCT	TGGTGTTTAT	ATGATTCACT	CTAAAAAACT	GTTTCAGTAT	660
GATACCATGT	TTGCCATTAT	TATTCTGGTG	TCGATTATCA	GTCTTTTGGG	TATGAAGCTG	720
GTCGATATCA	GTGAAAAATA	TGTGATTAAA	TGGAAACGTA	CTTAA		765

(2) INFORMATION FOR SEQ ID NO:1731:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2880 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2880

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1731:

AAAATGATGA	GCGTGGTCAG	GAAATCTTGT	GGAGTCTGGA	AGAAGGTCAT	GAAGAAAAAG	60
AGGCTGTTGA	AACCAAGGTG	CACCTTGGGT	GGCAAGTTTT	TGGATCGAAT	TTTATCTCCA	120
AAATCAGAAAT	GCGCCTATGA	GTTATCAGCT	GTGGGTCAGG	TGGAAGCAGG	AACCAATCAT	180
ATCTTGTTGA	CTCTGAGAAT	CGGTCAAATC	AATAGCCAAA	AATACTATGT	CATTCGGGAT	240
ATTCCACTTT	TTTTAAGGAT	TGTCGAGCAG	AGAAAGTCGT	ATATGATTGG	CAAGATTTAT	300
GAGGAGTCTC	TTTCTTGGGA	AGCCTTTGAT	GATGCCAGCC	AAGAACTTTT	GACTTTCTTG	360
CACGGACTAA	CGGAGGAAGG	GCTGGTTTTCA	GACCTCTTTT	GCCAAAACCA	AGGTCGGCAC	420
CTCTTTTTCC	CTCTGACCTT	TTTTGAGCAG	GGTGTGAATT	TACTGATGGC	CTTGCCCCAT	480
TTTCAATTTG	ACCATCAAGT	GGATAGCTAC	CAAACCTGTC	TTTTTCAGGA	TATGCATGCT	540
GATGCCAATC	TATTTGCCTT	TACAGTAACA	GAATACTCGG	ACTATTTTGA	AATGGAAATC	600
AGTGAGAGTC	CTAGGGTCAA	TGTCCTTTTAT	CAGGGAGCAG	TACTTTTCCA	TAAAGGTCAG	660
GTTTATTTTT	TAACAGACCA	GCAGATGCGT	CTTCTCAAGG	AAATTAAAGC	GTTACCTGTG	720
GGTCAACAAG	GAAAGAAATA	CCTGCAATTT	GATAGCAGTG	ATCGAGACAA	ATTGGCCTCC	780
TGTCTGACTC	TTTTTATCCA	GATGGGCACC	GTTTCAGCTC	CAGAACGTCT	ACAAATCAAA	840
ACTTTTGCGC	CCTCTTTTTA	CTTTGACAGG	GAAGAAGATA	ATCGGATTCTG	TTTAGAAATT	900
CAGTTTGATT	ATGGAAATAG	ACAGGTATCT	AGCCGACAAG	AGCTAGAAGA	ATTACCATTT	960
TCAAGTGACG	CGGACTTAGA	AGAAAAGAAAT	TTCCAAGTCT	GTTTGGCTGC	GGGCTTTGAA	1020
GCCGATTTTC	AATCTTGGCG	TCAGGCCCTTA	AAAGCGGAGT	CTGTCTATCA	TTTTTTTCAT	1080
GATATCATTC	CAGTCTTTGA	AAAACTCGGG	CATGTTGACC	TATCAGATAA	ACTAGAAGAG	1140
CTTTATAGCC	TAGCGAGTCC	TCAGGTGCAG	ATTGCCCTCA	AGGGAGGTCT	CTTGGAATC	1200
CAGTTTGATT	TTCAAGATAT	TGCCCAGGAG	GAAATCGACC	AAGCCATGCA	GGCCTTG GTT	1260
GCCAAATCAGG	ATTTTTATAT	TGATTCTGCT	AATCAAGTTT	ACTTTTTTCGA	TGAAGAAACC	1320
AAGAAAATTC	GCCAAAATCT	ACAGGAACTG	GGGCAATTTG	AATTAAAAGA	TGGGACCTTG	1380
CAGGCTCGGA	AATCCTTGGC	CTACAGTTTA	GCTCATCTCT	TTGAAGGGCG	AGACCGTGTT	1440
TCTTTTTTAC	AAGAATTCCA	GAATCTGGCC	CAGGATTTGA	CACATCCAGA	GGACTTTCCT	1500
CGACAGGCAA	CTCAGGTTCA	GGCTGACTTG	CGAGATTATC	AGGAAAAGGG	AATTGGCTGG	1560
TTGCAGATGC	TCCATCATT	TGGTTTTGGT	GGGATTTTGG	CTGATGATAT	GGGACTTGGG	1620
AAAACCCCTC	AGACCATTGC	TTTTTTGACT	AGTCAAGTGA	CAAAAGAAAG	TCGGGTTTTG	1680
ATTCTCGCTC	CGTCAGGTTT	GATTTACAAC	TGGGCAGATG	AGTTTCAGAA	ATTTGCCCCA	1740
CAGTTGGATG	TGGCTGTTGT	TCATGGTTTG	AAAGCAAGTC	GTGAGGAGAT	TCTTGCCGAG	1800
AGCCATCAAA	TCTATGTGAC	TAGCTATGCC	ACCTTCCGTC	AGGACAGTGA	GTTTTATCAG	1860
GGGATGCGCT	TTTACTTCCT	TTTCTTAGAT	GAGGCTCAGG	TCATGAAAAA	TGCCCAGACC	1920
AAGATTGCCC	AGACCTTGAG	ACAAATTTGTG	GTGCCGTCGG	TCTTTGCCTT	GTCAGGAACT	1980
CCGATTGAAA	ACCATCTGGG	TGAGTTGTGG	TCTATTTTCC	AAATCGTCAT	GCCCGGACTT	2040
TTGCCAAGCA	AGAAAGAAAT	TATGAAATTG	CCAGCAGAGC	GAGTGGCTCA	GTTTATCAAG	2100
CCTTTCTGTA	TGCGACGCAA	GAAAGAAGAA	GTTCTGACTG	AATTGCCAGA	CTTGATTGAG	2160
GTGGTTTATA	AAAATGAACT	GGAAGACCAG	CAAAAGGCTA	TTTACCTTGC	CCAGTTACAA	2220
CAGATGCGAG	ACCATCTGGC	TCAAGTGTC	GAACAGGAAT	TTCAGCGAAG	TCGTGTGGAA	2280

ATTTTATCTG	GTTTGATGCG	CTTGCGTCAA	ATATGTGACA	CTCCTGCCCT	GTTTATGGAA	2340
GATTATCAGG	GAGCCAGCGG	CAAAC TAGAT	AGTCTCCGAG	ACCTACTGGT	ACAGGTGGCA	2400
GACGGCAGAC	ACCGTGTCTT	GATTTTCTCT	CAGTTCAAGG	GAATGTTGGA	AAAAATTGAA	2460
CAAGAACTGC	CAGACTTGGG	CCTGACATCC	TTTAAAATTA	CGGGTTCAAC	CCCAGCCAAG	2520
GAAAGACAA	ACATGACCAA	GGCCTTTAAC	CAAGGAGAAA	GAGATGCCTT	TCTGATTTCC	2580
CTCAAGGCTG	GTGGGGTCGG	TCTGAACCTG	ACAGGTGCAG	ATACAGTGAT	CTTGGTTGAC	2640
CTTTGGTGGA	ATCCTGCGGT	GGAAGCGCAA	GCCATTGGCC	GTGCCCATCG	GATGGGTCAG	2700
GAAGAAACGG	TTGAGGTCTA	TCGCTTGGTG	ACCAAGGGAA	CCATTGAAGA	AAAAATTCAG	2760
GAACTCCAAG	AACAAAAGAA	ACATCTGGTG	TCACAAGTAT	TGGATGGCAC	AGAGTCACGT	2820
GGTAGTCTGA	CCCTAGCAGA	AATTAGAGAA	ATTTTGGGAA	TTTCTGAAGC	CAACACTTGA	2880

(2) INFORMATION FOR SEQ ID NO:1732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1732:

TTTACGATGA	GAAGGAAGTG	TCAC TCAGAG	AGATTTTACT	TTATTATTTC	CGAGTTATCG	60
ATCCTCTCAT	CTATCAATCA	ACAAGGGAAT	GACCGTGGTC	GCCAATATCG	AACTGGGATT	120
TATTATCAGG	ATGAAGCAGA	TTTGCCAGCT	ATCTACACAG	TGGTACAGGA	GCAGGAACGC	180
ATGCTGGGTC	GAAAGATTGC	AGTAGAAGTG	GAGCAATTAC	GCCACTACAT	TCTGGCTGAA	240
GA CTACCACC	AAGATTATCT	CAGGAAGAAT	CCTTCAGGTT	ACTGTCATAT	CGATGTGACC	300
GATGCTGATA	AGCCATTGAT	TGATGCAGCA	AACTATGAAA	AGCCTAGTCA	AGAGGTGTTG	360
AAGGCCAGTC	TATCTGAAGA	GTCTTATCGT	GTCAACACAAG	AAGCTGCTAC	AGAGGCTCCG	420
TTTACCAATG	CCTATGACCA	AACCTTTGAA	GAGGGGATTT	ATGTAGATAT	TACGACAGGT	480
GAGCCACTCT	TTTTTGCCAA	GGATAAGTTT	GC TTCAGGTT	GTGGTTGGCC	AAGTTTTAGC	540
CGTCCGATTT	CCAAAGAGTT	GATTCATTAT	TACAAGGATC	TGAGCCATGG	AATGGAGCGA	600
ATTGAAGTTC	GTTCTCGTTC	AGGCAGTGCT	CAC TTGGGTC	ATGTTTTTAC	AGATGGACCG	660
CGGGAGTTAG	GCGGCCCTCC	TTACTGTATC	AAT TCTGCTT	CTTTACGCTT	TGTGGCCAAG	720
GATGAGATGG	AAAAAGCAGG	ATATGGCTAT	CTATTGCCTT	ACTTAAACAA	ATAA	774

(2) INFORMATION FOR SEQ ID NO:1733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1733:

AAGCAGATGA	GTATAAGTCC	TCGTTTTGAA	ACCTTAGAGC	AGGCCATTGC	CTCCAAAGAT	60
TTGGAAAAAG	TCCGAGAAGC	TTTAAGAAA	ATGATTTC	CTTGGACCAT	CAATGAAAGT	120
GTGGTTCGTG	ACAATAGTAC	AGCTCATTAT	GGACGTGTTG	AAACAGNTAT	TTCCTTCCTG	180
CCTAGTAGCA	TGGAAACCGA	ACCTACAGAT	GAGTTTGGAA	CATGA		225

(2) INFORMATION FOR SEQ ID NO:1734:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 924 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1734:

AAAAAGATGA	GTTATTTGAA	AGGCTTTAAC	CTAATCAAAT	CAGCTGACCT	GAGGCAAAC	60
CGAGCTGGGA	AAAAC	TACCT	AGCCTTTACC	TTCCAAGATG	ATAGTGGCGA	120
AAGCTCTGGG	ATGCCCAACC	TCATAACATT	GAGGCCTTTA	CCGCAGGTAA	GGTTGTCCAC	180
ATGAAAGGAC	GCCGAGAAGT	TTATAACAAT	ACCCCTCAAG	TCAATCAAAT	TACTCTCCGC	240
CTGCCTCAAG	CTGGTGAACC	CAATGACCCA	GCTGATTTC	AGGTCAAAGT	ACCAGTTGAT	300
GTCAAGGAAA	TTCGTGACTA	CATGTCGCAA	ATGATTTTC	AAATTGAAAA	TCCTGTCTGG	360
CAACGGATTG	TCCGAAATCT	CTACACCAAG	TATGATAAGG	AATTCTACTC	CTATCCAGCC	420
GCCAAGACCA	ACCACCATGC	CTTTGAAACG	GGCTTGGCTT	ATCATACGGC	GACCATGGTA	480
CGTTTGGCAG	ACGCTATTAG	CGAAGTTTAT	CCTCAGCTCA	ATAAGAGCTT	ACTCTATGCG	540
GGGATTATGC	TGCATGACTT	AGCTAAGGTT	ATCGAGTTGA	CGGGGCCAGA	CCAGACAGAG	600
TACACAGTGC	GAGGTAATCT	TCTTGGACAT	ATCGCTCTCA	TTGATAGCGA	AATTACCAAG	660
ACAGTTATGG	AACTCGGCAT	CGATGATACC	AAGGAAGAAG	TCGTTTTGCT	TCGTCATGTC	720
ATCCTCAGTC	ACCACGGCTT	GCTTGAATAT	GGAAGTCCAG	TCCGTCCACG	TATTATGGAG	780

GCAGAGATTA TCCATATGAT TGACAATCTG GATGCAAGTA TGATGATGAT GTCAACAGCT	840
CTGGCTTTGG TGGATAAAGG AGAGATGTCC AATAAAATCT TCGCTATGGA TAATCGTTCC	900
TTCTATAAAC CAGATTTAGA TTGA	924

(2) INFORMATION FOR SEQ ID NO:1735:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 729 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...729
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1735:

AAGAAGATGA GAATCAATAA GTATATTGCC CACGCAGGTG TGGCCAGTAG GAGAAAAGCA	60
GAAGAGCTGA TTAAGCAAGG CTTGGTGACG GTTAACGGCC AAGTGGTGCG TGAAC TAGCA	120
ACCACTATCA AGTCAGGCGA CAAGGTCGAA GTTGAAGGTC AACCTATCTA CAACGAAGAA	180
AAGGTCTACT ATCTGCTTAA CAAACCACGC GGTGTGATTT CCAGTGTGAC AGATGATAAG	240
GGTCGCAAGA CGGTGTGCGA CCTCTTGCCC AATGTCAAAG AGCGTATTTA CCCTGTGGGT	300
CGTTTGGACT GGGATACATC AGGTGTCTTG ATTTTGACCA ATGATGGGGA CTTTACAGAC	360
GAGATGATTC ACCCTCGTAA TGAGATTGAC AAGGTTTATG TCGCGCGTGT TAAAGGTGTG	420
GCCAATAAGG ACAATCTCCG CCCCTTGACC CGTGGTCTTG AGATTGATGG TAAGAAAACC	480
AAGCCAGCTG TTTATGAAAT TCTCAAAGTG GACCCAGTCA AAAATCGCTC TGTGGTGCAG	540
TTGACCATCC ATGAAGGGCG TAACCATCAG GTTAAAAAGA TGTTTGAAGC TGTTGGTCTC	600
CAAGTAGATA AGTTGTCTCG GACTCGTTTC GGACACCTAG ACTTGACAGG ACTCCGTCCA	660
GGAGAATCCC GTCGTCCTAA TAAAAAAGAA ATCAGCCAAC TACACACCAT GGCTGTAACT	720
AAGAAATAA	729

(2) INFORMATION FOR SEQ ID NO:1736:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1266 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1736:

ACTATGGTGA	GTAGACAAGA	ACAATTTGAA	CAGGTACAGG	CTGTTAAAAA	ATCGATTAAAC	60
ACAGCTAGTG	AAGAAGTGAA	AAACCAAGCC	TTGCTAGCCA	TGGCTGATCA	CTTAGTGGCT	120
GCTACTGAGG	AAATTTTAGC	GGCTAATGCC	CTCGATATGG	CAGCGGCTAA	GGGGAAAATC	180
TCAGATGTGA	TGTTGGATCG	TCTTTATTTG	GATGCAGATC	GTATAGAAGC	GATGGCAAGA	240
GGAATTCGTG	AAGTGGTTGC	CTTCCCAGAT	CCAATCGGTG	AAGTTTTAGA	AACAAGTCAG	300
CTTGAAAATG	GTTTGGTTAT	CACAAAAAAA	CGTGTAGCTA	TGGGTGTCAT	CGGTATTATC	360
TATGAAAGCC	GTCCAAATGT	GACGTCTGAT	GCGGCTGCTT	TGACTCTTAA	GAGTGGAAAT	420
GCGGTTGTTT	TTCGTAGTGG	TAAGGATGCC	TATCAAACAA	CCCATGCCAT	TGTCACAGCC	480
TTGAAGAAGG	GCTTGGAGAC	GACTACTATT	CACCCAAATG	TGATTCAACT	GGTGGAAGAT	540
ACTAGCCATG	AAAGTAGTTA	TGCTATGATG	AAGGCCAAGG	GCTATCTAGA	CCTCCTCATT	600
CCTCGTGGAG	GAGCTGGGCTT	GATCAATGCA	GTGGTTGAGA	ATGCCATTGT	ACCTGTTATC	660
GAGACAGGGA	CTGGGATTGT	CCATGTCTAT	GTGGATAAGG	ATGCAGACGA	AGACAAGGCG	720
CTGTCTATCA	TCAACAATGC	TAAAACCAGT	CGTCCTTCTG	TTTGTAATGC	CATGGAGGTT	780
CTGCTGGTTC	ATGAAGACAA	GGCAGCAAGC	ATCCTTCCTC	GCTTGGATCA	AATGCTGGTT	840
GCAGAGCGTA	AGGAAGCTGG	ACTGGAACCA	ATTCAATTCC	GCTTGGATAG	CAAAGCAAGC	900
CAGTTTGTTT	CAGGTCAAGC	AGCTGAGACC	CAAGACTTTG	ACACCGAGTT	TTTAGACTAT	960
GTCCTTGCTG	TTAAGGTTGT	GAGCAGTTTA	GAAGAAGCGG	TTGCGCACAT	TGAATCCCAC	1020
AGCACCCATC	ATTCCGATGC	TATTGTGACG	GAAAATGCTG	AAGCTGCAGC	ATACTTTACA	1080
GATCAAGTGG	ACTCTGCAGC	GGTGATGTTT	AATGCCTCAA	CTCGTTTCAC	AGATGGAGGA	1140
CAATTTGGTC	TTGGTTGTGA	AATGGGGATT	TCTACTCAGA	AATTGCACGC	GCGTGGTCCA	1200
ATGGGCTTGA	AAGAGTTGAC	CAGCTACAAG	TATGTGGTTG	CTGGTGATGG	GCAGATAAGG	1260
GAGTAA						1266

(2) INFORMATION FOR SEQ ID NO:1737:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1737:

TTATTTTCGA	GGAGAAAAAC	AGTGAAAAAA	AGAAAAAAGC	TTGCTCTGTC	TCTTATCGCT	60
TTTTGGCTGA	CGGCTTGTTT	AGTAGGCTGT	GCTAGCTGGA	TTGATCGTGG	AGAATCCATA	120
ACGGCTGTTG	GCTCAACTGC	CTTGCAACCC	TTGGTTGAAG	TAGCGGCAGA	TGAATTTGGC	180
ACGATCCATG	TTGGAAAAAC	GGTCAATGTC	CAAGGGGGAG	GTTCTGGTAC	AGGCTTGTC	240

CAGGTTTCAGT	CTGGGGCAGT	TGATATAGGA	AACTCAGATG	TATTTGCTGA	GGAAAAAGAC	300
GGAATTGATG	CTTCTGCTCT	TGTTGACCAC	AAGGTCGCGG	TACGTGGCTT	GGCTCTGATT	360
GTCAATAAGG	AGGTTGATGT	TGATAACCTA	ACGACAGAGC	AACTTCGTCA	AATCTTCATA	420
GGTGAGGTAA	CCAAATTGGAA	AGAGGTTGGT	GGTAAGGACT	TACCCATCTC	TGTTATCAAT	480
CGGGCAGCCG	GCTCTGGTTC	TCGTGCTACC	TTTGATACTG	TCATTATGGA	AGGTCAGTCT	540
GCCATGCAAA	GTCAGGAGCA	GGATTCAAAT	GGAGCGGTAA	AATCAATCGT	ATCAAAAAGT	600
CCAGGAGCTA	TCTCTTATTT	ATCTCTTACC	TATATAGATG	ATTTCGGTCAA	AAGCATGAAG	660
TTGAATGGCT	ATGACTTAAG	TCCAGAAAAT	ATAAGTAGCA	ATAATTGGCC	CTTGTGGTCT	720
TATGAGCATA	TGTATACATT	GGGGCAGCCC	AATGAGTTGG	CTGCAGAATT	TCTCAATTTT	780
GTTCTCTCGG	ATGAGACCCA	AGAAGGGATT	GTCAAAGGAT	TGAAGTATAT	TCCGATTAAAG	840
GAAATGAAGG	TTGAAAAAGA	TGCTGCCCGA	ACTGTGACAG	TGTTGGAAGG	GAGACAATAA	900

(2) INFORMATION FOR SEQ ID NO:1738:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1413 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1413
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1738:

GTCATTTTCTGA	GCTTTTTTATG	GTACAATGGA	AACATGTTAT	TCAAATTATC	TAAGGAAAAA	60
ATAGAGCTAG	GCTTATCTCG	TTTATCGCCA	GCCCCGCTGA	TTTTTTTGAG	TTTTGCCTTG	120
GTCATTTTAC	TAGGCTCTCT	TCTTTTGAGC	TTGCCCCTTG	TCCAAGTTGA	AAGCTCACGA	180
GCGACTTATT	TTGATCATCT	TTTCACTGCT	GTCTCTGCAG	TCTGTGTGAC	AGGTCTCTCA	240
ACCCCTCCAG	TAGCTCACAC	CTATAATATA	TGGGGCCAAA	TAATCTGTTT	GCTCTTGATT	300
CAGATCGGTG	GTCTAGGGCT	CATGACCTTT	ATTGGGGTTT	TCTATATCCA	GAGCAAGCAA	360
AAGCTTAGTC	TTCGTAGCCG	TGCAACTATT	CAGGATAGTT	TTAGTTATGG	AGAAACTCGA	420
TCTTTGAGAA	AGTTTGTCTA	TTCTATTTTT	CTCACGACCT	TTTTGGTTGA	GAGCTTGGGA	480
GCTATTTTGC	TTAGTTTTTC	CCTTATTCCT	CAACTTGGCT	GGGGACGTGG	TCTTTTTAGT	540
TCCATTTTTT	TAGCGATCTC	AGCCTTCTGT	AATGCCGGTT	TTGATAATTT	AGGGAGCACC	600
AGTTTATTTG	CTTTTCAGAC	CGATTTACTG	GTCAATCTGG	TGATTGCAGG	CTTGATTATT	660
ACAGGCGGCC	TTGGTTTTAT	GGTCTGGTTT	GATTTGGCTG	GTCAATCTAGG	AAGAAAGAAA	720
AAAGGACGTC	TGCACTTTCA	TACGAAGCTT	GTACTATTGT	TGACTATAGG	TTTGTGTGTTA	780
TTTGGAACGG	CAACTACTCT	CTTTCTTGAG	TGGAACAATG	CTGGAACGAT	TGGCAATCTC	840
CCTGTTGCCG	ATAAGGTTTT	AGTTAGCTTT	TTTCAAACAG	TGACGATGCG	AACAGCTGGC	900
TTTTCTACGA	TAGATTATAC	TCAGGCTCAT	CCTGTGACTC	TTTTGATTTA	TATCTTACAG	960
ATGTTTCTAG	GTGGGGCACC	TGGAGGAACA	GCTGGGGGAC	TCAAGATTAC	GACATTTTTTT	1020
GTCTCTTGG	TCTTTGCACG	AAGTGAGCTT	CTAGGCTTGC	CTCATGCCAA	TGTTGCGAGA	1080
CGAACGATTG	CGCCGCGAAC	GGTTCAAAAA	TCCTTTAGTG	TCTTTATTAT	CTTTTTTGATG	1140
AGCTTCTTGA	TAGGATTGAT	TCTGCTAGGG	ATAACAGCCA	AAGGCAATCC	TCCCTTTATC	1200
CACCTCATAT	TTGAAACCAT	TTCAGCTCTT	AGTACAGTTG	GTGTAACGGC	AAATCTGACT	1260
CCTGACCTTG	GGAAATTGGC	TCTCAGTGTT	ATCATGCCAC	TTATGTTTAT	GGGACGAATT	1320

GGTCCCTTGA CCTTGTTTGT TAGCTTGGCA GATTACCATC CAGAAAAGAA AGATATGATT	1380
CACTATATGA AAGCAGATAT TAGTATTGGT TAA	1413

(2) INFORMATION FOR SEQ ID NO:1739:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...201
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1739:

GGCTTTCCGA GTTTTCGGAG AGCCTGTTTT TTTATTTTGA TACCCATACT TTTTAATATG	60
TATAGTGGAT TGATACTCTT CGAAAATCAA ATTCAAACCA CGTCAATTTT ACCTTGCCGT	120
ACTCAAGTAC AGCTGCGGC TAACTTCCTA GTTTGCACTT TAATTTTCAT TGAGTATGAA	180
TCTGGAATAG AACACTGTTA A	201

(2) INFORMATION FOR SEQ ID NO:1740:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...288
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1740:

ATACTTCCGA GAAACAAAAG TATTTTTATC ATCTTTTTTA GCCAATCTCT CCACTGTATA	60
TTTCAACATC ATTTATTCAA AGAATGTGAA ACAATCACCC TACAACTTTT GGTATTAGCA	120
GAAGAATTAA AAATATACGA TATTCTTGGA TTCTCTCAAG TACGCTTGGG AATACTACAA	180

CATAACTCCG ATTTGATTGA TAAAGGAATA ACTTTATTAC GACTAACCAA AGAAGAGGCA	240
TTAGTTAAAA TACTCGAAAA AGAAATTAAT GATTTTTCAA ACCTATAA	288

(2) INFORMATION FOR SEQ ID NO:1741:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 669 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...669
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1741:

CGACTTCAGA GCAAGATAAA CCAAAGGGGG CGGAGAAAAC GAGGAGTTCT GAGAGAGCAA	60
GCAACACGTG ATAAAAAAGA AAATGATGCG AAGTCTTCAG ATTCTAGCGT AGGTGAAGAA	120
GCTCTTCCAA GCCCATCCCT GAAACCAGAA AAAAAGGTTG CAGAAGCTGA GAAGAAGGTT	180
GCAGAAGCTG AGAAAAAAGC CAAGGCTCAA AAAGAAGAAG ATCGCCGTAA CTACCCAACC	240
AATACTTACA AAACGCTTGA ACTTGAAATT GCTGAGTCCG ATGTGAAAGT TAAAGAAGCG	300
GAGCTTGAAC TAGTAAAAGA GGAAGCTAAG GAATCTCGAA ACGAGGAAAA AGTTAATCAA	360
GCAAAAGCGA AAGTTGAGAG TAAAAAAGCT GAGGCTACAA GGTTAGAAAA AATCAAGACA	420
GATCGTAAAA AAGCAGAAGA AGAAGCTAAA CGAAAAGCAG CAGAAGAAGA TAAAGTTAAA	480
GAAAAACCAG CTGAACAACC ACAACCAGCG CCGGCTCCTC AACCAGAAAA ACCAACTGAA	540
GAGCCTGAGA ATCCAGCTCC CGCACCAAAA CCAGACAAGC CAGCTGAACA ACCAAAAGCA	600
GAAAAACAG ATGATCAACA AGCTGAAGAA GACTATGCTC GTAGATCAGA AGAAGAATAT	660
AATCGTTGA	669

(2) INFORMATION FOR SEQ ID NO:1742:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 207 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1742:

AGGCTACAGA	GGCAGGAGAA	TTTGTACAA	TACCTTATTT	CAGGCTTATA	TCGTTCTTAC	60
ACACGTGATG	CCTTCTATCA	ACTGTTGAAG	CGCCATGGTT	GGCGAAATAT	TATGCCACGT	120
CCAGAACATC	CTAAGAAAGC	AGACGCTCAA	ACCATGTGTCG	CGTCTAAAAA	TAAAACTCA	180
ATTCAAGAAG	AAAAGAAAGC	GCTTTTAA				207

(2) INFORMATION FOR SEQ ID NO:1743:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 789 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1743:

CTGGGACAGA	GAAGGAGGAC	TTGCATGTTT	AAGTTATCAT	TTCAGTCCAT	CGGACACGTT	60
GTGGTACGCA	ACTACATGAG	TTTTAGAAAT	TTATTTAAAA	TTTCAATTGT	CCCCAACCTT	120
ATCGACCCCC	TCTTTTATCT	TTTAGCAATG	GGATTTGGAG	TTGGTGCCTA	TTTGACGCAT	180
GTTAACGGTA	TGCTCTACCG	TGATTTTGTC	ATTACAGGTT	TAATTGCTGC	GA CTGCCATG	240
TCTGCGGCCA	CCGCAGAAAC	AACGGTCAAT	GCCTTTATCC	AGTATAAGAT	TGAAAAGACT	300
TATGATGCTA	TGTTGATGAC	GCCAATCAAT	ACGAGTGATA	TTGTGGTGGG	TCAGGCTATC	360
TGGGCAGGTA	TTCGTGCAGT	GATTTTCGGT	GGGATTTTTT	GGCTGATTTT	CATGCTTATC	420
ACAGCGCATT	TTCATGTCTT	GATGTTATTG	ATTCCTCTGA	TTTTATTTAT	AGTGGGTTAT	480
TTGTTTGGTG	TTTTGGGACT	AATCTTTACC	TACTTGGCGC	CGTCTAGGGA	ATTTCTGAAT	540
TACTACAATG	TTTTGGTAAT	CCGTCCTCTT	TATATGTTTT	CAGATACCTT	CTTTCCCATT	600
ACTTCCTTGC	CCCCAATACT	TGGTGATTTG	ACTTGGTTTT	CTCCCTTGTA	TCATGCTACT	660
CGCATGATTC	GTATTATATG	GGGAGGTGAG	GTGACAGGTT	TGTATCTTCA	TCTTATCTGG	720
TTGATAGCCT	TGGCGCTCTT	GATAACGGTG	CTTCCTATGT	ATATGTTACA	TCGTAGATAT	780
TATAGATAG						789

(2) INFORMATION FOR SEQ ID NO:1744:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3675 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...3675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1744:

AAAAATAAGA	GAGGAGTTAA	ATCGATGAAG	CTTATTCCCT	TTTAAAGTGA	GGAGGAGATT	60
CAAAAACCTGC	AAGAAGCAGA	AGCAAATTCG	AGCAAGGAAC	AGAAGAAAAC	TGCCGAACAA	120
ATCGAAGCTA	TCTACACTTC	TGGTCAGAAAT	ATCCTGGTCT	CAGCATCGGC	TGGTTCCTGGA	180
AAGACCTTTG	TCATGGTAGA	GCGCATTTCTG	GACCAATTGG	CGCGTGGTGT	CGAAATTTCT	240
CAACTCTTTA	TCTCAACCTT	TACCGTCAAG	GCTGCAACTG	AACTTAAAGA	ACGTTTAGAG	300
AAAAAAATCA	GCAAGAAAAT	CCAAGAAACA	GATGATGTCG	ACCTCAAACA	ACACTTGGGT	360
CGCCAGTTGG	CAGACCTACC	CAACGCTGCC	ATCGGAACCA	TGGA CTCTTT	CACACAAAAA	420
TTCTTGGCA	AACATGGTTA	TCTGCTTGAT	ATTGCACCTA	ATTTCCGTAT	TTTACAAAAC	480
CAAAGCGAGC	AACTTCTTCT	CGAAAACGAA	GTCTTTCATG	AGGTCTTTGA	AGCGCATTAC	540
CAAGGTAAAC	AGAAAAGAGAC	CTTTAGTCAT	TTGCTGAAAA	ACTTTGCTGG	GCGTGGCAAAG	600
GACGAACGGG	GTCTGCGGCA	GCAAGTCTAT	AAAACTATG	ACTTCCTCCA	ATCCACCAGT	660
AATCCTCAAA	AGTGGCTGAG	TGAATCTTTC	CTCAAAGGCT	TTGAGAAAGC	TGATTTTACC	720
AGTGA AAAAG	AAAAACTGAC	TGAGCAAATC	AAACAAGCCC	TTTGGGATTT	GGAAAGCTTT	780
TTCCGTTACC	ATCTGGATAA	CGATGCCAAG	GAGTTTGCAA	AGGCTGCCTA	TTTAGAAAAT	840
GTTCA GTTAA	TTCTGGATGA	AATTGGCTCC	CTAAATCAGG	AGTTCGATAG	TCAGGCTTAT	900
CAGGCAGTAC	TTGCGCGTGT	TGTCGCCATC	TCTAAGGAGA	AAAACGGTCG	TGCTCTGACT	960
AATGCCAGCC	GTAAGGCTGA	TTTGAAGCCC	CTGGCTGATG	CCTACAACGA	AGAGAGAAAG	1020
ACCCAGTTTA	CTAAACTAGG	ACAATTATCA	GACCAGATAG	CGATTCTCGA	CTATCAAGAA	1080
CGTTATCATG	GAGACACTTG	GAAACTAGCT	AAAACCTTCC	AATCTTTCAT	GAGCGATTTT	1140
GTAGAGGCTT	ATCGTCAGAG	AAAACGACAG	GAAAATGCCT	TTGAATTTCG	TGATATCAGC	1200
CATTACACCA	TTGAGATTTT	AGAAAATTTT	CCACAAGTTC	GTGAGTCTTA	TCAGGAGCGC	1260
TTCCATGAAG	TCATGGTCGA	TGAGTATCAG	GATACCAACC	ATATTCAAGA	ACGGATGCTG	1320
GAATTGTTGT	CTAATGGCCA	CAATCGCTTT	ATGGTGGGAG	ATATCAAGCA	ATCCATCTAT	1380
CGTTTCCGTC	AGGCAGACCC	GCAGATTTTC	AATGAGAAAT	TCCAACGCTA	TGCGCAAAAT	1440
CCTCAAGAA	GCAAGCTCAT	TCTCCTCAAG	GAAAATTTCC	GTAGTAGTTC	AGAAGTGCTG	1500
TCAGCAACCA	ATGATGTCTT	TGAACGTCTC	ATGGACCAAG	AGGTCGGCGA	AATCAACTAT	1560
GATAACAAGC	ACCAGCTTGT	TTTTGCCAAT	ACCAAATCTG	CTCCCAATCC	AGACAACAAG	1620
GCAGAATTTT	TCCTCTACGA	CAAGGACGAT	ACAGGTGAGG	AAGAAGAGAG	TCAAACAGAA	1680
ACGAAACTAA	CAGGCGAAAT	GCGCTTAGTT	ATCAAGGAGA	TTCTGAAACT	TCATCAAGAA	1740
AAAGGTGTTG	CCTTTAAGGA	AATTGCCCTT	CTGACCTCCA	GCCGCAGTCG	TAATGACCAG	1800
ATTCTCCTCG	CCCTGTCTGA	GTACGGGATT	CCTGTCAAAA	CTGACGGAGA	GCAAAACAAT	1860
TATCTCCAAT	CCCTAGAAGT	GCAAGTCATG	CTAGACACTC	TTCGTGTCAT	TCACAATCCC	1920
CTGCAAGACT	ACGCCTTGGT	TGCCCTTATG	AAGTCTCCAA	TGTTTGGTTT	TGATGAGGAT	1980
GAGCTAGCAC	GTTTGTCCCT	TCAGAAAGCA	GAGGATAAAG	TCCACGAAAA	TCTCTATGAG	2040
AAACTGGTCA	ATGCACAAAA	AATGGCAAGT	AGTCAAAAAG	GCTTGATTCA	CACAGCTCTA	2100
GCTGAAAAAC	TAAAGCAATT	CATGGATATC	CTAGCTTCTT	GGCGCTTGTA	TGCCAAAACC	2160
CACTCTCTCT	ATGACTTGAT	TTGGAAGATT	TACAACGACC	GTTTTTTATTA	TGACTATGTT	2220
GGGGCTTTTG	CGAATGGTCC	TGCTAGGCAG	GCCAATCTCT	ATGCCCTAGC	ACTGCGTGCT	2280
GATCAATTTG	AAAAAGAGCA	TTTCAAAGGT	TTGTCGCGTT	TTATTCTGAT	GATTGACCAA	2340
GTCTTAGAAG	CCCAGCACGA	TTTGGCAAGC	GTGGCCGTCG	CACCGCCAAA	AGATGCAGTA	2400
GAGCTCATGA	CCATCCACAA	GAGTAAAGGG	CTGGAGTTTC	CTTACGTCTT	TATCCTCAAT	2460
ATGGATCAAG	ATTTCAACAA	GCAAGACTCT	ATGTCAGAAG	TCATTCTCAG	TCGTCAGAAT	2520

GGTCTTGGTG	TCAAATATAT	TGCCAAGATG	GAGACAGGGG	CAGTAGAAGA	CCACTATCCT	2580
AAAACCATCA	AACTCTCCAT	TCCTAGTCTG	ACCTATAGGC	AGAACGAAGA	GGAATTACAG	2640
CTAGCAAGCT	ATTCTGAGCA	GATGCGTTTG	CTGTATGTTG	CTATGACGCG	GGCTGAGAAA	2700
AAGCTCTATC	TTGTCGGCAA	GGGTTCTCGT	GAAAAGCTGG	AATCCAAGGA	ATACCCAGCA	2760
GCCAAAAATG	GGAAACTAAA	TAGCAATACT	AGACTGCAAG	CACGGAATTT	CCAAGATTGG	2820
CTTTGGGCTA	TCAGTAAAGT	GTTTACTAAG	GACAAGCTCA	ACTTTAGTTA	TCGTTTTTAT	2880
GGCGAAGATC	AGTTGACCAG	AGAAGCTATC	GGAGAGTTGG	AAACCAAGAG	TCCTCTCCAA	2940
GATAGCTCCC	AAGCAGACAA	TCGTCAGTCA	GATACCATCA	AAGAAGCTCT	GGAAATGCTG	3000
AAGGAGGTGG	AAGTTTATAA	TACTCTTCAC	CGCGCAGCTA	TTGAACTTCC	TAGTGTTCAA	3060
ACCCCAAGTC	AAATCAAGAA	ATTCTACGAA	CCAGTTATGG	ATATGGAAGG	TGTCGAGATT	3120
GCTGGTCAAG	GTCAGTCAGT	AGGCAAGAAA	ATCAGCTTCG	ATTTGCCAGA	TTTTTCAACC	3180
AAAGAAAAGG	TAAGTGGAGC	TGAGATTGGT	AGCGCTACTC	ACGAAGTCAT	GCAGAGAATT	3240
GACCTCAGCC	AGCAACTAAC	CCTTGCTAGC	CTAACAGAAA	CACTCAAACA	AGTTCAAAC	3300
AGCCAAGCTG	TCAGAGACAA	GATCAATCTT	GATAAAATTC	TTGCTTTCTT	TGACACAGTA	3360
CTCGGTCAGG	AAATTCTTGC	TAATACCGAC	CATCTCTATC	GCGAGCAACC	TTTCTCCATG	3420
CTCAAACGAG	ACCAAAAGAG	TCAGGAAGAC	TTTGTGTGCC	GTGGTATCCT	TGATGGCTAT	3480
CTGCTTTTACG	AAAACAAAAT	TGTTCTGTTC	GACTACAAGA	CAGACCGCTA	TGATGAACCA	3540
AGTCAACTCG	TAGACCGCTA	TCGTGGTCAG	TTAGCTCTAT	ACGAAGAGGC	TTTATCACGA	3600
GCCTATTTCGA	TTGAAAATAT	TGAAAAATAC	TTGATTTTAC	TCGGTAAAGA	CGAGGTTCAA	3660
GTTGTAAAAG	TATAA					3675

(2) INFORMATION FOR SEQ ID NO:1745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1745:

AGAAATAAGA	GGAAGAAAAAT	GGAACAAAAA	CACCGTTCAG	AATTTCCAGA	GAAGGAACTC	60
TGGGATTTAA	CAGCCCTATA	CCAAGACCGT	GAGGATTTCT	TGCGTGCAAT	CGAGAAAGCT	120
CGTGAAGACA	TCAACCAGTT	TAGCCGTGAT	TACAAGGGCA	ATCTTCACAC	TTTTGAGGAT	180
TTGAGAGAAG	CCTTTGCGGA	ATTGGAACAG	ATCTACATTC	AGATGAGCCA	TATTGGCAAC	240
TATGCTTTTA	TGCCTCAGAC	GACGGACTAT	AGCAATGACG	AATTTGCCAA	TATTGCCCAA	300
GCTGGGATGG	AATTTGAAAC	AGATGCCAGC	GTAGCCTTGA	CCTTCTTTGA	CGATGCCTTG	360
GTGGTAGCAG	ACGAGGAAGT	CTTGGACCGT	TTGGGTGAAT	TGCCTCACTT	GACGGCAGCT	420
ATTCGTCAGG	CCAAAATCAA	AAAAGCCCAC	TATCTAGGGG	CTGATGTGGA	GAAGGCCTTG	480
ACCAATCTCG	GTGAAGTTTT	CTATAGTCCG	CAGGACATTT	ATACTAAGAT	GCGAGCTGGG	540
GATTTTGAAA	TGGCTGACTT	TGAAGCCCAT	GGCAAGACCT	ATAAAAAACAG	CTTTGTCACC	600
TATGAGAATT	TCTACCAAAA	TCACGAGGAT	GCTGAGGTTT	GTGAGAAATC	CTTCCGTTCC	660
TTCTCAGAGG	GACTTCGTAA	GCACCAAAAT	ACGGCTGCAG	CAGCCTATCT	GGCTCAGGTC	720
AAGTCTGAAA	AACTCTTGGC	TGATATGAAG	GGATACGACT	CTGTCTTTGA	CTATCTTCTA	780

GCTGAACAAG	AAGTGGACCG	TGTCATGTTT	GACCGCCAGA	TTGACCTCAT	CATGAAGGAC	840
TTTGCACCAG	TCGCTCAGAG	ATACCTCAAG	CATGTTGCCA	AGGTAAATGG	TCTTGAAAAG	900
ATGACCTTTG	CAGACTGGAA	ATTGGACTTG	GACAGCGCCC	TCAATCCTGA	AGTACTATT	960
GACGATGCCT	ATGATTTGGT	CATGAAGTCG	GTAGAACCTT	TGGGGCAAGA	ATATTGTCAG	1020
GAAGTTGCTC	GTTATCAAGA	AGAGCGCTGG	GTGGACTTTG	CTGCTAACAG	TGGCAAGGAT	1080
TCCGGTGGTT	ATGCGGCGGA	CCCATATCGC	GTACACCCTT	ATGTACTCAT	GAGCTGGACA	1140
GGCCGTTTGA	GCGATGTCTA	TACCTTGATT	CATGAAATCG	GGCATTCTGG	TCAATTCATC	1200
TTTTTCAGACA	ATCACCAAAG	CTATTTCAAC	GCCCACATGT	CGACCTATTA	TGTTGAAGCA	1260
CCGTCGACCT	TCAATGAATT	GCTACTCAGT	GATTACTTAG	AGAACCAATC	TAATGACCCA	1320
CGTCAAAAAAC	GCTTCGCTCT	GGCTCATCGC	TTGACAGACA	CCTACTTCCA	TAACTTTATC	1380
ACCCACCTCT	TGGAAGCCGC	CTTCCAGCGT	AAGGTGTATA	CATTGATTGA	AGAAGGAGAA	1440
ACCTTCGGAG	CAAGCAAAC	CAACAGCATT	ATGAAGGAAG	TTTTGACAGA	TTTTTGGGGC	1500
GATGCCATTG	AAATCGACGA	CGATGCAGCT	TTGACTTGGA	TGCGCCAAGC	TCACTACTAT	1560
ATGGGCTTGT	ATAGTTACAC	TTACTCTGCT	GGTCTTGTC	TCTCGACAGC	TGGTTACCTT	1620
CATCTTAAAA	ACTCAGAAAC	TGGAGCTGAA	GACTGGCTCA	ATCTCCTCAA	ATCAGGTGGT	1680
AGCAAGACAC	CACTTGAGTC	AGCCATGATT	ATCGGTGCTG	ATATTTCAAC	AGACAAACCA	1740
CTCCGTGATA	CCATCCAATT	CTTGTCTGAC	ACAGTTGACC	AGATTATCGC	CTACAGTGCT	1800
GAGTTGGGGG	AGTAA					1815

(2) INFORMATION FOR SEQ ID NO:1746:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1746:

AAAGATAAGA	GAACAAATAA	AATGATTAAT	ATCAAGCCTG	TTATTTATAA	AGAATTGCAA	60
AAGGTTGCAG	ATAATGTGAC	CGATACTTAT	CCTAGCGATT	GGGAGACTTT	CCCAGTCGTT	120
ATTTTTTTTG	AAGAACAAAA	CAAGCCGGGT	GATTGGTTTG	ATGACCAGGA	ACAAAAATCC	180
TCTATCCGCT	ACAAGGTGGA	TATCTTTGAT	GATACTAGCA	CTAGTGAGTT	AGCTGTTAAA	240
ATCAATCAGA	TTTTTGAGTC	TTTAGGTTTG	CGAAGAACTG	ACTGCCAAGA	CGTGCCAGAC	300
CCGTCTCATT	TGAGACATAA	GGTCATGCGT	TTTGAAGGTA	TCGTCGACTT	ACACTCAGAG	360
CTTGTTTTTC	AATTTAGAAT	GGAGAATTAA				390

(2) INFORMATION FOR SEQ ID NO:1747:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...693
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1747:

CAAGTAAAGA	GAGGAGAAGT	AAATATGGAA	ACACAAGACT	ATGCATTTCA	GCCAGGTTTG	60
ACTGTTGGAG	AATTATTAAA	AAGCAGTCAG	AAGGATTGGC	AGGCTGCAAT	CAATCATCGT	120
TTTGTTAAGG	AACTTTTTGC	GGGGACAATT	GAGAATAAGG	TCTTAAAGGA	CTATCTGATT	180
CAAGATTATC	ACTTCTTTGA	TGCCCTTCTTA	TCCATGCTGG	GTGCCTGCGT	AGCTCACGCA	240
GATAAACTTG	AATCCAAGCT	TCGTTTTGCC	AAGCAACTAG	GCTTTCTTGA	AGCAGATGAA	300
GATGGTTATT	TCCAAAAGGC	TTTTAAAGAG	TTAAAAGTAG	CAGAGATTAT	CTATCTAGAA	360
GTGACTTTGC	ACCCTGTAAC	AAAAGCCTTT	CAGGATCTAA	TGTATTCGGC	GGTGGCTTCA	420
TCAGACTATG	CCCATCTTTT	GGTCATGCTG	GTCATTGCAG	AAGGTCTCTA	TTTAGACTGG	480
GGTTCTAAAG	ATTTGGCTTT	ACCTGAAGTC	TATATTCATT	CGGAATGGAT	CAATCTCCAC	540
AGAGGTCCTT	TCTTTGCGAG	GTGGGTTCAA	TTTCTGGTTG	ACGAACTCAA	TCGTGTCGGT	600
AAAAATCGAG	AAGATTTGAC	AGAACTTCAG	CAACGCTGGA	ATCAAGCAGT	CGCTTTAGAA	660
TTAGCTTTTT	TTGATATTGG	TTACGATGTC	TAG			693

(2) INFORMATION FOR SEQ ID NO:1748:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1320 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1320
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1748:

GGAGTAAAGA	GAGGAGATAT	TCATATGAAA	AACTCAAAAT	TTATAGACCA	ATTTGCCACC	60
TTTGCTGGTA	AAC TAGGGAA	CCAAATTCAT	TTAAAAACCC	TAAGAGATGC	ATT CGTAACA	120
GTAATGCCAT	TATATATTTT	GGCAGGTTTA	ATCGTTCCTT	TGAACAACAC	GGTATTTAAG	180
TGGATTTTCC	AAGGGGATAC	ATTAACAAGA	TTCCAATATT	GGGGAATAAC	AATTGCAAAC	240

GGTACTTTTAA	GTATTTTCAGG	TATGATTATT	GCTGTAATGG	TTGGTTATTT	CTTAGCTAAA	300
AACAGAGATT	TCGAAAACCC	GTTAGCAGCA	TCAATGCTAT	CATTAGTTTC	T'TTAATTGTG	360
ATGATGCCAA	ATACAGTTTC	TGTAGTTCC	GACGGAGCAA	AAGATGCTGT	AAACATTTCA	420
GGTGTTCCTT	CATTCAACAA	CACAGGTACA	GGCGCAATGT	TCGCCGGGGT	TATCGTAGCG	480
ATTATTGCAA	CAGAATTATT	CATTGAATTA	TCAAATGTTA	AAGCTTTACA	AATGAACCTT	540
GGTGAAAATA	TTCCACCAGC	TGTTAGTAGA	TCATTTAGCG	TATTACTTCC	AGTCATGACC	600
GTCATCTCCT	TATTTGGGGT	TGTCTCAGCA	TTATTATTCA	ATATAACTGG	ATTGAACCTTA	660
ATCTCAATCA	TTACAATCTT	TATTCAAGAA	CCAATTCGTC	ATATTGGTAC	AAGCTTAATC	720
GGGGTCATTA	TTATTTACTC	TTTAGGAAAT	ATGTTATGGC	TATTTGGTAT	TCACCAAGCA	780
GTTATTTTACA	GTGCCATCCT	AGAACCATTA	CTATTAATTA	ACATTACTGA	AAACATCACT	840
GCAGCAAATA	ATGGACAAGC	CATTCCACAC	ATCATCAACC	TATCACAAAT	ACAAACATTC	900
GCTTTAATGG	GTGGTAGTGG	ATCTACATTA	TGTTTATTAA	TAGCAACATT	CTTAGTGAGT	960

CGCAATGCTG	TCTCTAAAAA	CGTGGCTAAA	TTATCTTTTG	GACCTGGTAT	CTTCAATATC	1020
AATGAACCAG	TATTATTCGG	TTACCCAATC	GTTTATAACA	TTTCATTAGC	TATTCCATTT	1080
ATCACAGTTC	CAGTCCCTTG	TATTTTAATC	AGCTACTTAG	CAACAGTTAC	AGGATTCATG	1140
AGTCCTGCAT	TTATACAAGT	TCCTTGGA	ACACCAGTAT	TCTTAAATGC	ATGGTTAGCA	1200
ACAGCAGGGG	ACGTGAGAGC	AGTTCCTAGT	CAATTCATCA	TCTTTGCACT	TGGAGTTCCT	1260
CTATACATTC	CATTTATCAA	AGTTAATGAC	AAAGTTGTTG	AACAAGAAAT	GGAAGGTTAA	1320

(2) INFORMATION FOR SEQ ID NO:1749:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1749:

TGTAGAAAGA	GAAGAACGAT	GAAAAAAATG	AGAAAGTTTT	TATGTCTAGC	TGGAATTGCG	60
CTAGCGGCTG	TTGCCCTGGT	AGCTTGTTCA	GGAAAAAAG	AAGCTACAAC	TAGTACTGAA	120
CCACCAACAG	AATTATCTGG	TGAGATTACA	ATGTGGCACT	CCTTTACTCA	AGGACCCCGT	180
TTAGAAAAGTA	TTCAAAAAATC	AGCAGATGCT	TTCATGCAAA	AGCATCCAAA	AACGAAAATC	240
AAGATTGAAA	CATTTTCTTG	GAATGACTTC	TATACTAAAT	GGA	TTTAGCAAAT	300
GGAAATGTGC	CAGATATCAG	TACAGCTCTT	CCTAACCAAG	TAATGGAAAT	GGTCAACTCA	360
GATGCTTTTG	TTCCGCTAAA	TGATTCTATC	AAGCGTATTG	GACAAGATAA	ATTTAACGAA	420
ACTGCCTTAA	ATGAAGCAAA	AATCGGAGAT	GATTACTACT	CTGTTCCCTCT	TTATTACAT	480
GCACAAGTCA	TGTGGGTTAG	AACAGATTTG	TTAAAAGAAC	ATAATATTGA	GGTTCCTAAA	540
ACTTGGGATC	A	AGCTTCTAAA	AAATTGAAAG	AAGCTGGAGT	TTATGGCTTG	600
TCTGTTCCGT	TTGGAACAAA	TGACTTAATG	GCAACACGTT	TCTTGAACCT	CTACGTACGT	660
AGTGGTGGAG	GAAGCCTCTT	AACAAAAGAT	CTTAAAGCAG	ACTTGACAAG	CCA	720
CAAGATGGTA	TTAAATACTG	GGTTAAATTG	TATAAAGAAA	TCTCACCTCA	AGATTCTTTG	780
AACTTTAATG	TCCTTCAACA	AGCTACCTTG	TTCTATCAAG	GAAAAACAGC	ATTTGACTTT	840

AACTCTGGCT	TCCATATCGG	AGGAATTAAT	GCCAACAGTC	CTCAATTGAT	TGATTTCGATT	900
GATGCTTATC	CTATTCCAAA	AATCAAAGAG	TCTGATAAAG	ACCAAGGAAT	TGAAACCTCA	960
AACATTCCAA	TGGTTGTTTG	GAAAAATTCA	AAACATCCAG	AAGTTGCTAA	AGCATTCCTTA	1020
GAAGCACTTT	ATAATGAAGA	AGACTACGTT	AAATTCCTTG	ATTCAACTCC	AGTAGGTATG	1080
TTGCCAACTA	TTAAGGGGAT	TAGCGATTCT	GCAGCCTATA	AAGAAAATGA	AACTCGTAAG	1140
AAGTTTAAAC	ATGCTGAAGA	AGTAATTACT	GAAGCTGTTA	AAAAAGGTAC	TGCTATTGGT	1200
TATGAAAATG	GACCAAGTGT	ACAAGCTGGT	ATGTTGACTA	ACCAACACAT	TATTGAACAA	1260
ATGTTCCAAG	ATATCATTAC	AAATGGAACA	GATCCTATGA	AAGCAGCAAA	AGAAGCAGAA	1320
AAACAATTAA	ACGATTTATT	TGAGGCTGTT	CAGTAG			1356

(2) INFORMATION FOR SEQ ID NO:1750:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1750:

CCAGGAAAGA	GGGAGACTGG	CTTTCTTGCA	GATGCTTGCT	CAAACCCTAC	AGGGCTTTTCG	60
TTAAAACTGT	CGAACATCAG	AGGGAAGACT	CTGGTGTTTT	TTGCTGATGA	GA CTATAAAAT	120
TTTGTAAGAAA	ATGTGATAAA	ATANACGACG	GATAAAATAA	CGGAAGATAG	CATGCAAAAT	180
AAACCAATCA	TTATTGGAGT	GACAGGTGGT	TCTGGTGGTG	GTAAAACCAG	TGTTTCAAGA	240
GCCATTTTAT	CGCATTTTCC	TGATGAAAAG	ATTTCCATGA	TTGAGCATGA	TTCATACTAC	300
AAGGATCAGT	CTCATTTGAC	CTTTGAAGAG	CGTGTCAAAA	CCAACTATGA	CCATCCTTTT	360
GCCTTTGATA	CAGACTTGAT	GATCGAGCAG	ATTAAGGAAT	TGTTGGCAGG	GCGTCCGGTG	420
GACATCCCGA	CCTACGACTA	TACAGAGCAT	ACACGGAGTA	GCAAGACCTA	TCGTCAGGAG	480
CCTCAAGATG	TCTTTATCGT	TGAGGGCATT	TTGGTCTTGG	AGGACAAGCG	TCTGCGCGAT	540
TTGATGGATA	TCAAGATTTT	TGTGGATACG	GATGACGATG	TGCGCATTAT	TCGTCGTATC	600
AAGCGTGATA	TGGAGGAGCG	TGGCCGTAGC	CTTGATAGCG	TTATTAACCA	GTACTTAGGT	660
GTGGTCAAAC	CAATGTACCA	CCAGTTTATC	GAGTCAACTA	AGCGTTATGC	TGATATCGTC	720
ATTCTCTGAAG	GGGTTAGCAA	TACCGTGGCT	ATCGACCTGT	TGACGACCAA	GATTGCAAAG	780
ATTTTGGAAG	AAGCTCGAAA	CAGCAAATAA				810

(2) INFORMATION FOR SEQ ID NO:1751:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...240
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1751:

ATTTTGAAGA	GGAGTTACAC	AATGGTAACC	GTttATTCTA	AAAACAATTG	TGTCCAATGT	60
AAAATGACCA	AGCGTTTCTT	GGACAGTAAT	AATGTCTCTT	ATCGTGAAAT	CAATCTTGAT	120
GAGCAACCTG	AGTACGTCGA	TCAAGTTAAA	GAGCTCGGTT	TTAGCGCAGC	TCCTGTTATC	180
CAAACACCAA	CTGAAGTCTT	TTCAGGTTTC	CAACCAGGAA	AACTGAAACA	ATTAGCATAA	240

(2) INFORMATION FOR SEQ ID NO:1752:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...198
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1752:

AGAATGAAGA	GAGGGATCAT	CTATTTCCTT	ATCGGCCTGT	CACTCTTGGT	ATGGTTAGTG	60
GAAATGTTTA	CTGATTGGTT	TGATCAAGCC	TTGCTTTGCC	AATTCATTCG	TGGTGCTTTG	120
GAGTTTGGAT	TTATGATTTT	CGTCGTTTTT	CCTATGGGAA	TGGAGTGGTT	GAAAGGAGAG	180
TCTCATGACG	GTGGTTAA					198

(2) INFORMATION FOR SEQ ID NO:1753:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1753:

ACGATGAAGA GTAGCACCAG CTGGGGCATG ATACGGATAA ATTCCAGATA CAATCGTGT	60
AAAAATCGTA TGATTCTAGA ATGGGAGGTC ATGATGATTC CCATGACTGT TCCGAACATC	120
ATGGATAAGA GGACAGACAG GATGGATATC CCAATCGTAA CGCCCAACCC CTGTAAGATT	180
CTCAGGAGAT TATTTCCCTTG A	201

(2) INFORMATION FOR SEQ ID NO:1754:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1320 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1754:

GAAAGGAAGA GACCTGAGGG CTCAGACAAA ATTATGACTT CAGTTGTTGT TGTAGGTACC	60
CAATGGGGTG ATGAAGGTAA AGGGAAGATT ACAGACTTCC TTTCAGCGAA TGCAGAAGTG	120
ATTGCACGTT ACCAAGGTGG TGATAATGCT GGTCACACGA TTGTGATTGA CGGTAAGAAA	180
TTTAAAGTTGC ACTTGATTCC ATCTGGGATT TTCTCCCTG AAAAAATATC TGTCATTGGG	240
AATGGTATGG TTGTAAATCC TAAATCTCTT GTAAAAGAGT TGAGCTATCT TCATGAGGAA	300
GGTGTAACAA CTGATAACTT GCGTATTTCT GATCGTGC GC ATGTTATTTT GCCTTATCAT	360
ATCGAGTTGG ATCGCTTGCA AGAAGAAGCT AAGGGCGACA ATAAGATTGG TACGACAATT	420
AAGGGAATTG GTCCAGCTTA TATGGACAAG GCTGCTCGTG TTGGAATTCG TATTGCAGAT	480
CTTTTAGATA AAGATATTTT CCGTGAGCGT TTAGAACGTA ACCTTGCTGA AAAGAATCGT	540
CTTTTGAAGA AATTGTATGA CAGTAAAGCG ATTGTTTTCG ATGATATTTT TGAAGAATAT	600
TACGAATATG GTCAACAAAT CAAGAAATAC GTGATAGATA CATCTGTTAT CTTGAATGAT	660
GCGCTTGATA ATGGCAACG TGTGCTTTTT GAAGGTGCAC AAGGTGTTAT GCTAGATATC	720
GACCAAGGTA CTTATCCATT TGTTACGTCA TCAAACCCTG TAGCTGGTGG TGTGACAATT	780
GGTTCTGGTG TCGGTCCAAG CAAGATTGAC AAGGTTGTAG GTGTATGTAA AGCTTATACG	840
AATCGTGTAG GAAATGGTCC TTTCCCAACT GAGTTGTTTG ATGAAGTGGG AGAACGTATC	900

CGTGAAGTGG	GTCATGAGTA	TGGTACAACA	ACTGGTCGTC	CACGTCGTGT	AGGTTGGTTT	960
GACTCAGTTG	TGATGCGTCA	TAACCGTCGT	GTTTCTGGTA	TTACTAACCT	TTCTTTGAAC	1020
TCTATTGATG	TTTTGAGCGG	TTTGGATACT	GTGAAAATCT	GTGTGGCCTA	TGATCTTGAC	1080
GGTCAACGTA	TTGACTACTA	TCCAGCTAGT	CTTGAGCAAT	TGAAACGTTG	CAAGCCTATC	1140
TATGAAGAGT	TGCCAGGTTG	GTCAGAAGAT	ATTACCGGAG	TTCGCAATTT	GGAAGATCTT	1200
CCTGAGAATG	CGCGTAACTA	TGTTTCGTCGT	GTGAGTGAAT	TGGTTGGCGT	TCGTATTTCT	1260
ACTTTCTCAG	TAGGTCCTGG	TCGTGAACAA	ACAAATATTT	TAGAAAGTGT	TTGGTCCTAA	1320

(2) INFORMATION FOR SEQ ID NO:1755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 933 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1755:

GTACCTGAGA	GCGGAGAAGG	CCATCCTAAA	AAAGTTAAGA	GAACTCCGAT	TGAAGGAGGA	60
AAAAGAGAAA	GAAGAAAGAC	AGAAATTGTT	CAAGAATTAA	TGACTGAGTT	TTCGTTAGAT	120
CTTCTTCTAA	AAGTCATTAA	ACTAGCTCGT	TCGACCTACT	ACTATCACTT	GAAACAGCTA	180
GACAAAACAG	ATAAGGACCA	AGAGCTTAAA	GCTGAAATTC	AATCCATTTT	TATCGAACAC	240
AAGGGAAATT	ATACTTATCG	CCGGGTTCAT	TTAGAACTAA	GAAATCGTGG	TTATCTGGTA	300
AATCATAAAA	GAGTTCAAGG	CTTGATGAAA	GTACTCAATT	TACAAGCTAA	AATGCGACAG	360
AAACGAAAAAT	ATTCTTCTCA	TAAAGGAGAC	GTTGGCAAGA	AGGCAGAGAA	TCTCATTTCAA	420
AGCCAATTTG	AAGGCTCTAA	AACAATGGAA	AAGTGCTACA	CAGATGTGAC	AGAATTTGCC	480
ATTCCAGCAA	GTACTCAAAA	GCTTTACTTA	TCACCAGTTT	TAGATGGCTT	TAACAGCGAA	540
ATTATCGCCT	ATCATCTTTC	TACTTCGCCC	AAC TTAGAAC	AAGTACAAAC	AATGTTGGAA	600
CAGGCATTCA	CAGAGAAGCA	CTACGAGAA	ACGATTCTCC	ATAGTGACCA	AGGCTGGCAA	660
TATCAACACG	ATTCTTATCA	TCGGTTCCTA	GAGAGTAAGG	GAACTCAAGC	ATCCATGTTA	720
CGCAAGGGAA	ACAGCCAAGA	CAACGGTATG	ATGGAATCTT	TCTTTGGCAT	TTTAAAATCG	780
GAAATGTTTT	ATGGCTATGA	GAAAAACATTT	AAATCACTTA	ATCAATTGGA	ACAAGCCATT	840
ATAGACTATA	TTGATTATTA	CAACAACAAG	AGAATTAAGG	TAAAACTAAA	AGGACTTAGC	900
CCTGTGCAAT	ACAGAACTAA	ATCCTTCGGA	TAA			933

(2) INFORMATION FOR SEQ ID NO:1756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 933 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1756:

GTACCTGAGA	GCGGAGAATG	CCATCCTAAA	AAAGTTAAGA	GAACTCCGAT	TGAAGGAGGA	60
AAAAGAGAAA	GAAGAAAGAC	AGAAATTGTT	CAAGAATTAA	TGACTGAGTT	TTCGTTAGAT	120
CTTCTTCTAA	AAGCCATTAA	ACTAGCTCGT	TCGACCTACT	ACTATCACTT	GAAACAGCTA	180
GATAAAACAG	ATAAGGACCA	AGAGCTTAAA	GCTGAAATTC	AATCCATTTT	TATCGAACAC	240
AAGGGAAATT	ATGCTTATCA	TCGGATTAT	TTAGAACTAA	GAAATCGTGG	TTATCTGGTA	300
AATCATAAAA	GAGTTCAAGG	CTTGATAAAA	GTACTCAATT	TACAAGCTAA	AATGCGACAA	360
AAACGAAAAT	ATTCTTCTCA	TAAAGGAGAC	GTTGGTAAGA	AAGCAGAGAA	TCTCATTCAA	420
GGCCAATTTG	AAGGCTCTAA	AACAATGGAA	AAGTGCTACA	CAGATGTGAC	AGAATTTGCC	480
ATTCCAGCAA	GTACTCAAAA	GCTTTACTTA	TTACCAAGTTT	TAGATGGCTT	TAATAGCGAA	540
ATTATCGCCT	ATAATCTTTC	AACTTCACCC	AACTTAGAAC	AAGTACAAAC	AATGTTGGAA	600
CAGGCATTCA	CAGAGAAGCA	CTACGAGAAT	ACGATTCTCC	ATAGTGACCA	AGGCTGGCAA	660
TATCAACACG	ATTCTTATCA	TCGGTTCCTA	GAGAGTAAGG	GAATTCAAGC	ATCTATGTCA	720
CGCAAGGGAA	ACAGCCCAGA	CAACGGCATG	ATGGAATCTT	TCTTTGGCAT	TTTGAAATCG	780
GAGATGTTTT	ATGGTTATGA	GAAGAACTTT	AGATCTTTAG	AAAACCTTGA	ACAAGCTATT	840
GTGGACTACA	TTGATTACTA	CAACAACAAA	CGAATTAAGG	TAAAACTAAA	AGGACTTAGC	900
CTTGTGCAGT	ACAGAACTAA	ATCCTTCGGA	TAA			933

(2) INFORMATION FOR SEQ ID NO:1757:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 933 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1757:

GTACCTGAGA	GCGGAGAATG	CCATCCTAAA	AAAGTTAAGA	GAACTCCGAT	TGAAGGAGGA	60
AAAAGAGAAA	GAAGAAAGAC	AGAAATTGTT	CAAGAATTAA	TGACTGAGTT	TTTGTTAGTT	120
CTTCTTCTAA	AATCCATTAA	ACTAGCTCGT	TGGACCTACT	ACTATCACTT	GAAACAGCTA	180

GACAAAACAG	ATAAGGACCA	AGAGCTTAAA	GCTGAAATTC	AATCCATTTT	TATCGAACAC	240
AAAGGAAATT	ATGCTTATCG	CCGGGTTCAT	TTAGAACTAA	GAAATCGTGC	TTATCTGGTA	300
AATCATAAAA	GAGTTCAAGG	CTTGATAAAA	GTACTCAATT	TACAAGCTAA	AATGCGACAG	360
AAACGAAAAT	ATTCTTCTCA	TAAAGGAGAC	GTTGGCAAGA	AGGCAGAGAA	TCTCATTCAA	420
GGCCAATTTG	AAGGCTCTAA	AACAATGGAA	AAGTGTCTACA	CAGATGTGAC	AGAATTTGCC	480
ATTCCAGCAA	GTACTCAAAA	GCTTTACTTA	TCACCAGTTT	TAGATGGCTT	TAACAGTGAA	540
ATTATTGCTT	TTAATCTTTC	TTGTTCGCCT	AATTTAGAAC	AAGTACAAAC	AATGTTGGAA	600
CAGGCATTCA	AAGAGAAGCA	CTACGAGAAT	ACGATTCTCC	ATAGTGACCA	AGGCTGGCAA	660
TATCAACACG	ATTCTTATCA	TCGGTTCCTA	GAGAGTAAGG	GAATTCAAGC	ATCCATGTCA	720
CGTAAGGGTA	ACAGCCCAGA	CAATGGTATG	ATGGAGTCCT	TCTTTGGGAT	TCTGAAATCG	780
GAAATGTTTT	ACGGTTATGA	GAAGTCGTTT	CAGTCGTTTA	AGCAATTGGA	ACAAGCTATT	840
ATAGACTATA	TTGATTACTA	CAACAATAAA	CGAATTAAGG	TAAAACTAAA	AGGACTTATC	900
CCTGTGCAAT	ACAGAACTAA	ATCCTTCGGA	TAA			933

(2) INFORMATION FOR SEQ ID NO:1758:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 516 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...516
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1758:

TATAATGAGA	GAAGAAAAC	GAAAGGATTT	ACCATGTCAA	AAGAAGTTAT	TGTCGAAAGT	60
TTTGAACCTG	ACCACACCAT	TGTCAAAGCA	CCCTATGTTT	GCTTGATTGG	GGAAGAAACA	120
GGACCAAAAG	GAGACATCAT	CTCCAATTAT	GATATTCGCT	TGGTGCAACC	AAACGAAGAC	180
TCTATCCCTA	CTGCCGGCCT	TCACACTATC	GAGCACCTCT	TAGCCAAACT	CATCCGTACC	240
CGCATTGACG	GCATGATTGA	CTGTTTACCA	TTTGGTTGCC	GCACAGGCTT	CCACATGATT	300
ATGTGGGGAC	GTCACACCAG	TGCTAAAATC	GCAGCTGTTA	TCAAGGATTC	GCTCAAGGAA	360
ATCGCTGAAA	CTACTACTTG	GGAAGATGTC	CCAGGGACAA	CCATCGAATC	TTGCGGAAAC	420
TACAAGGACC	ACAGCCTCTT	CTCTGCTAAA	GAATGGGCAA	AACTCATCTT	GGAACAAGGG	480
ATTTTCAGATG	ATGCCCTTGA	ACGTCATGTG	ATTTAA			516

(2) INFORMATION FOR SEQ ID NO:1759:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1759:

AGCACCGAGA	GATCCAAGGA	TTGGGCGTAC	TGTAAACCAG	AATACTGGGT	CACCGATACC	60
AGCAAGAGGT	CCCATCATAC	CGATTTTGAC	CCCTTGGATA	GCAGCGTCAT	CGATTTCCAC	120
ACCGTTAGCA	CGTTCTTCTT	CAAGCGCAAG	AGTAACCCCC	ATGACTGGAG	CAGCTACGTA	180
TGGATGAGTG	TTGAAGAACT	CAAGGTGACG	CTCAAGAGCA	GCGATTTGAT	CTTCTTTTTT	240
AGTATAGAGT	TTTTTGATAG	CTGGAATGAG	TGTATAAGCC	CAGCCCAAGT	TTTGCATCCG	300
TTCAAAGTTC	CAAGACCCCT	GTAA				324

(2) INFORMATION FOR SEQ ID NO:1760:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1760:

AAAACAGAGA	GGGAAGCTCA	TGGAAGAAGA	TTGAAAATCA	TTCAACAACA	GAGTGCTACA	60
ATTGATAGTC	TCACCAATGA	ACTTGCCCTT	CTGCGTGAAC	AAGTGGCTTA	TCTGACTCAA	120
AAGCTCTATG	GAAAATCCTC	TGAGAAAAGT	GTTTGCCCTT	CTGGACAACT	CAACCTTTTT	180
GAGGAAGAGT	CTCCATCTGA	GGAAGATGGA	GATGTTCCCA	GTTGA		225

(2) INFORMATION FOR SEQ ID NO:1761:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1761:

AAAGAAGAGA GTTGGGACTT GAATAAGCAA AAGATAAGTA ATCTCTTGGG GCTTGCTCAG	60
CGAGCAGGGC GCATCATATC GGGTGAAGAA TTGGTGGTCA AGGCCATTCA AGACGGCAAG	120
GCCAAAGTTGG TCTTTCTAGC TCATGATGCT GGACCCAATC TGGCCAAGAA GATTCAAGAT	180
AAAAGTCATT ATTATCAAGT AGAAATTGTA ACCGTGTTTT CAACACTGGA ATTAAGCATA	240
GCAGTCGGGA AATCGAGAAA GGTTTTGGCT GTAACAGATG CTGGATTTAC AAAGAAAATG	300
AGGTCTCTTA TGAATAG	318

(2) INFORMATION FOR SEQ ID NO:1762:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 789 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1762:

GGAAAGGAGA GAACGATGAA AAAATTTGCC AACCTTTATC TGGGACTGGT CTTATATGGT	60
CTCTACCTGC CTATCTTTTA CTTGATTGGC TATGCCTTTA ATGCTGGTGA TGATATGAAT	120
AGCTTTACAG GTTTTAGCTG GACTCACTTT GAAACCATGT TTGGAGATGG GAGACTCATG	180
CTGATTTTGG CTCAGACATT TTTCTTGGCC TTCCATATCAG CCTTGATAGC GACCATTATC	240
GGGACTTTTG GTGCCATTTA CATCTACCAG TCTCGTAAGA AATACCAAGA AGCCTTTCTA	300
TCACTCAATA ATATCCTCAT GGTTCGCCT GACGTTATGA TTGGTGCTAG CTTCTTGATT	360
CTCTTTACCC AACTCAAGTT TTCACCTGGC TTTTGTGACCG TTCTATCTAG TCACGTGGCC	420
TTCTCCATTC CTATCGTGGT CTTGATGGTC TTGCCTCGAC TCAAGGAAAT GAATGGCGAC	480
ATGATTTCATG CGGCCTATGA CTTGGGAGCT AGTCAATTTT AGATGTTCAA GGAAATCATG	540
CTTCCTTACC TGAATCCGTC TATCATTACT GGTATTTTCA TGGCCTTCAC CTATTCGTTA	600
GATGACTTTG CCGTGACCTT CTTTGTAACA GGAAATGGCT TTTCAACCCT ATCAGTCGAG	660
ATTTACTCTC GTGCTCGCAA GGGGATTTCC TTAGAAATCA ATGCCCTGTC TGCTCTAGTC	720

TTTCTCTTTA GTATTATCCT AGTTGTAGGT TATTACTTTA TCTCTCGTGA GAAGGAGGAG	780
CAAGCATGA	789

(2) INFORMATION FOR SEQ ID NO:1763:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1362 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1763:

AAAGAGGAGA GGATGAAACC AGAATTTTTA GAAAGTGCGG AGTTTTATAA TCGTCGTTAC	60
CATAATTTTT CCAGTAGTGT GATTGTACCC ATGGCCCTTC TGCTCGTGTT TTTACTTGGC	120
TTTGCAACTG TTGCAGAAAA GGAGATGAGT TTGTCCACTA GAGCTACTGT CGAACCTAGT	180
CGTATCCTTG CAAATATCCA GTCAACTAGC AACAATCGTA TTCTTGTCAG TCATTTGGAA	240
GAAAAATAAGC TGGTTAAGAA GGGGGATCTT TTGGTTCAAT ACCAAGAAGG GGCAGAGGGT	300
GTCCAAGCGG AGTCCTATGC CAGTCAGTTG GACATGCTAA AGGATCAAAA AAAGCAATTG	360
GAGTATCTGC AAAAGAGCCT GCAAGAAGGG GAGAACCCTT TTCCAGAGGA GGATAAGTTT	420
GGCTACCAAG CCACCTTTCC CGANTACATC AGTCAAGCAG GCAGTCTTAG GGCTAGTACA	480
TCGCAACAAA ATGAGACCAT CGCGTCCCAG AATGCAGCAG CTAGCCAAAC CCAAGCCGAA	540
ATCGGCAACC TCATCAGTCA AACAGAGGCT AAAATTTCGCG ATTACCAGAC AGCTAAGTCA	600
GCTATGGAAA CAGGTGCTTC CTTGGCCAGT CAGAATTTAG CCTACTCTCT TTACCAGTCC	660
TACAAGTCTC AGGGCGAGGA AAATCCCCAA ACTAAGGTTT AGGCAGTTGC ACAGGTTGAA	720
GCACAGATTT CTCAGTTAGA ATCTAGTCTT GCTACTTACC GTGTCCAGTA TGCAGGTTCA	780
GCTACCCAGC AAGCCTATGC GTCAGGGTTA AGCAGTCAAT TGGAATCCCT TAAATCCCCA	840
CATTTGGCAA AGGTTGGTCA GGAATTGACC CTTCTAGCCC AGAAATACTT GGAGGCAGAG	900
TCAGGTAAGA AGGTACAGGG AAATCTTTTA GACAAGGGGA AAATTACGGC GAGTGAGGAT	960
GGGGTGCTTC ATCTTAATCC TGAGACCAGT GATTCTAGCA TGGTTGCAGA AGGTGCCCTA	1020
CTAGCCCAAC TTTATCCATC TTTGGAAAGA GAAGGGAAAG CCAAACCTCAC AGCCTATCTA	1080
AGTTCAAAAAG ATGTAGCAAG AATCAAGGTC GGTGATTCTG TTCGCTATAC TACGACTCAT	1140
GATGCCGGGA ATCAACTTTT CCTAGATTCT ACTATTACAA GTATTGATGC GACAGCTACT	1200
AAGACTGAGA AAGGGAATTT CTTTAAAATC GAGGCGGAGA CTAATCTAAC TTCGGAGCAG	1260
GCTGAAAAAC TTAGGTACGG GGTGGAAGGC CGCTTGCAGA TGATTACGGG CAAGAAAAGT	1320
TATCTACGTT ATTATTTGGA TCAATTTTGT AACAAAGAGT AA	1362

(2) INFORMATION FOR SEQ ID NO:1764:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 708 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1764:

AACGATTGGA	GAAATCTTAT	GATATTTTCGA	GTGAAAGTAA	ATTCTTCTGT	TTCTAGGCCT	60
GTAACCGTTG	AAGACATTTG	CCCAAATTGT	AAAAAACCAA	CCAATCCAGA	TCTTGTGAAC	120
TCTTCTTATT	TTTCTCTTGG	AGAAAATAAA	ACAAGCTTAG	TATTAACATG	TAGATGCTTA	180
GGTTGTAAAG	ACTTTTGGAC	AGAGGAGTTT	ATAGCTACAA	GATTTTTTAAT	CAATGACTAT	240
ACCGAAAAAT	ACGAAATTGA	ACATATCAAA	GTAATCCCTA	ATCTTCCGAG	CGATATACCT	300
ATATCTGACG	ATGTAGAGAT	AGTTTCTCCA	ATTGGTAAGC	AAATCTATGT	CCAAGCACTG	360
AAAGCTGAAC	ACGAACAAC	AGACCACATT	GCAGGTATTG	GATACCGTAA	GGCGCTTGAG	420
TTCTTTGTTA	AAGATTTCTC	CATTGTTACA	AATCCTGATG	ATGAAGATAA	AATCATTAAA	480
ATGTCATTAA	AACAAGTTAT	TGAAAAATAT	ATCAAGGATG	AAGACCTTAA	AACATTTGCG	540
CTTGCACTCG	CTTATATCGG	TAACGACGAA	GGTCATTACT	ATAGAAATAA	TCCTGATAAA	600
GGTTTTACAG	ACCTAAAGAA	CTACCTACAC	GGAGTTATTC	ACTACATGGA	AATGAAACTC	660
AATTTCCCTG	ATGCTCAAGA	GCTTGTGAAT	CGTTCAAAGA	AATCTTAG		708

(2) INFORMATION FOR SEQ ID NO:1765:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 864 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1765:

CAAAGATGGA	GAATTTCTAT	GACTTGGAAG	ATTATTGCTG	ACTCTGGTTG	TGATTATCGT	60
CAACTGCCAA	CACCAGCTAT	TAACACAACC	TTTGTAAGTG	TCCCCTTAAC	CATTCAAGTA	120
GCTGATCAGG	TCTTTGTTGA	TGACGCCAGT	CTCGATATTG	ACCAAATGAT	GGAAACCATG	180
TATGCAACTG	CAGAAGCTTC	AAAATCGGCT	TGTCCAAGCC	CAGATGACTA	TTTGCGAGCA	240
TTTGAAGGTG	CCAAAAACAT	TTTCCTAGTA	ACCATCACAG	GTACCCTTTC	TGGCAGTCAC	300

AATAGTGCTC	AACTAGCAAA	GAATATTTAT	CTGGAAGACC	ATCCTGACAC	TAAGATTCAT	360
GTGATTGATA	GTTTATCTGC	TGGTGGTGAA	GTTGACCTAC	TCGTAGAAAA	ATTGAATGAC	420
TTGATTGACC	AGGGCTTGTC	TTTTGAAGAA	GTGGTTGAAG	CTATCACCGC	CTATCAAGAA	480
AAAAC TAAGT	TGCTCTTTGT	CCTAGCCAAA	GTCGATAACT	TGGTGAAGAA	CGGCCGTTTG	540
AGCAAGCTTA	TCGGTACGGT	CGTTGGCCCT	CTCAACATTC	GTATGGTCGG	AAAAGCTAGT	600
GAAACTGGAA	CTCTCGAATT	GCTACAAAAA	GCAAGGGGAT	CAAAGAAATC	AGTTCAAGCT	660
GCCTATGATG	AGTTAGTAAA	AGCTGGATAT	GCTGGTGGCC	GTATTGTCAT	GGCCCAACGC	720
AATAACGAAA	AATGTTGTCA	ACAACTCTCA	GAGCGAATCC	GTGAAACCTT	CCCACAAGCG	780
GATATTAAAA	TTCTACCAAC	CTCTGGTCTC	TGCAGTTTCT	ATGCAGAAGA	TGGCGGTTTG	840
CTGATGGGCT	ATGAAATTGA	TTAA				864

(2) INFORMATION FOR SEQ ID NO:1766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1821 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1766:

AAAGGATGGA	GGAATCTAAT	GGTATTACAA	AGAAATGAAA	TAAATGAAAA	AGATACATGG	60
GATCTATCAA	CGATCTACCC	AACTGACCAG	GC'TTGGAAG	AAGCC'TTAAA	AGATTTAACA	120
GAACAATTGG	AGACAGTAGC	CCAGTATGAA	GGCCATCTCT	TGGATAGTGC	GGATAACCTA	180
CTAGAAATCA	CTGAATTTTC	TCTTGAAATG	GAACGCCAGA	TGGAGAAGCT	TTACGTTTAT	240
GCTCATATGA	AGAATGACCA	GGATACACGT	GAAGCTAAGT	ATCAAGAGTA	CTATGCCAAG	300
GCCATGACAC	TCTACAGCCA	GTTAGACCAA	GCCTTTTCAT	TCTATGAGCC	TGAATTTATG	360
GAGATTAGCG	AAAAGCAGTA	TGCTGACTTT	TTAGAAGCTC	AACCAAAGCT	GCAGGTTTAT	420
CAACACTATT	TTGACAAGCT	CTTGCAAGGC	AAGGATCACG	TTCTTTTACA	ACGTGAAGAA	480
GAATTATTGG	CTGGAGCTGG	AGAAATCTTT	GGTTCAGCAA	GTGAAACCTT	CTCTATCTTG	540
GACAATGCGG	ATATTGTGTT	CCCTTATGTC	CTAGACGATG	ATGGTAAAGA	AGTTCAGCTA	600
TCTCATGGGA	CTTACACACG	TTTGATGGAG	TCTAAAAAAC	GTGAGGTTTCG	CCGTGGTGCC	660
TATCAAGCTC	TTTATGCGAC	TTACGAACAA	TTCCAACACA	CCTATGCCAA	AACCTTGCAA	720
ACCAATGTTA	AGGTGCAAAA	TTACCGTGCT	AAAGTTCGTA	ACTACAAGAG	TGCTCGTCAT	780
GCAGCCCTCG	CAGCGAATTT	TGTTCCAGAA	AGTGT'TTATG	ACAATTTGGT	AGCAGCAGTT	840
CGCAAGCATT	TGCCACTCTT	ACATCGCTAT	CTTGAGCTTC	GTTCAAAAAT	CTTGGGGATT	900
TCAGATCTCA	AGATGTACGA	TGTCTACACA	CCGCTTTTCAT	CTGTTGAATA	CAGTTTTTACC	960
TACCAAGAAG	CCTTGAAAAA	AGCAGAAGAT	GCTTTGGCAG	TCTTGGGTGA	GGATTACTTG	1020
AGCCGTGTCA	AACGTGCC'TT	CAGCGAGCGT	TGGATTGATG	TTTACGAAAA	TCAAGGCAAG	1080
CGTTCAGGTG	CCTACTCTGG	TGGTTC'TTAT	GATACCAATG	CCTTTATGCT	TCTCAACTGG	1140
CAGGACAATC	TGGACAATCT	CTTTACTCTT	GTTCATGAAA	CAGGTCACAG	TATGCATTCA	1200
AGCTATACTC	GTGAAACTCA	GCCTTATGTT	TACGGAGATT	ACTCTATCTT	TTTGGCTGAG	1260

ATTGCCTCAA	CTACCAATGA	AAATATCTTG	ACGGAGAAAT	TATTGGAAGA	AGTGAAGAC	1320
GACGCAACAC	GCTTTGCTAT	TCTCAATAAC	TTCCTAGATG	GTTTCCGTGG	AACAGTTTTTC	1380
CGCCAAACTC	AATTTGCTGA	GTTTGAACAC	GCCATTCCACC	AAGCAGATCA	AAATGGGGAG	1440
GTCTTGACAA	GCGATTTCCCT	AAATAAACTC	TACGCAGACT	TGAACCAAGA	GTATTATGGT	1500
TTGAGTAAGG	AAGACAATCC	TGAAATCCAA	TACGAGTGGG	CTCGTATTCC	ACACTTTTAC	1560
TATAACTACT	ATGTATATCA	ATATTCAACT	GGATTTGCGG	CCGCCTCAGC	CTTGGCTGAA	1620
AAAAATTGTCC	ATGGTAGTCA	AGAAGACCGT	GACCGCTATA	TCGACTACCT	CAAGGCAGGT	1680
AAGTCGGACT	ATCCACTTAA	TGTCATGAGA	AAAGCTGGTG	TTGATATGGA	GAAGGAAGAC	1740
TACCTCAACG	ATGCCTTTGC	AGTCTTTGAA	CGCCGTTTAA	ATGAGTTTGA	AGCCCTTGTT	1800
GAAAAATTAG	GATTGGCATA	A				1821

(2) INFORMATION FOR SEQ ID NO:1767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1761 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1767:

ATCTGTCGGA	GAAAGTGTGG	AATTATTTTAT	CACACCATCA	GACGTTCTGC	AATTTTAAAGG	60
AGGTGCAGTA	TGCGTCATAA	ATTAAATTTA	AAAGATTGGC	TTATTCGTTT	AGGGTTAATC	120
TGGTTCTTAG	TAACATTTAT	TATTTATCCA	AACTTTGATC	TAGTAGTGAA	TGTATTTGTA	180
AAAGGAGGAG	AATTTTCCCT	TGATGCTGTA	CATCGTGTTT	TAAAATCTCA	GAGGGCACTT	240
CAGAGTATTA	TGAACAGTTT	TAAGTTAGCA	TTTTCACTCA	TTATTACAGT	TAATGTCGTA	300
GGTATTCTTT	GTGTTCTATT	TACAGAGTAC	TTTGATATTA	AAGGTGCTAA	AATTTTAAAA	360
TTAGGTTATA	TGACCTCTTT	AATTTATGGA	GGAGTGGTTT	TAGCGACTGG	ATATAAATTT	420
GTCTATGGTC	CATATGGATT	GATTACAAAA	TTTTTACAAA	ATGTTATCCC	TTCTTTAGAC	480
CCTAACTGGT	TTATTGGGTA	TGGTGCAGTC	TTATTCAATTA	TGACATTTTC	AGGAACTGCT	540
AATCATACAT	TGTTTTTAAAC	AAATACAATT	CGAAGCGTTG	ACTATCACAC	TATTGAGGCT	600
GCTCGAAATA	TGGGAGCAAA	ACCATTTACT	GTTTTCCGAA	AAGTAGTGTT	ACCAACCTTA	660
ATTCCAACTC	TATTTGCACT	TACTATTATG	GTTTTTCTTA	GTGGTTTATC	TGCAGTAGCA	720
GCACCCATGA	TTGTTGGTGG	TAAAGAATTT	CAAACATAAA	ATCCAATGAT	TATTACATTT	780
GCAGGGATGG	GGAATTCTCG	TGATTTAGCT	GCCTTACTTG	CAATTATTTT	AGGTATTGCA	840
ACTACAATTT	TGCTTACTAT	CATGAATAAG	ATAGAAAAAG	GAGGAAATTA	TATTTCTATC	900
TCTAAGACTA	AAGCGCCTCT	TAAAAAACAA	AAAATTGCGT	CTAAGCCTTG	GAATATCATT	960
GCTCACATTG	TAGCATATGG	ATTGTTTACA	GTTTTTCATG	TTCCACTAAT	TTTTTATAGTA	1020
TTATACTCAT	TTACAGATCC	AGTTGCAATT	CAAACAGGTA	ACTTAACATT	ATCAAACTTT	1080
ACTTTAGAAA	ATTATCGCTT	ATTCTTTAGT	AATAGTGCGG	CATTCTCTCC	ATTCCTGGTC	1140
AGCTTTATTT	ATTCTATTAT	TGCTGCGACA	ACAGCAACAA	TTCTCGCAGT	TGTATTTGCT	1200
CGTGTGTGTC	GAAAAACATA	ATCTCGTTTT	GATTTCTTAT	TTGAATATGG	TGCTCTACTT	1260
CCTTGGTAC	TACCAAGTAC	ACTTTTAGCA	GTAAGTTTAT	TATTTACTTT	TAATCAGCCA	1320

CAATTTCTTG	TCTTGAATCA	GATTTTGGTA	GGTAGTTTGG	TAATTCTACT	TATTGCATAT	1380
ATAGTTGTAA	AAATCCCATT	TTCTTATAGA	ATGGTACGTG	CTATTTTATT	TAGTGTGAT	1440
GATGAGATGG	AAGATGCAGC	AAGAAGTATG	GGTGCTTCAC	CTTTTTTATAC	TATGATGAAG	1500
GTTATCATTC	CATTTATTTT	ACCGGTTGTT	CTCTCTGTTA	TTGCTTTAAA	CTTTAACTCT	1560
TTATTAAGTG	ACTTCGACTT	ATCTGTATTC	CTTTACCATC	CCCTAGCTCA	ACCATTAGGT	1620
ATTACGATTC	GATCTGCAGG	TGATGAAACA	GCAACATCTA	ATGCACAAGC	TCTGGTATTT	1680
GTTTATACAA	TTGTTCTGAT	GATTATTTCT	GGAACGGTAT	TATACTTCAC	ACAAAGACCG	1740
GGGCGTAAAG	TAAGGAAATA	A				1761

(2) INFORMATION FOR SEQ ID NO:1768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1768:

TTGAAACGGA	GAAAAAAGA	GGAGCGAGTC	CTGCTGATTG	GTGTGGAATT	GCAGGGTATG	60
GACAGTTTTG	ACCTCTCCAT	GGAAGAATTG	GCTAGTTTAG	CGAAAACGGC	AGGGGCAGTC	120
GTTGTAGATA	GCTACAGACA	AAAACGTGAA	AAATATGATT	CCAAGACCTT	CGTCGGCTCT	180
GGTAAGTTGG	AAGAGATTGC	GCTTATGGTG	GATGCAGAAG	AAATCACTAC	TGTCATCGTC	240
AACAATCGTC	TGACCCCAAG	GCAGAATGTC	AATCTAGAGG	AAGTTCTCGG	TGTTAAGGTC	300
ATTGACCGTA	TGCAGTTGAT	TTTGGATATC	TTTGCCATGC	GGGCTCGAAG	CCATGAAGGG	360
AAGCTCCAAG	TCCACCTAGC	CCAATTCAAA	TACCTCTTGC	CTCGCTTGGT	TGGTCAGGGG	420
ATTATGCTCA	GCCGTCAGGC	AGGGGGAATT	GGTTCCCGTG	GTCCCTGGTG	AAGCCAAGTG	480
GAGCTGAACC	GTCGTAGCGT	TCGCAATCAA	ATCACGGATA	TCGAGCGCCA	GCTTAAGGTG	540
GTTTGAGAAA	ATCGTGCGAC	TGTCAGAGAA	AAACGTTTGG	AGTCTAGCAC	TTTTAAGATT	600
GGTTTGATTG	GTTATACTAA	TGCTGGGAAA	TCAACTATCA	TGAACATCTT	GACCAGTAAG	660
ACCCAGTATG	AAGCAGATGA	GCTCTTTGCG	ACTCTGGATG	CGACAACCAA	GAGTATTCAT	720
CTGGGAGGCA	ATCTCCAAGT	AACTTTGACA	GATACCGTTG	GCTTTATCCA	AGATTTGCCG	780
ACAGAGTTGG	TGTCCAGTTT	CAAGTCAACC	TTGGAAGAAA	GCAAGCATGT	GGACCTTCTG	840
GTTTCATGTTA	TCGATGCTAG	CAATCCTTAC	CACGAGGAGC	ATGAAAAAAC	GGTTCTCTCC	900
ATCATGAAAG	ACCTGGACAT	GGAAGATATT	CCTCACTTGA	CGCTTTTATA	TAAAGCGGAT	960
TTGGTGGAGG	ATTTACAGCC	TACCCAAACG	CCATATACCC	TCATTTCTGC	CAAGTCTGAG	1020
GACAGTCGTG	AAAACCTTGA	AGCATTTATT	CTAGATAAGA	TTAAGGAAAT	TTTTGAAGCA	1080
TTTACCCTGC	GAGTGCCTTT	TTCAAAGTCC	TACAAGATTC	ATGATTTAGA	GAGTGTGCA	1140
ATTCTGGAAG	AACGTGATTA	TCAGGAAGAC	GGCGAAGTGA	TTACAGGCTA	CATTTCCGAG	1200
AAAAATAAAT	GGAGTTTAGA	AGAATTTTAT	GACTGA			1236

(2) INFORMATION FOR SEQ ID NO:1769:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1347 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1769:

AGCTTTAGGA	GGAGGAGCAG	TAAAAGGATG	AAACATACAC	TTGAAACTAT	CAATAGTAGA	60
ACTCAGTGGT	TTAGAGAAGC	AAGATTTGGG	ATGTTTCATC	ATTGGGGGTT	ATATTCTATT	120
CCAGGAAAAG	GGGAATGGAT	TCGTAGTCAT	CAGAAATTAT	CTATTGAAGA	TTATGAACCA	180
TATTTTCGAG	CTTTTGATCC	TAAGGAATAT	AACCCTAGAG	AATGGGCTAA	ACAAGCAAAA	240
GCTGCAGGGA	TGAAGTATAT	GGTTTTAACG	GCTAAACATC	ATGATGGGTT	TTGTTTGTTT	300
GATTCAAAAT	TTACAGATTA	TAAAGCAACA	AATACACCTG	CAGGTAGAGA	TTTAGTTAAA	360
GAATTTGTAG	ATGCTGTTTC	AGCTGAAGGT	TTAAAAGTAG	GCTTATATTT	TAGTTTGATT	420
GA CTGGCACC	ATCCTGATTT	CCCTAAATAT	GCTGATCTAA	ATCATCCAAT	GAGAGGAAAT	480
GAAGCCTATC	GAGATGAGAA	AATTAACTTT	GACAGTTATT	TGGAGTATTT	ACACAATCAA	540
GTTAAAGAAA	TTGTAAC TGG	TTATGGTCAG	ATTGACATAT	TATGGTTTGA	TTATTCTTAT	600
GAAGACATGG	TGGGTGAAAA	ATGGGGAGCT	TCAAAATTAA	TAGACATGGT	TCGTCATTAT	660
CAGCCAAACG	TTATCGTAGA	TAATAGATTA	GAAACATCAG	GTGAAGGATT	CGGAAGTATC	720
GTTACAGATG	AAATTACCTC	TTACGCTGGA	GATTTTGTTA	GTCCAGAGCA	AATTGTTCCCT	780
CACGAAGGTA	TTCGAAACTT	TAAAGGTGAA	CCTGTTCCCT	GGGAACTTTG	TCTAACTATG	840
AATAACAATT	GGGCTTATAA	TCCTACAGAT	TATCTATATA	AGTCTAGTCA	AACTTTGATA	900
AGAAAAGTTAG	TGGAATGTGT	TAGTAAAAAC	GGAAATATGA	TTCTTAATGT	AGGCCCAGAT	960
GCTTTGGGAA	GAATTAATGA	TTCAAGTAAG	AAAAATATTAG	ATAATTTTCA	TCGATGGATG	1020
TCTCGAAATG	GTGAGGCAAT	TTATGGATGT	AGTGGAGATG	AAAATTTACC	AAAACCAGAT	1080
TGGGGATACT	ATACTCGTAA	TGGAAATACG	GTTTATGCTC	ATGTATTTGA	ACAACCTATA	1140
GGTCCTTTAG	CTCTTCTTGG	TATTAGTAAA	GAAAACGTAA	AAAGAATGAG	CTTTC TTCAT	1200
GATGGAAGTG	AGGTGAAAAT	TTCAGAAAGC	TGGACGACCA	ATGCCTACAA	AGGAATTTGT	1260
TTTGACAGAT	TTGGAGAAGT	TCCACATTTT	ACCTATCCAT	TACCAGACTT	GATTGATAGC	1320
GTAATCAAAA	TTGAGTTGAG	AGAGTAG				1347

(2) INFORMATION FOR SEQ ID NO:1770:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 654 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1770:

TATAATAGGA	GTATGATTAC	AATAGTTTTA	TTAATCCTAG	CCTATCTGCT	GGGTTCGATT	60
CCATCTGGTC	TCTGGATTGG	ACAAGTATTC	TTTCAAATCA	ATCTACGCGA	GCATGGTTCT	120
GGTAACACTG	GAACGACCAA	CACCTTCCGC	ATTTTAGGTA	AGAAAGCTGG	TATGGCAACC	180
TTTGTGATTG	ACTTTTTCAA	AGGAACCCTA	GCAACGCTGC	TTCCGATTAT	TTTTCATCTA	240
CAAGGCGTTT	CTCCTCTCAT	CTTTGGACTT	TTGGCTGTTA	TCGGCCATAC	CTTCCCTATC	300
TTTGCAGGAT	TTAAAGGTGG	TAAGGCTGTC	GCAACCAGTG	CTGGAGTGAT	TTTCGGATTT	360
GCGCCTATCT	TCTGTCTCTA	CCTTGCGATT	ATCTTCTTTG	GAGCTCTCTA	TCTTGGCAGT	420
ATGATPTCAC	TGTCTAGTGT	CACAGCATCG	ATTGCGGCTG	TTATCGGGGT	TCTGCTCTTT	480
CCACTTTTTG	GTTTTATCCT	GAGTAACTAT	GACTTTCTCT	TCATCGCTAT	TATCTTAGCA	540
CTTGCTAGTT	TGATTATCAT	TCGTCATAAG	GACAATATAG	CTCGTATCAA	AAATAAAACT	600
GAAAAATTTG	TCCCTTGGGG	ATTGAACCTA	ACCCATCAAG	ATCCTAAAAA	ATAA	654

(2) INFORMATION FOR SEQ ID NO:1771:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1962 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1962

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1771:

ACGAATAGGA	GGTTCCTTGT	GTCAAAAAAG	GAAATCAATA	TTAACAATTA	TAATGATGAT	60
GCTATTTCAGG	TGCTAGAAGG	GTTGGATGCG	GTCCGAAAAC	GTCCGGGGAT	GTATATTGGA	120
TCGACCGATG	GCGCTGGTCT	TCATCACCTA	GTTTGGGAAA	TCGTTGATAA	TGCAGTCGAT	180
GAAGCCTTGT	CTGGGTTTGG	TGATCGTATT	GATGTAACCTA	TCAATAAAGA	CGGTAGTCTA	240
ACGGTTCAAG	ACCATGGACG	TGGGATGCCG	ACAGGTATGC	ACGCTATGGG	AATTCCAAC	300
GTTGAGGTTA	TCTTTACCAT	TCTTCATGCC	GGAGGGAAAT	TCGGTCAAGG	TGGCTATAAG	360
ACATCAGGTG	GACTTCACGG	AGTGGGTTCT	TCCGTTGTTA	ACGCCCTTTC	TAGCTGGTTA	420
GAAGTTGAAA	TTACCCGTGA	TGGCGCAGTT	TACAAGCAAC	GTTTCGAAAA	TGGTGGAAAA	480
CCTGTACACGA	CTTTGAAGAA	AATCGGTACA	GCACCCAGT	CTAAAACAGG	CACCAAAGTT	540
ACTTTTATGC	CTGACGCGAC	TATATTTTCT	ACGACAGATT	TCAAGTACAA	TACCATTTCA	600
GAGCGCCTTA	ATGAATCAGC	CTTCTCTTTG	AAAAATGTGA	CCTTGTCTTT	AACGGACAAG	660
CGAACAGATG	AAGCGATTGA	GTTCCACTAT	GAGAATGGAG	TACAAGATTT	TGTTTCTTAT	720

CTCAACGAAG	ATAAGGAAAT	CTTGACGCCA	GTTCTTTACT	TTGAAGGGGA	AGACAATGGT	780
TTTCAAGTGG	AAGTAGCCCT	CCAGTACAAT	GACGGATTCT	CAGATAACAT	TCTATCCTTT	840
GTCAATAACG	TTCGCACCAA	GGACGGTGGA	ACGCACGAGA	CAGGACTCAA	GTCTGCCATT	900
ACCAAGGTCA	TGAATGACTA	TGCACGTAAA	ACAGGCTCTC	TCAAGGAAAA	AGATAAAAAAC	960
CTTGAAGGTT	CAGACTATCG	TGAGGGACTA	GCGGCCGTTT	TTTCTATCTT	AGTTCCTGAA	1020
GAACACTTGC	AGTTTGAAGG	ACAGACCAAG	GATAAACTAG	GAAGCCCCCT	AGCTCGCCCA	1080
GTTGTGGATG	GAATAGTGGC	TGATAAGTTG	ACCTTTTTTCC	TTATGGAAAA	TGGGGAATTA	1140
GCTTCTAACC	TCATCCGCAA	GGCTATCAAG	GCCCCGTGAT	CTCGTGAAGC	AGCACGTAAG	1200
GCGCGTGATG	AGAGCCGAAA	TGGGAAGAAA	AACAAGAAAG	ATAAGGGCTT	GTTGTCTGGG	1260
AAATTGACCC	CAGCCCAATC	TAAGAATCCT	GCTAAGAATG	AACTCTATCT	AGTTGAGGGG	1320
GACTCTGCCG	GTGGTTCTGC	CAAACAAGGT	CGTGACCGCA	AGTTCCAGGC	TATTCTACCT	1380
CTTCGTGGTA	AGGTTATCAA	TACAGCCAAG	GCCAAGATGG	CGGATATCCT	CAAAAATGAA	1440
GAGATCAATA	CCATGATTTA	TACCATTTGGT	GCGGGTGTTG	GAGCAGACTT	CTCTATTGAA	1500
GATGCCAACT	ATGATAAGAT	CATTATCATG	ACCGATGCGG	ATACCGACGG	TGCCCATATC	1560
CAGACCTTGC	TCTTGACATT	TTTCTACCGT	TACATGCGTC	CGCTAGTCGA	GGCAGGTCAT	1620
GTCTATATTG	CCCTCCCACC	TCTTTACAAG	ATGTCCAAAG	GTAAAGGAAA	GAAAGAAGAA	1680
GTGGCCTACG	CTTGGACGGA	CGGAGAACTA	GAAGAACTCC	GTAAACAGTT	CGGTAAAGGC	1740
GCTACCCCTC	AACGATACAA	AGGACTTGGT	GAGATGAATG	CGGACCAGCT	CTGGGAAACA	1800
ACCATGAACC	CAGAAACACG	TACCCTCATC	CGTGTCACAA	TTGAAGATTT	AGCGCGCGCC	1860
GAACGCCGCG	TCAATGTTCT	CATGGGAGAT	AAGGTAGAAC	CACGCCGTAA	ATGGATTGAA	1920
GATAATGTCA	AGTTTACGCT	AGAAGAAGCG	ACAGTGTTTT	AA		1962

(2) INFORMATION FOR SEQ ID NO:1772:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 990 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...990
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1772:

CCATGTAGGA	GATACAGATA	CAGCCCTAGA	AGAATTGGAA	CGTTTAATTT	CCCCAAAGAG	60
AAGAATGGAG	TAATAATGGC	AACAAAACAA	AAAGAAGTAA	CAACATTTGA	CGTACAGGTA	120
GCAGAATTTA	TCCGTAAATCA	TAAGCAAAAA	GGGACAGCAA	CAGATGATGA	AATCAATGCA	180
AGTTTGGTTA	TTCTTTTAC	CTTGGACGCT	GATGGGATTG	AAGATCTCTT	GCAACGGATT	240
CAGGATGCAG	GAATTTCTAT	CACAGATAAC	GAAGGAAATC	CAAGTGCGCG	TGTTCTTAGC	300
AATGAAGAAG	AACCAGAACT	CAGCGATGAG	GACTTGATTG	GGTCAACTTC	TGCTAAGGTC	360
AATGACCCTG	TCCGTATGTA	CTTGAAAGAA	ATAGGGGTCG	TTCTCTCTT	GACCAATGAA	420
GAGGAGAAAG	AGTTGGCACT	GGCTGTTGAA	GCTGGTGATA	TCGAAGCCAA	ACAACGTCTT	480
GCGGAAGCCA	ATCTTCGTTT	GGTTGTTTCC	ATTGCCAAAC	GCTATGTCGG	TCGTGGTATG	540
CAGTTCCTTG	ACTTGATTCA	AGAAGGAAAT	ATGGGCTTGA	TGAAGGCGGT	TGACAAGTTT	600
GACTATTCTA	AAGGGTTCAA	GTTTTCAACT	TATGCAACTT	GGTGGATTCT	TCAGGCTATC	660
ACTCGTGCTA	TTGCAGACCA	AGCTCGTACC	ATCCGTATCC	CAGTTCACAT	GGTTGAAACT	720

ATCAATAAAT	TGGTTCGTGA	ACAGCGGAAT	CTCCTTCAAG	AATTGGGGCA	AGATCCGACA	780
CCAGAACAGA	TTGCTGAACG	AATGGATATG	ACACCTGATA	AGGTTTCGTGA	AATCTTGAAG	840
ATTGCCCAAG	AACCAGTATC	TCTTGAAACT	CCTATCGGTG	AAGAGGACGA	TAGCCACCTT	900
GGAGACTTTA	TCGAAGATGA	AGTGATTGAA	AATCCAGTGG	ATCTCATACG	ACTCGTATCG	960
TCTTGCGTGA	GCAATTGGAT	GAAATCTTAG				990

(2) INFORMATION FOR SEQ ID NO:1773:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1383
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1773:

AATAGTAGGA	GTAGAAATGG	AGTTCGAGAC	ATGAAAGTAA	TAGATCAATT	TAAAAATAAG	60
AAAGTCCTTG	TTTTAGGTTT	GGCCAAGTCT	GGTGAATCTG	CAGCTCGTTT	GTTGGACAAG	120
CTAGGTGCCA	TTGTGACAGT	AAATGATGGG	AAACCTTTTCG	AGGACAATCC	AGCTGCCCCA	180
AGTTTGCTGG	AAGAAGGGAT	CAAGGTCATT	ACAGGTGGCC	ATCCTTTGGA	ACTCTTGGAT	240
GAAGAGTTTG	CCCTTATGGT	GAAAAATCCA	GGTATCCCTT	ACAACAATCC	CATGATTGAA	300
AAGGCTTTGG	CCAAGGGAAT	TCCAGTCTTG	ACTGAGGTGG	AATTGGCTTA	TTTGATTTC	360
GAAGCACCGA	TTATTGGTAT	CACAGGATCG	AACGGTAAGA	CAACCACAAC	GACTATGATT	420
GGGGAAGTTT	TGACTGCTGC	TGGGCAACAT	GGTCTTTTAT	CAGGGAATAT	CGGCTATCCA	480
GCTAGTCAAG	TGGCCCAAAC	TGCGTCGGAC	AAGGACACGC	TTGTTATGGA	ACTTTCTTCT	540
TTCCAACCTCA	TGGGTGTTCA	AGAATTTTCAT	CCAGAGATTG	CGGTTATTAC	CAACCTCATG	600
CCAATCATA	TCGACTACCA	TGGGTCATTT	TCGGAATATG	TAGCAGCCAA	GTGGAATATC	660
CAGAACAAGA	TGACAGCAGC	TGATTTCCTT	GTCTTGAAC	TTAATCAAGA	CTTGGCAAAA	720
GACTTGACTT	CCAAGACAGA	AGCCACTGTT	GTACCATTTT	CAACACTTGA	AAAGGTTGAT	780
GGAGCTTATC	TGGAAGATGG	TCAACTCTAC	TTCCGTGGTG	AAGTAGTCAT	GGCAGCGAAT	840
GAAATCGGTG	TTCCAGGTAG	CCACAATGTG	GAAAATGCCC	TTGCGACTAT	TGCTGTAGCC	900
AAGCTTCGTG	GTGTGGACAA	TCAAACCATC	AAGGAAACTC	TTTCAGCCTT	CGGTGGTGTC	960
AAACACCGTC	TCCAGTTTGT	GGATGACATC	AAGGGTGTTA	AATTCCTATA	CGACAGTAAA	1020
TCAACTAATA	TCTTGCTTAC	TCAAAAAGCC	TTGTCAGGAT	TTGACAACAG	CAAGGTCGTC	1080
TTGATTGCAG	GTGGTTTGG	CCGTGGCAAT	GAGTTTGACG	AATTGGTGCC	AGACATTCTT	1140
GGACTCAAGA	AGATGGTCAT	CCTGGGTCAA	TCTGCAGAAC	GTGTCAAACG	GGCAGCAGAC	1200
AAGGCTGGTG	TCGCTTATGT	GGAGGCGACA	GATATTGCAG	ATGCGACCCG	CAAGGCCTAT	1260
GAGATTGCGA	CTCAAGGAGA	TGTGGTTCTT	CTTAGTCCTG	CCAATGCCAG	CTGGGATATG	1320
TATGCTAACT	TTGAAGTACG	TGGCGACCTC	TTTATCGACA	CAGTAGCGGA	GTAAAAAGAA	1380
TAA						1383

(2) INFORMATION FOR SEQ ID NO:1774:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1774:

ATTTTCAGGA GAATAAAAGA GATGACAGAA AAAGAAATTT TTGACCGTAT TGTGACCATT	60
ATCCAAGAGC GACAGGGAGA GGACTTTGTC GTGACAGAAT CCTTGAGTCT GAAAGACGAT	120
TTGGATGCGG ATTCTGTTGA CTTGATGGAG TTTATCTTGA CTCTGGAAGA TGAATTTAGT	180
ATCGAAATCA GCGATGAAGA AATTGACCAA CTCCAAAACG TAGGAGATGT GGTAAAAATC	240
ATTCAAGGAA AATAG	255

(2) INFORMATION FOR SEQ ID NO:1775:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 864 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1775:

ATTATAAGGA GATTAGACTG TATTGCCTAC TGTCTATCTA TAAAATATAT TTTATTGGAG	60
GCTTTTACTC AAATGGCAAA AGAAAAATAC GATCGTAGTA AACCACACGT TAACATTGGT	120
ACTATCGGAC ACGTTGACCA CGGTAAAACT ACCCTAACTG CAGCTATCAC AACTGTTTTG	180
GCACGTCGCT TGCCTTCATC AGTTAACCBA CCTAAAGACT ATGCGTCTAT CGATGCTGCT	240
CCAGAAGAAC GCGAACGCGG TATCACTATC AACACTGCGC ACGTTGAGTA CGAAACTGAA	300
AAACGTCACT ACGCTCACAT CGACGCTCCA GGACACGCGG ACTACGTTAA AAACATGATC	360
ACTGGTGCTG CTCAAAATGGA CGGAGCTATC CTTGTAGTAG CTTCAACTGA CGGACCAATG	420
CCACAAACTC GTGAGCACAT CCTTCTTTCA CGTCAGGTTG GTGTTAAACA CCTTATCGTC	480

TTCATGAACA	AAGTTGACTT	GGTTGACGAC	GAAGAATTGC	TTGAATTGGT	TGAAATGGAA	540
ATCCGTGACC	TATTGTCAGA	ATACGACTTC	CCAGGTGACG	ATCTTCCAGT	TATCCAAGGT	600
TCAGCACTTA	AAGCTCTTGA	AGGTGACTCT	AAATACGAAG	ACATCGTTAT	GGAATTGATG	660
AACACAGTTG	ATGAGTATAT	CCCAGAACCA	GAACGTGACA	CTGACAAACC	ATTGCTTCTT	720
CCAGTCGAGG	ACGTATTCTC	AATCACTGGA	CGTGGTACAG	TTGCTTCAGG	ACGTATCGAC	780
CGTGGTATCG	TTAAAGTCAA	CGACGAAAAC	TATATTGTTG	GTATCAAAGA	AGAAAACCTC	840
GAACCCCTTG	TTTCCGGGTG	TTGA				864

(2) INFORMATION FOR SEQ ID NO:1776:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 486 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...486
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1776:

AGAAAAAGGA	GAAAAGAGAT	GACTGAAAAA	AGACTGGCCT	GGGATGAGTA	TTTTGCAGCC	60
CAAGCTTTAC	TAATTGCGAA	TCGTTCCACT	TGTAAACGTG	CTAAAGTGGG	CGCGATTTTG	120
GTAAAAGATA	ATAAGGTTAT	TTCCACTGGT	TACAATGGTT	CGGTGTCAGG	GACTGAGCAT	180
TGTATTGATC	ACGAATGTTT	GGTCATTGAA	GGCCACTGTG	TTCGCACCCCT	TCACGCTGAG	240
GTCAATGCTA	TCCTTCAAGG	TGCTGAGCGT	GGTGTTCCCA	AAGGTTTTTAC	AGCCTATGTA	300
ACCCATTTTC	CTTGTTTCAA	CTGTACAAAA	CAATTGCTTC	AGGTCGGCTG	CAAGCGTGTG	360
GTTTATATCA	ACCAGTACCG	AATGGACGAC	TACGCCCAAT	ACCTTTATCA	AGAGAAAGGG	420
ACAGAATTGA	CCCATTTACC	ACTTGAGACA	GTACAGACAG	CTCTTAAAGA	GGCTGATCTA	480
ATGTAA						486

(2) INFORMATION FOR SEQ ID NO:1777:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1777:

AGTAGGAGGA	GTTGGATGGA	AATCAAAAAT	CACTTTGGGG	TCTACTGTGT	TTGCTTTGAA	60
AATGGAAAGT	TACTTTGTAT	TGAAAAAACG	AGAGGCCCTT	ATCAACATCG	GTATGATCTA	120
CCTGGAGGCA	GTCAGCAACT	TGGTGAAGGA	CTGACGGAAA	CGCTGACTAG	AGAAGTTATG	180
GAAGAGACGG	GATTTACTGT	TAGAAGCTAC	TCTAATCCTC	GAATCTACGA	TGTTTTTCGTC	240
AGAGAAGAGT	TAAAAAATTT	TATGGTTCAC	CATGTCATGG	CCTTGTATGA	TGTTGAAATG	300
AATGAGAGTG	CACCTCAAGT	TACGATTTTCG	GAAGCTGTGT	CTGATGGTGC	GAATGATTCA	360
CTTGGATATA	TTTGGATGGA	TATTCAAGAG	ATTACAGAAG	AAAATGCATC	GCCATTAGTC	420
TTGAAGGTTA	AGTCTGAATT	ATTAGGATTT	CCAGAACTGG	ACAAGACTTC	TTACATGAAT	480
TGGAAGGTGA	AGTAG					495

(2) INFORMATION FOR SEQ ID NO:1778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1778:

TTCTTAGGGA	GCTATTTTTA	TTTTTCAAG	AAGTTATCTT	CTTGTATTTT	ATACTCAATG	60
AAAATCAAAG	AGCAAGCTAG	GAAACTAGCC	GTAGGCTGCT	CAAAACACTG	TTTTGAGGTT	120
GTAGATAAGA	CTGACAAAGT	CAGGAACACA	TATCTACGGC	AAGGCGACGT	TGACGCGGTT	180
TGA						183

(2) INFORMATION FOR SEQ ID NO:1779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1779:

GAAACAGGGA	GAAATAAGAT	GACAGATTAT	TATGTAATTG	GAGATGTTCA	CGGAAAAGCT	60
GGGATGCTGG	AAGACCTTCT	TAAAACCTGG	GATGGTCAGA	CCCAGTTGCT	CTTTCTAGGT	120
GATTTGATTG	ACAGAGGTGA	GGATAGTCAC	CGTGTTCCTG	AAATGGTCAA	GGACTTGGTG	180
GACAATCAAG	GGGCTATCTG	TTTGTCTGGA	AACCACGAGT	ATATGTTTTT	GACTTGGCTA	240
GATTACCCAG	AAGAAAAGTTA	TGACCATTAT	CGTCGCAATG	GTGGAGATAC	AACCATTAAAG	300
TCTATCCTAG	GTCTGCCCTT	GGATGCACCA	GTTGATGGAG	TAGAAGATGC	CAAGCGGGTT	360
GCCGCTGAAG	CGGCAGACTT	GGTCGAAATC	ATTCGTCAAA	TGCCATTTGT	AGTAGAGACA	420
GACAAGTATA	TCTTTGTTCA	CGCAGGTATT	GATTTGACCT	TGGACGACTG	GCATGAAACA	480
ACAGATTATA	AAAAAGTATG	GCTTAGAAGA	CCATTCACG	GAGGTGCAAA	TTTACTGGA	540
TAG						543

(2) INFORMATION FOR SEQ ID NO:1780:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 444 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1780:

AGAGGGGGGA	GTTGTCGTTT	GACTAGTCGT	GTATTTATTG	ATGCAGATTG	TATTTTCAGTA	60
TTTTTATGGG	TTGGCACTGA	ACATCTTTTA	GAAAAGCTCT	ATTTGGGTAA	AATTGTTATT	120
CCACAAGAGG	TGTATGATGA	AATCAATATA	CCTACAATTC	CCCATTTAAA	ATCTAGGATA	180
GACCAGTTGG	TAACTAAGGG	TTCAGCTGAG	ATTGTGAGCA	TAGACATTGG	AACTGAAGAA	240
TACGCATTAT	ATAGAGATTT	AACAAGAAAT	CATGATAGTA	ACAAGATTAT	TGGTAAGGGA	300
GAAGCGACTT	CTATTTTCTT	AGCGAAAAAG	CATAATGGGA	TATTAGGAAG	TAATAACCTA	360
AGAGATGTTA	AACCATATGT	AGAAGAATTT	TCTTTAGAAC	ATATGACAAC	AGGAGATATA	420
CTGATTGAAG	CGTTTAAAGC	GTAA				444

(2) INFORMATION FOR SEQ ID NO:1781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1781:

ACGTCTTTTG	GGTCTGGACA	TCCAGTCATG	ATTCCTTCGA	CACCTGCAGG	AATTATGGAA	60
ATGTTTCATG	AATATGGGAT	TGACTTGGA	GGTAAAAATG	CGGTCGTAAT	CGGTCGTTCA	120
AATATCGTTG	GAAAACCTAT	GGCTCAGCTT	CTTTTGGCTA	AAAATGCGAC	AGTAACCTTG	180
GCCCACTCAC	GAAGTCATA	TCTTGCCAAG	GTGGCTGCTA	AAGCAGATAT	TCTTGTAGTC	240
GCAATCGGCC	GCGCCAAGTT	TGTGACTGCT	GACTTTGTCA	AACCAGGTGC	GGTTGTCATT	300
GACGTTGGGA	TGAATCGAGA	TGAAAAATGG	AAGCTCTGTG	GAGATGTTGA	TTATGAGGCA	360
GTTGCACCAC	TTGCTAGCCA	TATCACGCCA	GTCCCTGGAG	GTGTCGGTCC	TATGACCCAT	420
TACCATGCTG	ATGGAGCAAA	CTTATCAAGC	AGCACTTCGG	ACATTGGATA	G	471

(2) INFORMATION FOR SEQ ID NO:1782:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 546 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1782:

GAAACTTTTG	GAGGTATTTT	CATCATGGCA	AAGCAAACCA	TCATTGTAAT	GAGCGATTCC	60
CATGGCGATA	GCTTGATTGT	GGAAGAAGTC	CGTGATCGCT	ATGTGGGCAA	AGTCGATGCC	120
GTTTTTCATA	ACGGCGATTG	TGAAGTACGT	CCGGATTCTC	CACTTTGGGA	GGGCATCCGC	180
GTTGTTAAAAG	GGAACATGGA	CTTCTACGCC	GGCTACCCAG	AACGTCTGGT	GACTGAGCTT	240
GGTTCGACCA	AGATTATCCA	AACTCATGGT	CACTTGTTTG	ACATCAATTT	CAACTTTCAA	300

AAGTTGGACT	ACTGGGCTCA	GGAGGAAGAG	GCCGCTATCT	GCCTCTATGG	TCACTTGCAT	360
GTGCCAAGTG	CTTGGAATGGA	AGGCAAGATC	CTCTTTCTAA	ATCCAGGTTT	TATCAGCCAA	420
CCACGAGGTA	CCATCAGAGA	ATGTCTCTAT	GCTCGTGTGG	AGATTGATGA	TAGTTACTTC	480
AAAGTGGACT	TTTTGACACG	AGATCACGAG	GTGTATCCAG	GTTTGTCCAA	GGAGTTTAGC	540
CGATGA						546

(2) INFORMATION FOR SEQ ID NO:1783:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 903 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1783:

TCGGGTTTTG	GATGTGACCA	AGCTAAGCCC	AGAGGAAATT	ATAGAGGAAC	TAAGATGAAA	60
ATTGCTTATC	TAGGTCCCAA	AGGATCATTT	TCACACCACG	TTGTGCAGAC	AGCTTTTCCT	120
CATGAGGAAT	TGCAGGCTTT	TGCCAACATT	ACAGATGTCA	TCAAGGCTTA	TGAGCAAGGA	180
TTAGTGGACT	ATTCTGTGGT	GCCAGTTGAA	AATTCTATTG	AGGGTAGTGT	TCATGAAACC	240
TTGGACTATC	TTTTTCATCA	GGCTCACATC	CAAGCAGTAG	CAGAAATCGT	TCAGCCTATT	300
CATCAGCAGT	TGATGGTGGT	TCCAGGCCAT	ACTAAGATTG	AAAAGATTTT	TTCACATCCA	360
CAGGGCTTGG	CTCAAGGAAA	GAAATTTCATC	GATGAACAAT	ATCCAGAGGC	TCAAATCGAG	420
GTAACAGCTA	GTACAGCTTA	TGCGGCCCGT	TTTATTTCCG	AACATCCAGA	CCAGCCCTTT	480
GCAGCAGTTG	CACCTAGAAG	TTCTGCTGAA	GAATATGGAT	TGGAAC TGAT	TGCCGAGGAT	540
ATTGAGGAAA	TGGAAGCCAA	TTTCACACGT	TTCTGGGTTC	TAGGAGCTGA	AAAGCCTAGT	600
ATTCCCTTGC	AAGCACAAAC	TGAAAAGATG	AGTTTGGCCT	TGACATTACC	TGACAACCTT	660
CCAGGTGCAC	TTTATAAGGC	CTTGTCGACC	TTTGCTTGGC	GAGGAATTGA	CTTGACAAAA	720
ATTGAAAGTC	GTCCACTCAA	GACAGCACTG	GGTGAATACT	TTTTTCATTAT	CGATGTGGAT	780
TATATCGATA	AGGACTTGGT	CCACTTTGCC	CAAAAAGAAT	TAGAAGCGAT	TGGAATCCAG	840
TATAAAATTC	TGGGTGCCTA	TCCTATTTAT	CCAATATCAG	ACCATGGAAA	GGAGAGAAGA	900
TGA						903

(2) INFORMATION FOR SEQ ID NO:1784:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 756 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1784:

AAAGTATTTG	GAGGAGGAAG	AATTATGTTG	AATCAGGATC	TCTTTGATTC	GCTTGAGGCA	60
CAAAAAATTG	TAGATACTTT	GATGAAAGGG	CAAAAAGATT	ATGTAGATGA	ACGTCTAGAA	120
AAAAGAGAGA	CAATGATAGT	GTCGAATGGT	TATGCATGGA	CGCGACCTAA	TCATATTGAT	180
ACTGCATTTG	CATCAGCAGA	TTTGTGTTGAG	TATAAATTAC	AATTAGCAGG	ACAGACTTGG	240
GGATATTTAG	AATTTGAAAC	AAATACAGAA	AAATATGGGA	AAGTATTGTT	AATTATAAAG	300
GGTAAGAAGC	GACTTACGAA	CCAATTTCCCT	TTGGTACAAA	AAAATAAGAG	TGGCTACTTA	360
TTTGAATATG	CTCAGATGAA	TACACTTTAT	CTTAATCAAC	ATTCTTCCTA	CAAAAATGAT	420
GAAGATAGTC	ATTCCTTTCC	AATTCAGATG	GAGTTAGTTT	CTGATGAAAT	GATTCAAGAA	480
ATTGAACAAG	CTACTAAAAA	TTCGAATATC	GAAAAATTTA	TGATTTTAAAC	TTATGAGGCG	540
GACTCAGAAA	ACAATATTAT	ATCTGTAGAT	GTTGTTATGC	CTGATGCACG	AACTGGTCAG	600
TTACACTTGA	TTCAAGATTT	GTCTGAGTAT	ATTCAATCAA	GTTCGTACCA	TTTCGAAGAA	660
GCTAAATATC	AAGATATTCC	TAATTTTTC	GAATTATCGG	AAACAGAAGA	TTTTGAAATT	720
ATTCCAAGAA	TAGAAAAACA	AGAAGGTCAA	AAGTAG			756

(2) INFORMATION FOR SEQ ID NO:1785:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1785:

AGAAAATTTG	GAATCTATTT	GCTTATTATC	AATCGTTTTT	TTAGCTTATT	TGTCCTTAGAT	60
TGGTATAGAA	CTGAGCTATG	GATTAATACT	CTTGTATCTT	ATCCTGTTCC	TAAATATGTT	120
GGTAGAAAAA	TGAAGCAGTT	GTTACGAGTG	TCTGTATTGG	AAAAAATTTT	GTCTATAGAA	180
TTCTTTAAAT	GA					192

(2) INFORMATION FOR SEQ ID NO:1786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1786:

AAGATTCTTG GCTGGGATAT AACGAGAAAC TCCATTCTCC TCAAAGACAT AACCATCGCC	60
TACTTTTCGA ACAGCTTCTT TGACCAATTT CTCATCAATT GGATTGCTTG GAGCTGGTTG	120
AGGATTGGT GCAGGTGCG GACTTGACT AGGTCTGGA GTCGGTTGTG GACTTGTTTC	180
TTCTGGTCTT GA	192

(2) INFORMATION FOR SEQ ID NO:1787:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1787:

AAGATCCTTG GCTGGGATAT AACGAGAAAC TCCATTCTCC TCAAAGACAT AACCATCGCC	60
TACTTTTCGA ACAGCTTCTT TGACCAATTT CTCATCAATT GGATTGCTTG GAGCTGGTTG	120
AGGATTGGT GCAGGTGCA GACTTGACT AGGTCCGGA GTCGATTGTG GACTTGTTG	180
TTCTGGTCTT GA	192

(2) INFORMATION FOR SEQ ID NO:1788:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1914 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1914

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1788:

GGAAACCTTG	GAGAGATTGA	GAAAGTAAGA	ATGAAAAAGA	AATTAACTAG	TTTAGCACTT	60
GTAGGCGCTT	TTTTAGGTTT	GTCATGGTAT	GGGAATGTTC	AGGCTCAAGA	AAGTTCAGGA	120
AATAAAATCC	ACTTTATCAA	TGTTCAAGAA	GGTGGCAGTG	ATGCGATTAT	TCTTGAAAGC	180
AATGGACATT	TTGCCATGGT	GGATACAGGA	GAAGATTATG	ATTTCCCAGA	TGGAAGTGAT	240
TCTCGCTATC	CATGGAGAGA	AGGAATTGAA	ACGTCTTATA	AGCATGTTCT	AACAGACCGT	300
GTCTTTCGTC	GTTTGAAGGA	ATTGGGTGTC	CAAAAACCTG	ATTTTATTTT	GGTGACCCAT	360
ACCCACAGTG	ATCATATTGG	AAATGTTGAT	GAATTACTGT	CTACCTATCC	AGTTGACCGA	420
GTCTATCTTA	AGAAATATAG	TGATAGTCGT	ATTACTAATT	CTGAACGTCT	ATGGGATAAT	480
CTGTATGGCT	ATGATAAGGT	TTTACAGACT	GCTGCAGAAA	AAGGTGTTTC	AGTTATTCAA	540
AATATCACAC	AAGGGGATGC	TCATTTTTCAG	TTTGGGGACA	TGGATATTCA	GCTCTATAAT	600
TATGAAAATG	AAACTGATTC	ATCGGGTGAA	TTAAAGAAAA	TTTGGGATGA	CAATTCCAAT	660
TCCTTGATTA	GCGTGGTGAA	AGTCAATGGC	AAGAAAATTT	ACCTTGGGGG	CGATTTAGAT	720
AATGTTTCATG	GAGCAGAAGA	CAAGTATGGT	CCTCTCATTG	GAAAAGTTGA	TTTGATGAAG	780
TTTAATCATC	ACCATGATAC	CAACAAATCA	AATACCAAGG	ATTTTCATTAA	AAATTTGAGT	840
CCGAGTTTGA	TTGTTCAAAC	TTCGGATAGT	CTACCTTGGG	AAAATGGTGT	TGATAGTGAG	900
TATGTTAATT	GGCTCAAAGA	ACGAGGAATT	GAGAGAATCA	ACGCAGCCAG	CAAAGACTAT	960
GATGCAACAG	TTTTTGATAT	TCGACAAGAC	GGTTTAGTAC	ACATTTTTTAC	TTCTTACAAG	1020
CCGATTCCAA	GTTTTCAAGC	TGGTTGGCAT	AAGAGTGTCAT	ATGGGAACTG	GTGGTATCAA	1080
GCGCCTGATT	CTACAGGAGA	GTATGCTGTC	GGTTGGAATG	AAATCGAAGG	TGAATGGTAT	1140
TACTTTAACC	AAACGGGTAT	CTTGTTACAG	AATCAATGGA	AAAAATGGAA	CAATCATTGG	1200
TTCTATTTGA	CAGACTCTGG	TGCTTCTGCT	AAAAATTGGA	AGAAAATTGA	TGGAATCTGG	1260
TATTATTTTA	ACAAAGAAAA	TCAGATGGAA	ATTGGTTGGG	TTCAAGATAA	AGAGCAGTGG	1320
TATTATTTGG	ATGTTGATGG	TTCTATGAAG	ACAGGATGGC	TTCAATATAT	GGGGCAATTG	1380
TATTACTTTG	CTCCATCAGG	GGAAATGAAA	ACGGGCTGGG	TAAAAGATAA	AGAAGCCTGG	1440
TACTATATGG	ATTCTACTGG	TATCATGAAG	ACAGGTGAGA	TAGAAGTTGC	TGGACATCAT	1500
TACTATCTAG	AAGAATCAGG	AGCTATGAAG	CAAGGCTGGC	TTAAAAAGGC	AAATGATTGG	1560
TATTTCTACA	AGACAGGTGG	TTACAGAGCT	ATAGGTTGGA	TTAAAGACAA	GGATAAATGG	1620
TACTTCTTGA	AAGAAAATGG	TCAATTACTT	GTGAATGGTA	AGACACCAGA	AGGCTATACT	1680
GTGGATTCAA	GTGGTGCCTG	GTTAGTGGAT	GTTCCGATCG	AGAAATCTGC	TACAATTAAA	1740
ACTACAAGTC	ATTCAGAAAT	AAAAGAATCC	AAAGAAGTAG	TGAAAAAGGA	TCTTGAAAAT	1800
AAAGAAACAA	GTCAACATGA	AAGTGTTACA	AATTCTTCAA	CTAGTCAAGA	TTTGACATCC	1860
TCAACTTCAC	AAAGCTCTGA	AACGAGTGTA	AACAAATCGG	AATCAGAACA	GTAG	1914

(2) INFORMATION FOR SEQ ID NO:1789:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1789:

CATATGATTG	GAAGTATTGC	AGCAATTTTA	ACAACATTTG	CATTTTTTACC	ACAAGTTTTTT	60
CGTGTAAGTTA	AGACAAAGGA	CACAGGATCT	ATTGCTCTAG	GTATGTATGT	TATGCAAGTT	120
ATTGGTATTG	CATTGTGGCT	TGCTCATGGT	ATTCGTATAG	GAGACTTGCC	TTTGATTTTA	180
GCTAATAGTG	TTTCATTTCT	ACTTTCAGGA	ATAATTTTAT	TTTATAAAAT	GAAGTATAAA	240
TAA						243

(2) INFORMATION FOR SEQ ID NO:1790:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1790:

TTATGTGTTG	GGTACCTACC	ATACACACTC	ATATCGTTTC	TCCTGTTCAA	TTTATCTGTC	60
TTAGTATATC	AAAAAGTCCT	AGGATTGTCA	GCTTGCGATG	GCTGTTTGAG	TGATTTTTTG	120
CATAGTTTCA	CAAAGGTTTC	AATTTCCCGA	AAGCGGTGTA	AATGTGTCTG	TTTGAACTCA	180
ATCATATCAT	TCACTTCTTC	CTTAGTTAGC	ATGAATTTCC	CTCCTCTTTC	TTTCTATTCTG	240
TAA						243

(2) INFORMATION FOR SEQ ID NO:1791:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 711 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1791:

AAAGACGTTG	GTATGAAAGA	ATTACAAACT	GTACTAAAGA	ACCATTTTGC	AATCGAATTT	60
ACAGACAAAA	AGTTACTGGA	AACTGCCTTT	ACTCATACGA	GTTATGCCAA	TGAGCACCGC	120
CTCTTAAAAA	TTTCACACAA	TGAACGCTTG	GAATTTTTAG	GAGACGCTGT	TCTACAGTTA	180
TTGATTTTCAG	AATATCTGTA	TAAAAAATAT	CCTAAAAAGC	CTGAAGGTGA	CCTATCAAAA	240
CTCCGTGCTA	TGATTGTCCG	TGAGGAGAGT	TTAGCTGGTT	TTGCGCGTGA	TTGCCAGTTT	300
GACCAGTTTA	TCAAGTTGGG	TAAAGGGGAA	GAAAAATCTG	GTGGTCGCAA	TCGTGACACC	360
ATTCTTGGTG	ATGCCCTTGA	AGCCTTTCTT	GGTGCCCTTC	TTTTGGATAA	GGATGTGGCC	420
AAGGTCAAGG	AATTTATCTA	TCAAGTCATG	ATTCCTAAGG	TTGAAGCAGG	CGAGTTTGAG	480
ATGATTACAG	ACTATAAAAC	CCATCTCCAA	GAGTTGCTTC	AGGTCAATGG	TGATGTGGCT	540
ATTCTGTATC	AGGTGATTTT	TGAAACAGGG	CCTGCTCACG	ATAAGGTCTT	TGATGTAGAA	600
GTTCTTGTG	AAGGTAAGAG	CATCGGTCAA	GGCCAAGGTC	GTTCTAAGAA	ATTAGCAGAG	660
CAGGAAGCTG	CCAAAAATGC	CGTTGAGAAA	GGGCTGGATT	CATGTATTTA	A	711

(2) INFORMATION FOR SEQ ID NO:1792:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1107 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1792:

GAGTTGGTTG	GAGGTGTTAT	GAAGAAAATT	GGGACTTATT	TGGTTTATGT	GCTAGCTGTT	60
GTCTTTATTA	TGCTAGCTTT	TGCTTGTGGA	ACAATCGCAT	TTGCAGAGTT	GGGGTATTCC	120
GCAGTTTATAG	CCTTTACTTT	TGGTTATGCC	TTCGCTCTTC	TAAGCATGTA	TTTAATCTTT	180
ATTCTTCATG	AGCTGGGTCA	TGCTTTTGT	GGCTACTTGA	CAGGCTATCG	GCTGGTGGCT	240
TTTGGATTAG	GACATTTTAT	TTTGACCAAA	AAGTCAGGCA	GGTTTCATCT	GAGTAGAACA	300
GCCATTCTGA	AAAAATGTTG	TGCTCAATAC	ATTGGTTTAA	AAGAGGATGA	AAGCGATCAA	360
AGAATCATCC	TGATGCTTTC	AGGAGGCTTG	ATGGTTCATC	TCGGCTTGAT	ATTATTGGCG	420
ATAGTGTGTTG	GATTTTGTGAC	AAGAAGCTGG	TATTTTGCAG	GGACTTGGAT	TTTTCTTAAT	480
TTATCTTTCT	TCCTAAATAA	CATTTTGTCA	GTCGACATCA	CCGATGGAGC	AAAAATTTGG	540
GAATTACTAC	AACACCCTGA	AAATACCAAA	TACGCCTACC	TGGTATTGAG	ACATTCTGCT	600
CAAACTTTGC	TGGCTCCTCA	AGAATATGAT	TTGAAAGACT	TTGTTCAAGC	AGTTCCTGAG	660
GATGCACGAG	GGAGTTTTGC	GGATGGTGTA	TTAGGTATGC	AAGGTGAAGT	TTCCATTTTG	720
GAAGGGAAGG	AAGAAGTAGC	TAAACAGCAG	TTTCAAGCAT	TACTTGAGAG	GACAACTACT	780
CCGATGATGC	AGACAGTTGC	CCAACATATCC	CTGCTTCATA	TCGCCTTGTT	GGAAGGAGAT	840
TTTGAGCAAG	CGGAGCAATA	TGCTAGTATT	CGACAGGTCA	AATCGTTTCT	GTCTCTCAAA	900
CTGTCCAATC	TTCAAGTGAT	ACAAGCCTGG	TATCAATTTA	AGGTAAGGAA	AGATGTGGTT	960
CAAACTCACA	AGGCTATGAA	GATTGCTAGA	CAGAAAATGG	ATAGTAGTCG	AATGTTGAGG	1020
GACGAGAAAC	GCTATTATGA	AAACTTGTTA	GCAGAGCTGG	AAAAGGAAAT	GTTAGAAGGA	1080
ACTGAAGATG	GAAC TAGAAA	TTTCTGA				1107

(2) INFORMATION FOR SEQ ID NO:1793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...699

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1793:

CTTGTGGTTG	GTATCGCAAC	ACCAGCAACC	CAAAGGTTGG	CTAGTGCCAC	AAAAGACCTA	60
CCAGTTATCA	TGGCCGCTAT	TACAGACCCA	ATTGGTGCTA	ACTTGGTTAA	AGATTTGAAA	120
AAACCAGGTG	GCAACGTTAC	AGGGGTATCT	GACCACAATC	CAGCTCAACA	ACAAATTGAA	180
CTCATCAAGG	CTCTGACACC	GAATGTGAAA	ACAATCGGAG	CTCTTTACTC	AAGTAGCGAA	240
GACAATTCAA	AAACACAGGT	CGAAGAATTT	AAGGCTTATG	CTGAAAAAGC	AGGTCTGACA	300
GTGGAAACAT	TTGCAGTTCC	TTCAACAAAT	GAAATTGCCT	CAACTGTCAC	TGTTATGACT	360
AGCAAGGTAG	ATGCTATTTG	GGTTCCAATT	GATAACACCA	TTGCATCAGG	ATTTCCAACG	420
GTTGTCTCTA	GCAATCAAAG	TTCTAAGAAA	CCAATTTATC	CCAGTGCGAC	AGCTATGGTA	480
GAAGTAGGTG	GTTTGGCATC	AGTTGTAATT	GACCAACATG	ACCTTGGTGT	GGCAACAGGT	540
AAAATGATTG	TGCAAGTCTT	GAAAGGTGCA	AAACCAGCCG	ATACCCAGT	CAATGTCTTT	600
TCAACTGGTA	AGTCAGTCAT	CAATAAAAAA	ATAGCACAA	AAGTGGTAT	TACTATTCCT	660
GAGTCTGTTT	TCAAAGAAGC	AGGACAAGTC	ATCGAATAA			699

(2) INFORMATION FOR SEQ ID NO:1794:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...480
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1794:

CATATTTCTG	GTCAAACAAA	AGTTTCGTCT	TGGAGGCGAA	CGTTCGCTAT	CAAGGATGAC	60
AGGGGAGAAA	TTGCCTATCA	GGTGGAGGGA	TCATTTTAA	AGATTCCCAA	AACTTTACC	120
ATCTATGATG	CGGCTGGTGA	ACAAGTCAGT	CAGATCAGTA	AAGAAATCTT	GACCTTGCTT	180
CCTCGTTTTG	AGATTCAGCT	TCGGGATGGC	TCGAGTTTTG	TCATTCGTAA	GAAAGTTGACC	240
TTTGGGCGAG	ATAAGTATGA	GTTTGATAAT	CTAGGTCTTC	GTATCGAGGG	CAATATCTGG	300
GATTTGAATT	TCAAATTGCT	GGATGATCGC	GATCAGTTGA	TTGCGGAAAT	TAAGAAGGAA	360
CTCTTCCATC	TGACCTCTAC	CTATACCGTA	ACGGTTCTTG	AAGACGCTTA	TGCAGACCTA	420
GTCATTTCCC	TCTGTGTCGC	GATTGACTAT	GTGGAAATGC	TGGAAAGCCA	ATCACATTAA	480

(2) INFORMATION FOR SEQ ID NO:1795:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 537 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...537
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1795:

AACCATTTCTG	GGAGTTGGAT	GAAAGTGAAG	TACAGGCTAT	GCTTGAAAAT	ACAGACGTTT	60
CCACCAGCAA	ACCGCGAATA	CTTCCGTGGA	GGAGGATTCT	CAACTCGTTT	CTTGACGAAG	120

GGGGATATGC	CAGTAACAAT	GGTACGTCTC	AATCTTTTAA	AAGGGGTTGG	TCCAGTGCTA	180
CAAATTGCAG	AAGGTTACAC	ACTTGAACCT	CCTGAAGATG	TTCACCATAC	TTTAGATAAT	240
CGTACAGATC	CAGGATGGCC	AACTACTTGG	TTTGCTCCAC	GTTTGACAGG	AAAAGGTGCT	300
TTCAAGTCTG	TCTATGACGT	CATGAATAAT	TGGGGAGCTA	ATCACGGAGC	CATAACATAT	360
GGACACATTG	GAGCAGACTT	GATTACCTTG	GCTTCTATGT	TGAGAATTCC	TGTCAATATG	420
CATAATGTAC	CCGAGGAAGA	TATCTTTAGA	CCTAAAAATT	GGTCCTTATT	TGGAACAGAA	480
GATCTAGAAT	CAGCAGACTA	TCGTGCATGT	CAGTTGTTGG	GACCGCTACA	TAAATAA	537

(2) INFORMATION FOR SEQ ID NO:1796:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3873 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...3873
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1796:

GCTCCATCTG	GGACAGCTTC	TGTTCTAGTC	CGATTTGCCT	TCCAAGCACA	GACTGTTGCA	60
GCCGATGGAG	TTACTACTAC	TACAGAAAAC	CAACCGACCA	TCCATACAGT	TTCTGATTCC	120
CCTCAATCAT	CCGAAAATCG	GACTGAGGAA	ACACCTAAAG	CAGAGCTTCA	ACCAGAAACT	180
CCAGCTACTG	ATAAGGTAGC	TAGTCTTCCA	AAAACAGAAG	AAAAACCACA	AGAGGAAAGTT	240
AGTTCAACTC	CTAGTGATAA	AGCAGAGGTG	GTAACCTCCAA	CTTCTGCTGA	AAAAGAAACT	300
GCTAATAAAA	AGGCAGAAGA	AGCTAGCCCCT	AAAAAGGAAG	AAGCGAAAAGA	GGTTGATTCT	360
AAAGAGTCAA	ATACAGACAA	GACTGACAAG	GATAAACCCAG	CTAAAAAAGA	TGAAGCGAAA	420
GCAGAGGCTG	ACAAACCGGA	AACAGAGGCA	GGAAAGGAAC	GTGCTGCAAC	TGTAATGAA	480
AAACTAGCGA	AAAAGAAAAT	TGTTTCTATT	GATGCTGGAC	GTAAATATTT	CTCACCAGAA	540
CAGCTCAAGG	AAATCATCGA	TAAAGCGAAA	CATTATGGCT	ACACTGATTT	ACACCTATTA	600
GTGCGAAATG	ATGGACTCCG	TTTCATGTTG	GACGATATGA	GCATCACAGC	TAACGGCAAG	660
ACCTATGCCA	GTGACGATGT	CAAACGCGCC	ATTGAAAAAG	GTACAAATGA	TTATTACAAC	720
GATCCAAACG	GCAATCACTT	AACAGAAAAGT	CAAATGACAG	ATCTGATTAA	CTATGCCAAA	780
GATAAAGGTA	TCGGTCTCAT	TCCGACAGTA	AATAGTCCTG	GTCACATGGA	TGCGATTCTC	840
AATGCCATGA	AAGAATTGGG	AATCCAAAAC	CCTAACTTTA	GCTATTTTGG	GAAGGAATCA	900
GCCCGTACTG	TCAATCTTGA	CAACGAACAA	GCTGTGCTTT	TTACAAAAGC	CCTTATCGAC	960
AAGTATGCTG	CTTATTTTCG	GAAAAAGACT	GAAATCTTCA	ACATCGGACT	TGATGAATAT	1020
GCCAATGATG	CGACAGATGC	TAAAGGTTGG	AGTGTGCTTC	AAGCTGATAA	ATACTATCCA	1080
AACGAAGGCT	ACCCTGTAAA	AGGCTATGAA	AAATTTATTG	CCTACGCCAA	TGACCTCGCT	1140
CGTATTGTAA	AATCGCACGG	TCTCAAACCA	ATGGCCTTTA	ACGACGGTAT	CTACTACAAT	1200
AGCGACACAA	GCTTTGGTAG	TTTTGACAAA	GACATCATCG	TTTCTATGTG	GACTGGTGGT	1260
TGGGGAGGCT	ACGATGTCGC	TTCTTCTAAA	CTACTAGCTG	AAAAAGGTCA	CCAAATCCTT	1320
AATACCAATG	ATGCTTGGTA	CTACGTTCTT	GGACGAAACG	CTGATGGCCA	AGGCTGGTAC	1380
AATCTCGATC	AGGGGCTCAA	TGGTATTAAA	AACACACCAA	TCACTTCTGT	ACCAAAAACA	1440
GAAGGAGCTG	ATATCCCAAT	CATCGGTGGT	ATGGTAGCTG	CTTGGGCTGA	CACTCCATCT	1500
GCACGTTATT	CACCATCACG	CCTCTTCAAA	CTCATGCGTC	ATTTTGCAAA	TGCCAACGCT	1560

GAATACTTCG	CAGCTGATTA	TGAATCTGCA	GAGCAAGCAC	TTAACGAGGT	ACCAAAAGAC	1620
CTGAACCGTT	ATACTGCAGA	AAGCGTCGCG	GCCGTAAAAG	AAGCTGAAAA	AGCTATTTCGC	1680
TCTCTCGATA	GCAACCTTAG	CCGTGCCCAA	CAAGATACGA	TTGATCAAGC	CATTGCTAAA	1740
CTTCAAGAAA	CTGTCAACAA	CTTGACCCTC	ACGCCCTGAAG	CTCAAAAAGA	AGAAGAAGCT	1800
AAACGTGAGG	TTGAAAAACT	TGCCAAAAAC	AAGGTAATCT	CAATCGATGC	TGGACGCAAA	1860
TACTTTACTC	TGAACCAAGT	CAAACGCATC	GTAGACAAGG	CCAGTGAAC	CGGATATTCT	1920
GATGTCCATC	TCCTTCTAGG	AAATGACGGA	CTTCGCTTTC	TACTCGATGA	TATGACCATT	1980
ACTGCCAACG	GAAAAACCTA	TGCTAGTGAT	GACGTTAAAA	AAGCTATTAT	CGAAGGAAC	2040
AAAGCTTACT	ACGACGATCC	AAACGGTACT	ACACTAACAC	AGGCAGAAGT	GACAGAGCTA	2100
ATTGAATACG	CTAAATCTAA	GGACATCGGT	CTCATCCAG	CTATTAACAG	TCCAGGTCAC	2160
ATGGATGCTA	TGCTGGTTGC	CATGGAAAAA	TTAGGTATTA	AAAATCCTCA	AGCCCACTTT	2220
GATAAAGTTT	CAAAAAACAAC	TATGGACTTG	AAAAACGAAG	AAGCGATGAA	CTTTGTAAAA	2280
GCCCTCATCG	GTAAATACAT	GGACTTCTTT	GCAGGTAAAA	CAAAGATTTT	CAACTTTGGT	2340
ACTGACGAAT	ACGCCAACGA	TGCGACTAGT	GCCCAAGGCT	GGTACTACCT	CAAGTGGTAT	2400
CAACTCTATG	GCAAATTTGC	CGAATATGCC	AACACCCCTC	GAGCTATGGC	CAAAGAAAGA	2460
GGGCTTCAAC	CAATGGCCTT	CAACGATGGC	TTCTACTATG	AAGACAAGGA	CGATATTTCAG	2520
TTTGACAAAG	ATGTCTTGAT	TTCTTACTGG	TCTAAAGGCT	GGTGGGGATA	TAACCTCGCA	2580
TCACCTCAAT	ACCTAGCAAG	CAAAGGCTAT	AAATTCCTGA	ATACCAACGG	TGACTGGTAC	2640
TACATTCTTG	GTCAAAAACC	AGAAGATGGT	GGTGGTTTCC	TCAAGAAAGC	TATTGAGAAT	2700
ACTGGAAAAA	CACCATTCAC	TCAACTAGCT	TCTACCAAAT	ATCCTGAAGT	AGATCTTCCA	2760
ACAGTCGGAA	GTATGCTTTC	AATCTGGGCA	GATAGACCAA	GCGCTGAGTA	CAAGGAAGAG	2820
GAAATCTTTG	AACTCATGAC	TGCCTTTGCA	GACCACAACA	AAGACTACTT	CCGTGCTAAT	2880
TATAATGCTC	TCCGCGAAGA	ATTAGCTAAA	ATTCCCTACAA	ACTTAGAAGG	ATATAGTAAA	2940
GAAAGTCTTG	AGGCCCTTGA	CGCAGCTAAA	ACAGCTCTAA	ATTACAACCT	CAACCGTAAT	3000
AAACAAGCTG	AGCTTGACAC	ACTTGTAGCC	AACCTAAAAG	CCGCTCTTCA	AGGCCCTCAA	3060
CCAGCTGCAA	CTCATTCAGG	AAGCCTGGAT	GAAAAATGAAG	TGGCTGCCAA	TGTTGAAACC	3120
AGACCAGAAC	TCATCACAAG	AACTGAAGAA	ATTCCATTTG	AAGTTATCAA	GAAAGAAAAT	3180
CCTAACCTCC	CAGCTGGTCA	GGAAAATATT	ATCACAGCAG	GAGTCAAAGG	TGAACGAAC	3240
CATTACATCT	CTGTACTCAC	TGAAAATGGA	AAAACAACAG	AAACAGTCCT	TGATAGCCAG	3300
GTAACCAAAG	AAGTTATAAA	CCAAGTGGTT	GAAGTTGGCG	CTCCTGTAAC	TCACAAGGGT	3360
GATGAAAGTG	GTCTTGCACC	AACTACTGAG	GTAAAACCTA	GACTGGATAT	CCAAGAAGAA	3420
GAAATTCCAT	TTACCACAGT	GACTCGTGAA	AATCCACTCT	TACTCAAAGG	AAAAACACAA	3480
GTCATTACTA	AGGGCGTCAA	TGGACATCGT	AGCAACTTCT	ACTCTGTGAG	CACTTCTGCC	3540
GATGGTAAGG	AAGTGAAAAC	ACTTGTAAT	AGTGTCTGAG	CACAGGAAGC	CGTTACTCAA	3600
ATAGTCGAAG	TCGGAACAT	GGTAACACAT	GTAGGCGATG	AAAACGGACA	AGCCGCTATT	3660
GCTGAAAGAA	AACCAAAACT	AGAAAATCCA	AGCCAACCAG	CTCCATCAAC	TGCTCCTGCT	3720
GAGGAAAGCA	AAGCTCTTCC	TCAAGATCCA	GCTCCTGTGG	TAATAGAGAA	AAAAC'TTCC	3780
GAAACAGGAA	CTCACGATTC	TGCAGGACTA	GTAGTCGCAG	GACTCATGGC	CACACTAGCA	3840
GCCTATGGAC	TCACTAAAAG	AAAAGAAGAC	TAA			3873

(2) INFORMATION FOR SEQ ID NO:1797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1797:

GACAAGTCTG	GCGGCAGGAA	TTTTAACGAG	AGATATAGGA	GGTCAGGCTT	CAACAAAGGA	60
AATGATGGAA	GCTATTATTG	CAAGGTTATG	AAGTTAGACG	AAAAAATTAC	TCTAGTCCTT	120
TTGATTTGGA	ATGTCATCAT	TTTCTTGATT	TATGGCATTG	ACAAATTCAA	GGCAAGAAGA	180
AGAGCTTGGC	GCATCCCAGA	GAAAATCTTA	CTCATTTTAG	CCCTTACTTG	TGGTGGTTTT	240
GGGGCCTGGT	TAGCTGGAAT	CACTTTTTCAC	CACAAGACTC	GAAAATGGTA	CTTTAAAACA	300
GTTTGGTTTC	TTGGGATGGT	GACCACACTA	GTAGCCTTAT	ATTTTATTTG	GAGGTAA	357

(2) INFORMATION FOR SEQ ID NO:1798:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2226 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1798:

GAAAGGGCTG	GATTCATGTA	TTTAAAGGAA	ATCGAAATTC	AGGGGTTCAA	GTCTTTTGCT	60
GATAAGACCA	AGGTCGTTTT	TGACCAAGGT	GTGACGGCAG	TTGTTGGACC	CAATGGATCT	120
GGAAAGTCCA	ATATTACAGA	AAGTCTGCGT	TGGGCTTTGG	GGGAGTCTAG	TGTCAAGAGT	180
CTCCGTGGGG	GCAAGATGCC	GGATGTCATC	TTTGCTGGAA	CAGAAAGTCG	CAAACCGCTC	240
AATTATGCTT	CTGTAGTTGT	GACTCTGGAT	AATCATGACG	GATTTATCAA	GGATGCAGGT	300
CAAGAAATCA	GGGTGGAACG	CCATATCTAT	CGTAGTGGAG	ATAGCGAATA	CAAGATTGAC	360
GGCAAGAAAAG	TCCGTCTGCG	TGATATTCAT	GACCTCTTCT	TGGATACTGG	ATTGGGACGA	420
GATTCCCTTCT	CTATTATTTT	CCAAGGGAAG	GTTGAGGAGA	TTTTTAATTC	CAAGCCTGAG	480
GAACGACGAG	CTATTTTTTGA	AGAAGCTGCT	GGAGTTTTTAA	AATACAAGAC	TCGCAGAAAA	540
GAAACCGAGA	GTAAACTGCA	GCAAACTCAG	GATAATCTGG	ACCGCTTAGA	GGACATTATC	600
TACGAGTTGG	ATAATCAAAT	CAAGCCTCTT	GAGAAGCAAG	CTGAGAATGC	CCGTAAGTTT	660
TTAGACTTGG	AAGGACAACG	TAAGGCTATT	TATTTAGACG	TTCTGGTTGC	TCAAATCAAG	720
GAAAAATAAGG	CAGAACTAGA	GTCGACAGAA	GAAGAGTTGG	CTCAGGTTCA	AGAACTCTTG	780
ATGAGTTATT	ACCAAAAGCG	TGAAAAATTA	GAAGAAGAAA	ATCAAACTCT	TAAAAAGCAA	840
CGCCAAGATT	TACAGGCTGA	AATGGCCAAA	GACCAAGGCA	GTTTGATGGA	CTTGACTAGT	900
CTGATTAGTG	ATTTAGAAAAG	AAAATTAGCC	CTATCGAAAC	TGGAGTCCGA	GCAAGTGGCC	960
CTGAATCAAC	AGGAGGCACA	AGCTCGTTTG	GCTGCTTTGG	AGGATAAGAG	AAATTCACTC	1020
AGCAAAGAAA	AGTATGATAA	AGAAAGCTCT	TTAGCTCTGT	TAGAGGGAAA	TCTAGTCCAA	1080
AATAATCAAA	AACTCAATCG	TTTAGAAGCT	GAATTGCTGG	CTTTCTCAGA	CGATCCTGAT	1140
CAGATGATTG	AGCTCTTACG	TGAACGCTTT	GTAGCTCTTT	TACAAGAAGA	AGCGGATGTC	1200
TCAAACCAGT	TGACCCGTAT	TGAGAATGAG	TTGGAAAATA	GTCGTCAGCT	TTCTCAAAAA	1260

CAAGCAGATC	AACTAGAAAA	GCTGAAAGAG	CAATTAGCTA	CAGCTAAAGA	GAAGGCTAGT	1320
CAGCAAAAAG	ACGAGCTTGA	AACTGCCAAG	GTGCAGGTTT	AGAAATTAT	GGCTGACTAT	1380
CAAGCTATTG	CCAAGGAGCA	AGAGGAGCAG	AAAACCTTCT	ATCAAGCTCA	ACAAAGTCAA	1440
CTCTTTGACC	GTCTGGATAG	TCTCAAAAAC	AAGCAGGCCA	GAGCTCAAAG	TTTGGAAAAT	1500
ATCCTGAGAA	ATCATAGTAA	CTTTTATGCA	GGTGTTAAGA	GTGTTCTCCA	AGAAAAAGAT	1560
CGCCTAGGTG	GGATTATTGG	TGCAGTCAGT	GAGCATCTGA	CCTTTGATGT	TTATTATCAA	1620
ACTGCCCTAG	AGATTGCCTT	AGGGGCAAGT	AGCCAGCATA	TCATCGTAGA	AGATGAAGAG	1680
TCGGCAACCA	AAGCTATTGA	TTTCCTCAAA	CGAAACAGAG	TCGGTCGTGC	AACCTTTCCT	1740
CCTTTGACCA	CTATTAAGGC	GCGTACGATT	TCTAGTCAGA	ACCAAGATGC	TATCGCTGTA	1800
AGCCCAGGTT	TCCTTGGGAT	GGCAGATGAG	TTGGTGACTT	TTGATACTAG	ACTGGAAGCC	1860
ATTTTCAAGA	ACTTGCTAGC	TACGACGGCT	ATCTTTGATA	CCGTAGAACA	TGCGCGTGAA	1920
GCTGCTCGAC	AAGTTCGTGA	TCAGGTTTCG	ATGGTGACAT	TGGATGGGAC	AGAATTACGC	1980
ACGGGTGGTT	CCTATGCGGG	TGGTGCCAAT	CGCCAAAATA	ACAGTATTTT	CATCAAGCCA	2040
GAAGTGGAGC	AATTACAAAA	AGAAATTGCT	GCAGATGAAG	CAAGCTTGGG	TTTCAAGAGAA	2100
GCGGCTTTGA	AGACCTTGCA	AGACCAGATG	GCTGCATTGA	CAGAAAGATT	AGAAGCCATC	2160
AAACTCTCAA	GGAGAGCAGG	CACGTATTCA	GGAGCAAGGC	TTGTCCCTCG	CTTATCAGCA	2220
AACTAG						2226

(2) INFORMATION FOR SEQ ID NO:1799:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...237
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1799:

TTGCCCCATG	GTTGTTTGT	CATGAAAGAC	GGAAAAATGT	CTAAGTCAAA	AGGGAATGTC	60
GTTTACCCTG	AAATGTTGGT	AGGAGCGTTA	TGGACTAGAT	CCACTTTGTT	ACTAACCTCA	120
TGCGTAACTT	TCCAGTTGTT	TCAGACGGAC	CTTTTACTCC	TGAAGACTAT	GTTGGCCGTA	180
TCAACTATGA	ATTGGCTAAT	GACTTTGGGA	ACCTCCTTAA	CCGTACGTTT	TCCATGA	237

(2) INFORMATION FOR SEQ ID NO:1800:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1800:

CACCAGCATG	GTGTAAGTGT	AATTGTTGCG	CAAACATTTG	ATTTTTTAAA	CAACTCATGG	60
GAAGCTGCAG	CCTCTGGAAC	ACGACCAATG	GATAGTGGAG	AAATCACACA	TTCCACAGGT	120
TCCCCATCTG	GATATTTCAA	TGTGCTTGAA	ATCAAATCTG	CCACACTTTT	AGCCATGTTC	180
ATTGTTTGTA	CTTCAAGTGA	TTCGCGTACA	CCTTGA			216

(2) INFORMATION FOR SEQ ID NO:1801:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1152 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1801:

ATGTTTAATG	GTCTGGTATT	GAAAGAATTA	CGGCTGTAA	ATGGTTTAA	GAGAGCAGAA	60
TTAGCTCAGA	GAATTAATTT	AACGGAACAA	GCCATTTGGC	AGTTTGAGTC	CAACGAAACG	120
AAACCTAAAT	TATCAACCAA	AATGCATTTG	GCCAACCAAT	TTCATGTTGA	TTTAACTTAT	180
TTTGAACAGG	AAGAAGAGAG	CATTCGATTT	GATTCTTCTG	TAATTGCCTT	TAGAAATGCA	240
GACCTAGCAA	CACGGAAAAAC	AATAGATATT	CAAACATATG	ATTTACATAA	GGTAGATAGT	300
TTGATTGATT	ATTTTGAAAAG	TTTGTAAATT	ATACCTAATA	TTATAATTCA	TGACCTAAGT	360
AATGTAGTGA	GTGAATCTTA	TCATAAGGGA	GAATCCATTG	AGGAATTGGC	TCTTTATGCC	420
AGGGAAAAAT	TAGGTATTTT	AAAAGATAAT	CATGATTTGC	TTTATAAATT	AGAACGTTCA	480
GGCATCTATA	TCGTGGAACG	ATTAATTAAT	GGCCAAGCTG	ATGCTTATAG	CGCATGGTCA	540
AAATTGGGAA	GACCTTATAT	TGTGTTGGGA	ACGAATAAAT	CATCTGTACG	TCGAAATTTT	600
GACTTAGCTC	ATGAGCTAGG	ACATATTTCT	TTACATAAAT	ATAAAGATAT	GAATGAAGAT	660
GGCGATCGTT	TGGAGCAAGA	AGCAAATTAT	TTTGCATCAT	GTTTTTTTAT	GCCAAAAGAA	720
GAGTTTTTAG	TCAAATTTGA	AGAGAGGGTT	GGCAAGCGTG	TCAGCAATCC	TGATAGTTAT	780
ATTTTATTGA	AGTCGGATTT	GAATGTTTCG	ATACAGGCTT	TAGAGTATCG	AGCTTTTAA	840
TTAGGATTAT	TGACTCCAAA	GCAACATTCT	TACTTTTATC	GTCAAATTGC	GCAAAAAGGT	900
TACAAAATGA	TTGAACCTTT	GGATGATCAA	ATTTTTGTGA	AAAAACCAAG	CAAAGTAAAG	960
AGTATTCTGG	ACGTCGTTTT	GAGTAATCAT	CTAGTCAGTC	TAGCGACTAT	AATGTCATAA	1020

CAAAGTATTC GTTTACAGTT TATAAGCGAA ATATTTTCAG TCGAAATGAA ATTTTTTGAT	1080
CAGTATCAAG AAGATAGAAG AACAGATCGA TTTGATAACA TCATCCCTTT GTACAAAAGA	1140
AATAATTTAT AA	1152

(2) INFORMATION FOR SEQ ID NO:1802:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...318
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1802:

TTCCCTAATG GGAGCTTTTT GCGTGCTCTG AACATTTCCC ATTTTGGAAG GAGTACTGTG	60
AAACGTCAAT CAGCCTTGGT CGTCTTTAGT GGTGGTCAAG ATTCAACAAC CTGCCTTTTC	120
TCGGGCCCCAC GGCAGTATGA AACAGTCGAA GCTGTCACCT TTGGCCTACG GCAACATCAT	180
CACCTCGAAA TTCAAATTGC TAGAGAAATC GCCAAGGAAC AGGGGCATTC GTCACCCATA	240
TCCTCGATAT GTCTCTGCTG GGACAAATCA CTGCTCAACC ACGACTTTGC GACGATTTCA	300
TATTTCTTAC ATTTCTGA	318

(2) INFORMATION FOR SEQ ID NO:1803:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 402 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...402
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1803:

AAAGAAAATG	GTACAATATT	TCTAAGAGAA	AATACAATGG	GAGGTAAAAAT	GAGGTTATTA	60
CCTATAAGAA	AAATATCACG	TCAGTCTAAA	AGGTTAGCAC	TTTTTTTGAC	GTTTGTGCT	120
GGATATGTGG	ATGCTTACAC	TTTTATTGTT	CGCGGGAATA	CCCTTGTAGC	TGGACAAACT	180
GGAAATGTTG	TCTTCTTTC	AGTAGAATTA	ATTAAAAATA	ATGTTTCGGA	TGTTAGGGAC	240
AAGGTTCTCA	CCTTGCTAGC	GTTTATGATG	GGAGTCTTTT	TATTAACGAT	TTATAAGGAA	300
AAATTGAGAA	TTGTGAAAAA	ACCTATTCTG	TCCTTGATTC	CCTTGGCAAT	CTTATCAATC	360
ATTATTGCTT	TTGTGCCGCA	AACTGTGGAT	AATATCTATC	TA		402

(2) INFORMATION FOR SEQ ID NO:1804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1804:

AGAGTGAATG	GGAGGAATAA	GATGAGCGAT	GTAAAAGAGG	AAGTAAGCTC	TCTATCTGAG	60
AAGCAGTTAC	GCCAAATTGA	TGTTGAGTAT	GCTGAATTAA	ATGATAGTGA	TATTATCGAG	120
CGATTAGCTT	ATTTAGAAAT	TAACAACAAT	GAAAAACGTA	TTGTCATCTC	TGATATTGAA	180
CCAACCAAGG	AAATAATGTC	AGTCTCGGAC	CAAAATTTTGT	AGATTCAAAA	GAATTTTCAA	240
AAAATCAAGA	ATATGTTTGA	ATTGTTTATT	TCAGATGTCT	CGGATTTTTT	AAGTATTAAA	300
AATAAACTTG	AGTCAAAGGA	ATTAGAAATT	GAAGAGGCAG	ATGTAAATCG	TTTCATGATT	360
CATTTATTAT	CCAGTGGAAG	ATTGTTTGTC	GATTTTAAAC	AAAACCAAAT	TAAACAAAAA	420
TATTCCAAAG	ATAGTGAGGA	GTTTGATTGT	ATACATGGTT	TTGCAAGCTA	TCAGTATGAT	480
ATCAATTTTA	CTTATCGATT	TTGCCATTCT	TTGAGAAATT	ATTCGCAACA	TACTGACTTA	540
CCAATAAATG	AGGTAAAAGC	TGTTAGCCCA	GATGATGAGA	CTGTTATAAT	AGATTTCTAT	600
ATTGATTTAG	ATTATCTTTT	AAATTCCAAC	TTTAAATGGA	AAAAATTGAA	AGGGGAGTTG	660
ATAAACTAA	ACCAAGAAAC	ATCTAAGATT	GACGCTATAG	CTCTAGTGAA	AGAATACTTT	720
AATGCTCTTA	CAGAGCTCTA	TGGTAATTAT	AATAAGTTGT	TTTTAAAGTT	AAACCATAAT	780
ACATTAGTAG	ATATTAAATC	AAAGTTGGAA	TCATTAAAAAT	TGAAACACTC	TAGGTATTAT	840
ATTTCAAAGA	TAAGCAAGTA	TGATCTTAAA	TATAATCCTG	GAAATTATAC	TATGTCACCA	900
CTTGACGAT	TTGCTGAAAT	TGAAGAGATT	TATATTGAAC	TTTCAAAAAT	TGGTTTGGTT	960
AAAATTGTCA	ATAAAAGTAA	TTAA				984

(2) INFORMATION FOR SEQ ID NO:1805:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...519
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1805:

GCAGGGAATG	GACATCGTAA	AGGATTTTCCT	GAAAGCTATG	ATATGGAAGC	TCTTCTCAAC	60
TTCTTGGAAC	GCATCAAAAA	TGGACAAGAT	GTAGATATTC	CTGTCTATTC	TCATGAAGTT	120
TACGACATCG	TACCCAAAAA	GAAACAAAGT	GTCAAAGCTG	CTGATTTTGT	AATCGTTGAG	180
GGAATTAATG	TCTTTCAAAA	TCCACAAAAC	GATCGTCTCT	ATATCACTGA	CTTCTTTGAC	240
TTTTCCATCT	ATGTAGATGC	TGGAGTGGAT	GATATTGAAA	GTTGGTATCT	GGACCGTTTC	300
TTGAAAATGC	TGAGTCTAGC	CCAAAACGAC	CCTGATAGCT	ACTATTATCG	TTTTACTCAG	360
ATGCCGATTG	GGGAAGTGGA	GTCCTTTGCC	CATCAGGTCT	GGACCAGTAT	CAATCTCACA	420
AATCTGCAAA	ATTATATTGA	ACCAACCAGA	AATCGTGCAG	AAGTGATTCT	TCATAAAAGC	480
AAGAACCATG	AAATCGATGA	AATTTACTTA	AAAAAGTAA			519

(2) INFORMATION FOR SEQ ID NO:1806:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 756 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...756
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1806:

TCGCGTGATG	GGAGAAATCC	TGAGCGTAAG	TTTGCCATCA	TCACAGGACT	TAAC TTACCG	60
ATGTTGATTG	AAGCCTACAC	AGAGCGCCTC	ATGGACGCTG	CTGCAGGTGT	AGAAAAAGTC	120
GCTGCTAATA	TCATTAAAGA	AGCCAAGGAT	GGCATCAAAG	CTCTTCCAGA	AGAGCTAAAT	180
CCAGTTGAAG	AAGTTGCAAG	CGCTGCAGCT	GCTCCAGTTG	CCCAAGCTGC	TATCCCAGAA	240
GGAACGTGTA	TCCGAGACGG	TAAATTGAAA	ATCAATCTTG	CCCGTCTTGA	CACACGTCTA	300
CTTCACGGTC	AGGTTGCAAC	TGCTTGGAAT	CCAGATTCAA	AAGCAAATCG	TATCATCGTT	360
GCTTCAGATA	ACGTGGCTAA	AGACGACCTT	CGTAAAGAAT	TGATTAAACA	AGCAGCTCCA	420
GGTAATGTCA	AGGCTAACGT	GGTTCCAATT	CAAAAAC TGA	TTGAGATTTT	AAAAGACCCA	480
CGTTTTGGAG	AAACACATGC	CCTTATCTTG	TTTGAAACAC	CTCAAGATGC	CCTTCGTGCC	540

ATCGAAGGCG GCGTGCCAAT CAAGACTCTT AACGTTGGTT CTATGGCTCA CTCAACAGGT	600
AAAACATTGG TCAATACCGT TTTGTCTATG GACAACGCCG ATGTTGCGAC ATTTGANAAA	660
ATGCGTGACT TGGGTGTCAC GTTTGATGTC CGTAAAGTAC CAAATGATTC TAAAAAAGAT	720
NTGTTTGA CT TGCTTAACAA AGCCAATGTC AAATAA	756

(2) INFORMATION FOR SEQ ID NO:1807:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 207 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...207
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1807:

TCGAAAGATG GAAAAAAGAA GGAAAATCAA ATAGAGAAAT TGCCTCTCTA CTTGGAAAAG	60
CTCCTCAAAC TATCCACACT AAAATCAAGC GTAGGACAGT CCGAAAATGT CTTGGAAAAG	120
GGCGCTTCAA AGAGGTTTAT TCTGCCGACT ATGCTCAACA GTCTTATGAA AACAATCGCA	180
AGCGCTCGGT CAAGAAATCA AGCTTGA	207

(2) INFORMATION FOR SEQ ID NO:1808:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 207 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...207
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1808:

TCGAAAGATG GAAAAAAGAA GGAAAATCAA ATAGAGAAAT TGCCTCTCTA CTTGGAAAAG	60
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CTCCTCAAAC TATCCACACT AAAATCAAGC GTAGGACAGT CCGAAAATGT CTTGGAAAAG	120
GGCGCTTCAA AGAGGTTTAT TCTGCCGACT ATGCTCAACA GTCTTATGAA AATAATCGCA	180
AGCACTCGGT CAAGAGATCA AGCGTGA	207

(2) INFORMATION FOR SEQ ID NO:1809:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...294
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1809:

AGGAATTGTG GATTGCCAAA TTGTATCATT GAAATTATTG CTCAAATTTG TTATGATATA	60
AATATGAATA AAAGTAGACT AGGACGTGGC AGACACGGGA AAACGAGACA TGTATTATTG	120
GCTTTGATTG GTATTTTAGC AATTTCTATT TGCCTATTAG GCGGATTTAT TGCTTTTAAG	180
ATCTACCAGC AAAAAAGTTT TGAGCAAAAG ATTGAATCGC TCAAAAAAGA GAAAGATGAT	240
CAATTGAGTG AGGGAAATCA GAAGGAGCAT TTTCGTCAGG GCAAGCCGAA GTGA	294

(2) INFORMATION FOR SEQ ID NO:1810:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...330
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1810:

AGGTCATGTG GGATTAGGCT NNTTNGGCTG GTTGTNGANA ACGAAGCACG GTGTACCGAT	60
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GAAAATGGAG	TTATCGATGA	CGTGTATCGT	ATTGAATTTT	ATGAAGAACA	TTTAAGATGG	120
CTACATAAAG	CCATTGAAGA	AGGAAGTCAC	TGTTTTGGAT	ACCACGCTTG	GACCGCATTT	180
GATTGCTGGT	CTTGGAATAA	TGCATATAAG	AATCGTTACG	GATTTATCTC	CGTTGATTTA	240
GAAACGCAAA	AGAGAACCAT	CAAGAGCTCA	GGAAGATGGT	ATCGCAAAGT	AAGTGACAAT	300
AACGGTTTTG	AAGTAGAAAT	TGAGGAGTAA				330

(2) INFORMATION FOR SEQ ID NO:1811:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...297
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1811:

GCCCCTCGTG	GTGAAACTTT	TCAGGANANG	GTCAGCATCA	CGACTTATCA	AAACAATCAA	60
GTTTCTAACA	ATAAATTTC	AACTTCACTT	CATTTTCATCG	AGGTTGTTTC	CAAAGATTTG	120
GGAGTAGACA	AGTCAGAAAGT	CTATGTTAAT	ACTTCCACAA	ACACAGATGG	CGCACTTATC	180
AAGGTGGGAG	ATCGCTATTA	TCGTGCCCTA	AACGGAAGTG	AGCCAGACAA	GTACCTGTTA	240
GAGAAAGTCG	AATTGTATAA	GACAGACGCA	ATTGAACTGG	TGGATGTGAA	CAAATGA	297

(2) INFORMATION FOR SEQ ID NO:1812:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 783 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1812:

AGGGCTAGTG	GTGTTTACCA	TGGAGCTCTT	AGTATCATGA	TTATGGCGAC	TTATGAAACC	60
TTTGCGGCGG	TCTATGATGC	GGTCATGGAC	GATAGTTTAT	ACGACAAATG	GACGAATTTT	120
TCTCTGCGTC	ATTTGCCTAA	GACCAAGGAG	AGAAAGAAAC	TCTTGGAATT	GGCTTGTGGG	180
ACAGGAATTC	AATCAGTGCG	CTTCTCTCAG	GCTGGTTTTG	ATGTGACTGG	ACTTGACTTG	240
AGTGCGGATA	TGTTGAAGAT	TGCGGAGAAG	AGAGCAACTT	CAGCCAAGCA	AAAGATTGCT	300
TTTATAGAAG	GTAATATGCT	GAATTTGTCC	AAGGCAGGGA	AATACGATTT	TGTCACGTGT	360
TATTCGGAAT	CTATCTGCTA	TATGCAGGAT	GAGGTGGAAG	TAGGGGACGT	CTTTAAGGAC	420
GTGTACAATG	CGCTGAATGA	AGAGGGAGTT	TTCATCTTTG	ACGTGCACTC	GACCTACCAG	480
ACAGATGAAG	TATTCCCTGG	CTATTCCTAC	CATGAAAATG	CGGAAGATTT	TGCCATGCTT	540
TGGGATACAT	ATGAGGACGA	AGCTCCTCAC	TCCATCGTGC	ATGAGCTGAC	TTTCTTTATC	600
AAGGAGGCTG	ACGGTTCCCT	TAGTCGCCAC	GATGAAGTAC	ATGAGGAGAG	GACCTATGAG	660
ATCTTGACCT	ATGATATCTT	GCTGGAACAG	GCTGGATTTA	AGTCCTTCAA	ACTCTATGCA	720
GACTTTGAGG	ATAAGGAGCC	AACAGAAACT	AGCACCCGTT	GGTTTTTTGT	GGCGCAGAAG	780
TAG						783

(2) INFORMATION FOR SEQ ID NO:1813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1813:

GCAAAAAGTG	GCTTTCGAAC	GAGTAGAGCC	CTTGTTAAAA	ATGTTCCGTT	TGGACAGAAA	60
TTAGACTGGT	TCCCTGTTCA	TTTTTCAAAA	GGGATGAAGC	AGAAGGTCAT	GATTATCTGT	120
GCTTTTGTGG	TGGATCCAAG	TCTTTTCATC	GTGGATGAGC	CTTTCCTTGG	TCTTGATCCG	180
CTGGCTATTT	CTGATTTGAT	TCAGCTTTTG	GAAGTGGAGA	AGCAAAAGGG	CAAGTCTATT	240
CTCATGAGTA	CCCACGTGCT	GGATTCGGCG	GAGAAGATGT	GTGATGCCTT	TGTCATTCTT	300
CACAAGGGAG	AGGTGCGTGC	AAACGAATCT	CCTGCAACTA	CGTGA		345

(2) INFORMATION FOR SEQ ID NO:1814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1814:

GTTCCAGGTG	GTTCGAAAA	TATTCGCCAA	GTCCCTTAAAA	TAAATGACAC	AGAAAATAAG	60
GAAGCTGGTG	CCTATCAATT	CGTTACGGTT	GGTGTTC AAC	ATGCCACTTT	AGCTCATATG	120
ATTTATGCTT	GGTTGACACC	TTTTACAGAT	ATTCGTAGTG	CTCAGGAAAC	TACAGGTGGT	180
TCTTCCGATG	TTAAATTTAT	GCAAATCAAT	CAATTCTACA	TGCAAACATC	GCAAAATATG	240
GCCAAGTATC	AAGGACTAAA	AACAGCTGGT	AAGGATATCG	AACTCAAGTA	CTTTGGAGTT	300
TATGTTTTGA	ATGTGACGGA	TAATTCAACC	TTTAAAGGGA	TTCTCAATAT	CTCTGATACA	360
GTCACAAACAG	TCAATGATCA	GACCTTTGAT	AATTCCAAAG	AATTGATTGA	TTACGTCAGT	420
GCTCAAAAAAT	TAGGGGATTC	CGTCAAGGTC	ACCTATGAAG	AGGATGGGCA	AACCAAGTCT	480
GCAGAATGA						489

(2) INFORMATION FOR SEQ ID NO:1815:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1815:

GGTGGTATCG	GTGGTACTTA	TGGTGCTATG	CCAGAACTCT	TCTTGAAACT	CAATCAGTTG	60
ATTGCGGATA	AGGACCTAAA	AACAGCGCGT	GAATTGCAGT	ATGCTATCAA	CGCAATCATT	120
GGTAAACTCA	CTTCTGCTCA	TGGAAATATG	TACGGTGTCA	TTAAAGAAGT	CTTGAAAATC	180
AATGAAGTCT	TGAATATTGG	ATCTGTTCGT	TCACCATTGA	CACCAGTGAC	TGAAGAAGGT	240
CGTCCAGTTG	TAGAAGCGGC	TGCTGCCTTG	ATTCGTGAAA	CCAAGGAGCG	CTTCCTCTAA	300

(2) INFORMATION FOR SEQ ID NO:1816:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 582 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...582
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1816:

ATGAAAATCG	GAATATTGGC	CTTGCAAGGG	GCCTTTGCAG	AACATGCAAA	AGTGCTAGAT	60
CAATTAGGTG	TCGAGAGTGT	AGAACTCAGA	AATCTAGATG	ATTTTCAGCA	AGATCAGAGT	120
GACTTGTCGG	GTTTGATTTT	GCCTGGTGGT	GAGTCTACAA	CCATGGGCAA	GCTCTTACGT	180
GACCAGAACA	TGCTACTTCC	CATCCGAGAA	GCCATTCTAT	CTGGCTTACC	AGTGTTTGGG	240
ACCTGTGCGG	GCTTAATTTT	GCTGGCTAAG	GAAATCACTT	CTCAGAAAGA	GAGTCATCTA	300
GGAACATATG	ATATGGTGGT	CGAGCGTAAT	GCTTATGGGC	GCCAATTAGG	AAGTTTCTAC	360
ACGGAAGCAG	AATGTAAGGG	AGTTGGCAAG	ATTCCAATGA	CCTTTATCCG	TGGTCCGATT	420
ATCAGTAGTG	TTGGTGAGGG	TGTAGAAATT	CTAGCAACAG	TGAACAATCA	AATTGTTGCA	480
GCCCAAGAAA	AAAATATGTT	GGTAAGTTCT	TTTCATCCAG	AATTGACTGA	TGATGTGCGC	540
TTGCACCAGT	ACTTTATCAA	TATGTGTAAA	GAAAAAAGTT	GA		582

(2) INFORMATION FOR SEQ ID NO:1817:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 855 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...855
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1817:

GGACCAGTCG	GTTATAGCTT	GTATGGAGGG	CTTATAATGG	CAGATATAAA	ATTGATTGCA	60
TTGGACTTGG	ACGGGACCTT	GCTGACTACT	GATAAAAGGC	TGACGGATCG	TACCAAGGAA	120
ACCTTGAAAAG	CTGCGCGTGA	TCGTGGTATC	AAGGTCGTAT	TGACAACTGG	TCGTCCCTTA	180
AAAGCTATGG	ATTTCTTTCT	CCATGAGCTA	GGGACTGACG	GTCAGGAAGA	AGAGTATACC	240
ATTACTTTTA	ATGGTGGTTT	GGTTCAGAAA	AATACAGGTG	AAATCCTTGA	TAAGACAGTC	300

TTTTCATATG	ATGATGTGGC	ACGCTTGTAT	GAAGAAACAG	AGAAATTATC	ACTGCCTCTT	360
GACGCTATCT	CAGAAGGAAC	TGTTTATCAA	ATTCAATCGG	ACCAAGAAAAG	TCTTTATGCC	420
AAATTCAATC	CAGCTTTGAC	TTTTGTTCCA	GTTGATTTTG	AAGACCTGTC	TAATCAAATG	480
ACCTACAACA	AATGCGTGAC	CGCCTTTGCT	CAAGAACCCT	TGGATGCAGC	CATTCAGAAG	540
ATTTCTCCAG	AATTGTTTGA	CCAATATGAA	ATCTTTAAAT	CACGTGAAAT	GTTGCTAGAA	600
TGGTCACCAA	AGAATGTTCA	TAAAGCAACA	GGTTTGGCAA	AACTAATTAG	CCATCTTGGA	660
ATTGATCAAA	GTCAAGTGAT	GGCCTGTGGT	GACGAGGCCA	ATGACCTCTC	TATGATTGAA	720
TGGGCAGGGC	TCCGTGTTGC	CATGCAAAAC	GCTGTTTCCTG	AAGTCAAGGC	AGTCGCAAAT	780
GTGGTAACTC	CTATGACCAA	TGATGAAGAA	GCTGTCGCCT	GGGCTATCGA	AGAATATGTG	840
CTAAAGGAGA	ACTAA					855

(2) INFORMATION FOR SEQ ID NO:1818:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 186 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...186
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1818:

TTTTCTTACG	GGCATGATTC	TCTCCTTAAC	AGTACATACC	TATTTTATCA	TTTTTTTCGGC	60
AGAGAATTAT	TACAGAAAAG	TTACAAAAAG	AATAAAGTCC	CTTTTCATTT	TCAAAGCATG	120
GCTGATTTTG	GAGAAATGTG	GTATAATTTT	TCTTATGGAA	AAGATTGTCA	TTACAGCAAC	180
TGCTGA						186

(2) INFORMATION FOR SEQ ID NO:1819:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 390 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1819:

AGAAAATACG	GAATCGAGGG	GAATTCTATG	GAGCAAATTG	GAAAAGTCTT	TAAACAATTA	60
CAAGAATCAA	GAAATATCTC	ACTGATACAA	GCAACCGGAG	GACAATTTTC	GCCGTCATG	120
TTGTCCCGTT	TTGAAACAGG	TCAAAATGAG	CTTTCGGTGG	AAAAGTTTCT	ATTTGCTCTG	180
GAAAATATAT	CTGCCAGTGT	GGAGGAAATC	CTCTTTCTGG	CAAGAGGTTT	CCATTATGAT	240
ACAAATCCTG	AGTTGAGAAA	AGAAATTACA	GATGTCTTGG	AACCAAAGAA	TATACCACCT	300
CTTGAGGACT	TATATCGCAG	GGAGTATCAA	AAGCATGCCC	ATTCTCACAA	CAAACAGAAA	360
CATATTCTAA	ATGCCATTAT	TATCAAGTCT				390

(2) INFORMATION FOR SEQ ID NO:1820:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 936 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1820:

GGAGAAAACG	GAGGTAATAG	AAGTATGATT	TATACAGTCA	CACTCAATCC	ATCCATTGAC	60
TATATCGTTC	GTNTGGACCA	AGTCAAAGTT	GGTAGTGTA	ATCGTATGGA	CAGTGATGAT	120
AAGTTTGCTG	GTGAGAAAGG	AATCAATGTC	AGCCGTGTC	TGAAACGTTT	GAATATATCA	180
AATACAGCGA	CGGGATTTAT	CGGTGGCTTT	ACTGGTAAAT	TTATCACAGA	TACTTTAGCA	240
GAGGAAGAAA	TCGAGACACG	TTTTGTCCAG	GTGGCAGAAG	ATACTCGTAT	CAATGTTAAA	300
ATCAAAGCAG	ACCAAGAAAC	AGAAATCAAC	GGAACGGGTC	CAACTGTTGA	ACCGGTTAAG	360
CTAGAAGAAT	TGAAAGCTAT	TTTATCTAGT	CTGACAGCAG	AAGATACAGT	TGTCTTTGCA	420
GGTTCGAAGT	CTAAAAATCT	AGGCAATGTT	ATCTATAAGG	ATTTGATTTT	CTTGACGCGC	480
CAGACTGGTG	CGCAAGTGGT	CTGTGACTTT	GAAGGACAGA	CCTTAATTGA	TAGTTTGGAC	540
TACCAGCCTC	TTCTTGTA	ACCAAATAAT	CATGAACTTG	GAGCGATTTT	TGGGGTTAAA	600
CTCGAAAGTT	TAGATGAAAT	TGAGAAATAC	GCTCGTGAGT	TACTGGCTAA	GGGTGCTCAA	660
AATGTTATTA	TCTCTATGGC	TGGTGATGGT	GCCCTTCTTG	TCACATCTGA	GGGAGCTTAC	720
TTTCGTA	CAATCAAAGG	AACAGTCAAA	AATTCAAGTTG	GAGCTGGTGA	TTCTATGGTT	780
GCTGGATTCA	CAGGTGAATT	TGTCAAATCA	AAAGACGCAG	TAGAACCTTT	CAAATGGGGA	840
GTGGCTTGCG	GAACGGCAAC	TACCTTCTCA	GATGACTTGG	CAACGGCGGA	ATTTATTAAA	900
GAAACATATG	GAAAAGTTGA	GGTAGAAAAA	CGATGA			936

(2) INFORMATION FOR SEQ ID NO:1821:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 831 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1821:

TTTGAAACG	GGTCCAGTCC	TTTATCACCA	TTCAAGGAGG	TTAGTATGAA	AAAATATCAA	60
CGAATGCATC	TGATTTTTAT	CAGACAATAC	ATCAAAACAA	TCATGGAATA	TAAGGTGGAT	120
TTTGTGGTTG	GTGTCTTGGG	AGATCTTTCT	GGCTCAAGGC	TTGAATCTCT	TGTTTCTCAA	180
TGTCATCTTT	CAACATATTC	CATTCCTAGA	AGGTGGACCT	TTCAAGAGAT	AGCTTTCATT	240
TATGGATTTT	CCTTGATTCC	CAAGGGAATG	GACCATCTCT	TTTTTGACAA	TCTCTGGGCA	300
CTAGGGCAAC	GCCTAGTCCG	AAAAGGAGAG	TTTGACAAGT	ATCTGACTCG	TCCCATCAAT	360
CCTCTCTTTC	ACATCCTAGT	TGAAACCTTT	CAGATTGATG	CCTTGGGTGA	ACTCTTAGTC	420
GGTGGTATTT	TATTGGGAAC	AACAGTGACC	AGCATTGTTT	GGACTCTTCC	AAAATTCCTG	480
CTTTTCCTAG	TTTGATTCC	TTTTGCGACC	TTGATTTATA	CTTCTCTTAA	AATCGCAACA	540
GCCAGTATCG	CCTTTTGGAC	TAAGCAGTCA	GGCGCCATGA	TTTACATCTT	CTATATGTTC	600
AATGACTTTG	CTAAGTATCC	GATTTCTATT	TACAATTCTC	TTCTTCGTTG	GTTGATTAGC	660
TTTATCGTGC	CTTTCGCCTT	TACAGCCTAT	TATCCAGCTA	GCTATTTCTT	ACAGGAAAAG	720
GATGTGTTCT	TTAACGTAGG	AGGTTTGATG	TTGATTTCTC	TGGTTTCTT	TGTTATTTCC	780
CTTAAACTTT	GGGATAAGGG	CTTAGATTCC	TACGAAAGTG	CGGGTTCGTA	A	831

(2) INFORMATION FOR SEQ ID NO:1822:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 615 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1822:

ATCAATGACG	GGAAAAATAG	TTTAAATGTT	AAATCGAAAG	GATTGTATAT	GTCAAAAGCA	60
AAGAAAATAT	GTTTCATTAT	TTTCTGTATT	TTAATCTTGA	CAATTTTCCT	TCCTGTTTTG	120
ATAGATTATC	ATCAAGTTAG	TGATCTAGGT	ATTCTATCTAC	TTAGCTGGAG	ACAGAACTCC	180
GTAGTTGAAT	TCTATCTTGC	TAGATATGTC	TTTTGGGGGA	CAGTGGTTCT	ATCAACTTTA	240
GTTTTATTAT	CCATTTTAGT	TGTGATGTTT	TATCCTAAAC	GTTACTTGGA	AATCCAACCT	300
GAAACTAAAA	ACGATACATT	AAAATTAAAG	AATTCGGCAA	TCGAAGGTTT	TGTTAGAAGT	360
TTGGTGAGTG	ATCATAGATT	GATCAAGAAC	CCAAC'TGTT	ATGTAAATTT	ACGAAAAAAT	420
AAATGTTTCG	TTCATGTAGA	AGGTAAATTT	CTTCCTTCAG	ACAACATCGC	TGACAGATGC	480
CAAATAATTC	AAAATGAAAT	AAC'TAATGGA	TTGAAGCAGT	TTTTTGGTAT	TGAGCGTCAA	540
GTAAACCTTG	AAGTTGCAGT	AAAAAATTAC	CAACCAAAAC	CTCAAAACAA	AAAGACTGTT	600
AGTCGTGTGA	AGTAA					615

(2) INFORMATION FOR SEQ ID NO:1823:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1823:

TCAAAAGACG	GAGGAAACGC	TATGCTCGGA	ATTTTAACCT	TTATTCTGGT	TTTTGGGATT	60
ATTGTAGTGG	TGCACGAGTT	CGGGCACTTC	TACTTTGCCA	AGAAATCAGG	GATTTTAGTA	120
CGTGAATTTG	CCATCGGTAT	GGGACCTAAA	ATCTTTGCTC	ACATTGGCAA	GGATGGAACG	180
GCCTATACCA	TTCGAATCTT	GCCTCTGGGT	GGCTATGTCC	GCATGGCCGG	TTGGGGTGAT	240
GATACAACTG	AAATCAAGAC	AGGAACGCCT	GTTAGTTTGA	CACTTGCTGA	TGATGGTAAG	300
GTTAAACGCA	TCAATCTCTC	AGGTAAAAAA	TTGGATCAAA	CAGCCCTCCC	TATGCAGGTG	360
ACCCAGTTTG	ATTTTGAAGA	CAAGCTCTTT	ATCAAAGGAT	TGGTTCCTGA	AGAAGAAAAA	420
ACATTTGCAG	TGGATCACGA	TGCAACGGTT	GTGGAAGCAG	ATGGTACTGA	GGTTCGGATT	480
GCACCTTTAG	ATGTTCAATA	TCAAAATGCG	ACTATCTGGG	GCAAACCTGAT	TACCAATTTT	540
GCAGGTCCTA	TGAACAATTT	TATCTTAGGT	GTCGTTGTTT	TTTGGGTTTT	AATCTTTATG	600
CAGGGTGGTG	TCAGAGATGT	TGATACCAAT	CAGTTCCATA	TCATGCCCCA	AGGTGCCTTG	660
GCCAAGGTAG	GAGTACCAGA	AACGGCACAA	ATTACCAAGA	TCGGCTCACA	TGAGGTTAGC	720
AACTGGGAAA	GCTTGATCCA	AGCTGTGGAA	ACAGAAACCA	AAGATAAGAC	GGCACCAGCT	780
TTGGATGTGA	CTATTTCTGA	AAAGGGGAGT	GACAAACAAG	TCACTGTTAC	ACCCGAAGAT	840
AGTCAAGGTC	GTTACCTTCT	AGGTGTTCAA	CCGGGGGTTA	AGTCAGATTT	TCTATCCATG	900
TTTGTAGGTG	GTTTTACAAC	TGCTGCTGAC	TCAGCTCTCC	GAATTCTCTC	AGCTCTGAAA	960
AATCTGATTT	TCCAACCGGA	TTTGAACAAG	TTGGGTGGAC	CTGTTGCTAT	CTTTAAGGCA	1020
AGTAGTGATG	CTGCTAAAAA	TGGAATTGAG	AATATCTTGT	ACTTCTTGGC	AATGATTTCC	1080
ATCAATATTG	GGATTTTTTA	TCTTATTCCG	ATTCCAGCCT	TGGATGGTGG	TAAGATTGTG	1140
CTCAATATCC	TAGAAGCCAT	CCGCCGCAAA	CCATTGAAAC	AAGAAAT'TGA	AACCTATGTC	1200
ACCTTGGCCG	GAGTGGTCAT	CATGGTTGTC	TTGATGATTG	CTGTGACTTG	GAATGACATT	1260
ATGCGACTCT	TTTTTAGATA	A				1281

(2) INFORMATION FOR SEQ ID NO:1824:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1824:

TCTTACTGCG GTTATGATGA AAAAATAATC TTGGAAAATA TAAATATAAA AATACCTGAA	60
GAAAAAATAT CAGTTATTAT TGGGTCAAAT GGTGTGGGA AATCAACACT CATTAAAACC	120
TTGTCTCGAC TTATAAAGCC ATTAGAGGGA GAAGTATTGC TTGATAATAA ATCAATTAAT	180
TCTTATAAAG AAAAAGATTT AGCAAAACAC ATAGCTATAT TACCTCAATC TCCAATAATC	240
CCTGAATCAA TAACAGTAGC TGATCTTGTA AGCCGTGGTC GTTTCCTAC AGAAAGCCTT	300
TTAAGAGTCT TGGAAAAGAT GACCTTGAAA TAA	333

(2) INFORMATION FOR SEQ ID NO:1825:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1825:

GGCCGGTGCG GTGTGGGCCC GGGGTGGGGC GGCGGATTCC TGCGGGGGGG GGCGTGGGGG	60
GTTTGGCGTG CGGCGGGCGG TGGTGGGGGT GGGGGGGGGG AGTTGCTCGC GCGCGGTGGG	120
GGATTGGCCG CGTGGAGGGG GCGGCGATGC GGGGGAACGG GGGGTGGAGG GAAGTGGGGT	180

(2) INFORMATION FOR SEQ ID NO:1826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1826:

AAAGAAAGCG GTAACAATAT GCTTAATGCG AAAATTTTTT ATATATTTTT ATGTTTGATC	60
GTTATCGAAA CTACAGGCTT GTTGTTGTTG AAAAGAGGTC TCGAAATGGG TTATTTAGAC	120
ACAGAAGCTA TTATCCTCGC AGTTTTTCA TTTGCTTTTT ACAACCTATG TTCATTCGCT	180
TGGGTCTGCT CTACAATAAA AAACAATAAA AAATAA	216

(2) INFORMATION FOR SEQ ID NO:1827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1827:

GAAAGCGGCG GAAGAATTTT AAAAATATCC GAAGCTTTGA AAAGGCAGAC TACTCAACAC	60
TATCCAGCCT TGATACTTTT TGATGGGCTT ATGTACCGCA ACATTAAGAG AGATAAGCTG	120
ACCGAGGCGG AACAAAGATTA TCTTGAAAAT CATGCTTCA TTACCTCGGC TTTGTACGGT	180
GTTGTTCAG CCTGTACC CATGGCTCCT CACCGTTTG ATTTTTTGAT GAAATTAAAA	240

GTTGCTGGTA	AGACTTTGAA	GAGCCATTGG	AAGGCAGTCT	ATGATGAAGC	TCTGAAGATG	300
GAAGAAGTGA	TTTTCTCTCT	CTTGTCATCA	GAGTTTGAGA	CTGTATTTTC	TAAGGAAATC	360
AGAGCAAAGA	TGGTGACCTT	CAATTTCATG	GAGGATAGAG	AGCGGTCACT	GAAGATTCAC	420
TCAACTATCT	CCAAGAAAGC	GCGCGGGGCC	TTTTTAACAG	CTTTAATAGA	AAATCAAGTA	480
CAAACTGTGG	GGGAAGCACG	TCGCTTGAAC	TTTGCTGGAT	TTGTTTACCG	AGAAGATTG	540
TCACAACCAC	AGGGATTGGT	TTTGTTAAAG	GAAGTATAG			579

(2) INFORMATION FOR SEQ ID NO:1828:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 393 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1828:

GTNGGCGGCG	GGGCGGGGTG	GGTGGCGGGG	GGGTTTGGG	GCTGGCGTGG	GGCGGGGCGG	60
CTCGTTCGTT	GGGGGTGTGG	TAGGGGGGCC	GGTGTGGGCT	GGTGGCGGAG	TGGGGGGGGT	120
GTGCGGGGGC	GGGGTGGGGC	GGTGAGGCCG	GTGCGGTGTG	GGCCCGGGGT	GGGGCGGCGG	180
ATTCTGCGG	GGGGGGGCGT	GGGGGGGTTG	GCGTGCGGCG	GGCGGTGGTG	GGGGTGGGGG	240
GGGGGAGTTG	CTCGCGCGCG	GTGGGGGATT	GGCCGCGTGG	AGGGGGGCGG	CATGCGGGGG	300
AACGGGGGGT	GGAGGGAAGT	GGGGTGGCCG	GGGTTGAGGC	GGGGGCGGTC	CGGGGACGGG	360
TGGAGTGGGG	TGAGTGGGGG	GCA GTTGGTG	TGA			393

(2) INFORMATION FOR SEQ ID NO:1829:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1221 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...1221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1829:

AAGATTTTAG	GAAAAGTCGT	TATATCATGC	TATACCTATT	CTTTGTGGTA	TAATTGCAAG	60
AGGTTTAATC	CGATAATTTA	TAAAGAGAGA	AAGATATTCA	TGAGAGATTT	ATTATCTAAA	120
AAAAGTCATA	GGCAATTAGA	ATTATTAGAA	TTATTATTTG	AACATAAACG	TTGGTTTCAT	180
CGTTCTGAAC	TAGCAGAGTT	ATTAAATTGT	ACAGAACGTG	CAGTCAAAGA	TGATCTATCC	240
CATGTTAAAT	CTGCTTTTCC	TGACTTGATT	TTTCATTCTT	CTACTAATGG	TATACGCATT	300
ATTAATACCG	ATGATAGTGA	TATTGAAATG	GTTTACCATC	ATTTCTTTAA	ACATTCAACT	360
CATTTTTCGA	TTTTAGAATT	CATCTTCTTT	AATGAAGGTT	GTCAAGCTGA	GAGTATTTGT	420
AAAGAATTTT	ATATCAGTTC	ATCTTCGCTC	TATCGTTTTA	TTAGCCAAAT	CAATAAAGTG	480
ATTAAGAGGC	AATTTCAATT	TGAAGTCAGT	CTGACCCCTG	TTCAAATCAT	TGGAAATGAG	540
AGAGACATTC	GTTACTTTTT	TGCACAATAT	TTTTCAGAAA	AATATTATTT	CCTAGAATGG	600
CCATTTGAAA	ATTTTTCATC	AGAGCCACTA	TCTCAATTGT	TAGAATTGGT	TTATAAGGAA	660
ACAAGCTTTC	CAATGAATTT	GTCAACGCAT	AGAATGCTAA	AGTTGCTCCT	AGTTACGAAC	720
CTATATAGAA	TAAAGTTTGG	TCATTTTATG	GAAAGTAGATA	AAGATTCTTT	TAACGACCAA	780
AGTTTGGAAT	TTTAAATGCA	GGCAGAAAGG	ATAGAAGGTG	TTGCTCAGAG	TTTTGAATCA	840
GAATACAATA	TCTCTTTAGA	TGAAGAAAGT	GTTTGCCAAT	TATTTGTGTC	TTACTTTCAA	900
AAAATGTTTT	TCATAGATGA	AAGTCTCTTT	ATGAAATGCG	TAAAAAAGGA	TAGTTATGTT	960
GAAAAATCTT	ACCATCTATT	GAGTGATTTT	ATTGATCAGA	TTTCAGTCAA	GTATCAGATT	1020
GAAATGGAGA	ATAAGGATAA	TCTGATTTGG	CATCTGCATA	ATACCGCACA	TCTGTATCGT	1080
CAAGAGTTGT	TTACTGAGTT	TATTTTATTT	GATCAAAAAG	GGAATACAAT	CAGGAACTTT	1140
CAAAATATTT	TTCCAAAATT	TGTTTCAGAT	ATAAAAAAAG	AGATTTCTCA	CTATTTAGAG	1200
ACTCTTGAGG	TGTGTTCTTA	G				1221

(2) INFORMATION FOR SEQ ID NO:1830:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1830:

ACCATCATAG	GTCTCATTAT	TGGACTTGCC	ATTGGTGTCT	TCCGTACTGC	TCCTCTCTCT	60
GAAAACAAAG	CCATTTATGG	CCTTCAAAAA	CTAGTCGGCT	GGGTTCTCAA	TGTTCTACATT	120
GAAATTTTCC	GTGGTACGCC	AATGATTGTT	CAATCGATGG	TTATCTACTA	TGGAAC TGCC	180
CAAGCTTTTCG	GGATCAACCT	TGACCGTACA	CTGGCTGCTA	TCTTCATCGT	TTCAATCAAT	240
ACCGGTGCCT	ACATGACTGA	AATCGTCCGT	GGTGGTATCC	TAGCAGTTGA	CAAGGGACAA	300
TTTGAAGCTG	CGACTGCTCT	TGGTATGACC	CATAACCAGA	CCATGCGTAA	GATTGTCCCTA	360
CCTCAGGTAG	TCCGTAACAT	CCTACCTGCA	ACTGGTAATG	AATTTGTTCAT	CAATATCAAA	420
GATACATCTG	TATTGAACGT	TATCTCTGTT	GTCGAACTTT	ATTTCTCAGG	AAATACCGTG	480

GCAACACAAA CCTATCAATA CTTCCAGACA TTTACAATCA TCGCCGTGAT TTACTTTGTC	540
CTCACCTTCA CCGTAACACG TATCCTACGA TTTATCGAGC GCCGAATGGA CATGGATACC	600
TATACTACAG GTGCTAACCA AATGCAAACG GAGGATTTGA AATAA	645

(2) INFORMATION FOR SEQ ID NO:1831:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...363
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1831:

TGGATGGTAG GGTCTTCGAG GGAACACGCT GCTTGGGCTC TAGCGGACTA TGGTTTTAAG	60
GTCGTGATTG CAGGATCTTT CGGTGACATT CATTACAATA ATGAACTCAA TAATGGCATG	120
TTGCCAATCG TTCAGCCTAG AGAGGTTAGA GAGAACTAG CCCAGCTAAA ACCAACCGAC	180
CAGGTAAC TGACTTGGA ACAACAAAA ATCATCTCAC CAGTTGAAGA ATTCACCTTC	240
GAGATAGATA GCAAGTGGA ACATAAACTC CTAAATAGTT TGGATGATAT CGGTATTACC	300
TTGCAGTATG AAGAGTTGAT TGCTGCTTAT GAAAAACAAC GACCAGCCTA CTGGCAGGAT	360
TAG	363

(2) INFORMATION FOR SEQ ID NO:1832:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 423 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...423
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1832:

TTACAATCAG	GATCTGGGCA	ATTAGCAGAC	AAATCCAGTC	AGTTACTTTC	AGGTGCTTCT	60
CCATTAGAGA	ATAGAGCTAA	TAAATTGGCA	GATGGATCTA	GGAAACTAGC	AGAAGGTGGA	120
ACAAAGTTAA	CTTCTGGATT	GGAAGATTTA	CAGACAGGAC	TTGCTTCTTT	AGGACAAGGA	180
CTAGGTAAATG	CTAGTGATCA	ACTCAAATCA	GTATCAACAG	AATCTAAAAA	TGCAGAGATT	240
TTGTCAAATC	CACTCAATCT	TTCAAAAACA	GACAATGATC	AAGTTCCCTGT	AAATGGAATC	300
GCAATAGCTC	CTTATATGAT	ATCAGTTGCT	CTTTTTGTTG	CAGCAATATC	AACAAATATG	360
ATATTTGCGA	AATTGCCTTC	AGGACGTCAT	CCAGAGAGCC	GTTGGGCTTG	GTTGAAATCT	420
TGA						423

(2) INFORMATION FOR SEQ ID NO:1833:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1833:

AAAAAATCAG	GGAGATTTTG	GATGAAGCTT	GATGGCTATA	CACGTTTAGC	TGCAGTTGTT	60
GCCAATCCTA	TTAAGCATTC	TATTTCTCCC	TTCATCCACA	ATAGAGCCTT	TGAGGCGACA	120
GCTACCAACG	GTGCTTATGT	GGCTTGGGAG	ATTGAAGCGA	GTGACTTGGT	AGAAACAGTG	180
GCCAATATTC	GTCGCTACCA	GATGTTTGGC	ATCAATCTGT	CCATGCCCTA	TAAGGAGCAG	240
GTGATTCCTT	ATTTGGATAA	NCTGAGCGAT	GAANCGCGCT	TGATTGGTGC	GGTTAATACG	300
GTTGTCAATG	AGAATGGCAA	TTGGATTGGA	TATAATACAA	ATGGCAAGGG	ATTTTTTAAG	360
TGCTTGCCCT	CTTTTACCAT	TTCAGGTAAA	AAGAATAACC	TGCTGGGTGC	ACGTGGTGCG	420
GCTAAATCAA	TCTTGGCACA	GGCTATTTTG	GATGGCGTCA	GTCAGATTTT	GGTCTTTGTT	480
CGTTCCGTTT	CTATGGAAAA	AACAAGACCT	TACCTAGACA	AGTTACAGGA	GCAGACAGGC	540
TTTAAAGTGG	ATTTGTGTGC	TTTAGAATAT	GTTTCTGAAC	TGCAAGCAAG	GATTGCCGAG	600
TCGGATTTGC	TAGTTAATGC	CACCAGTGTG	GGCATGGATG	GCCAATCCTC	TCCTGTTCTT	660
GAAAACATAG	TCTTACCAGA	AACTCTTTTA	GTTGCAGATA	TCATATACCA	ACCCTTTGAA	720
ACACCGTTTT	TGAAATGGGC	TAGAAGTCAG	GGCAATCCAG	CAGTCAATGG	TCTGGGAATG	780
TTACTCTATC	AAGCTGCAGA	AGCTTTTCAA	CTGTGGACAG	GCAAGGAAAT	GCCGACAGAA	840
GAGATTTGGC	AGTCTTTAAC	AGAAAAATAC	CAATAA			876

(2) INFORMATION FOR SEQ ID NO:1834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1834:

CGGAAATCAG	GCGCATACTT	AAATATTCAA	CATGATTATA	ACACGAAAGG	AGCAAAAATG	60
GAAGCAGTTG	AAATTGTAAG	AATTAAAGAT	GTGATTATTG	AAAAAGTCTC	TGCTAATGAT	120
GAAGAGTTAA	AACGTATCTT	TGGATGTTCA	AAACGACAAG	CAGGAGAGCG	AAGAAGAGAA	180
ATGCAAAAAC	TCCCTAGTCA	GCAAAAACAT	CTTTTGGATA	GTGGACAACT	TGTAACGATT	240
AAAGGTTTCT	ATGAATACTT	GCAATATCGT	GGAACATAAG	CTTGGAAAAA	AGAAATGGAA	300
ACAAGCAAGA	AAATGAGGTC	AGCAGGATGA				330

(2) INFORMATION FOR SEQ ID NO:1835:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 849 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1835:

GTAGGATCAG	GTTCAAGTTT	TAAAAAACCA	AGCAAAATATG	ATATACTAAA	GAGCGAGTAT	60
TCTAGTAGAA	TTAGGACAAA	TAATATGAAA	CAAACGATTA	TTCTTTTATA	TGGTGGACGG	120
AGTGCGGAAC	GCGAAGTCTC	TGTCCTTTCA	GCTGAGAGTG	TCATGCGTGC	GGTCAATTAC	180
GACCGTTTCA	CAGTCAAGAC	TTTCTTTATC	AGTCAGTCAG	GTGACTTTAT	CAAAACACAG	240
GAATTTAGTC	ATGCTCCGGG	GCAAGAAGAC	CGTCTCATGA	CCAATGAAAC	CATTGATTGG	300
GATAAGAAAG	TTGCACCAAG	TGCTATCTAC	GAAGAAGGTG	CAGTGGTCTT	TCCAGTCCTT	360
CACGGGCCAA	TGGGAGAAGA	TGGCTCTGTT	CAAGGATTCT	TGGAAGTTT	GAAAATGCCT	420
TACGTTGGTT	GCAACATTTT	GTCATCAAGT	CTTGCCATGG	ATAAAATCAC	GACTAAGCGT	480
GTTCTGGAAT	CTGCTGGTAT	TGCCCCAAGT	CCTTATGTGG	CTATCGTTGA	AGGCGATGAT	540
GTGACTGCTA	AAATCGCTGA	AGTGGAAGAA	AAATTGGCTT	ATCCAGTCTT	CACTAAGCCG	600
TCAAACATGG	GGTCTAGTGT	CGGTATTTCT	AAGTCTGAAA	ACCAAGAAGA	ACTCCGTCAA	660
GCCTTAAAC	TTGCCTTCCG	ATATGACAGC	CGTGCTTGG	TTGAGCAAGG	AGTGAATGCC	720

CGTGAAATTG AGGTTGGCCT CTTGGGTAAC TACGATGTCA AGAGCACGCT ACCTGGAGAA	780
GTTGTCAAGG ACGTTGCCTT TTATGACTAC GATGCCAAGT ATATTGATAA CAAGATTACT	840
ATGGATATT	849

(2) INFORMATION FOR SEQ ID NO:1836:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 519 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...519
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1836:

AGCGTGTCTAG GGCTACTAGG GGCAGATAGG CTTATAGCTA AATGTAGACG ATTGGCTAGT	60
AAAAAACTG GCGAGGATAT CGTCTTACGT GCGGTGCACA ATGCTACTAT AAAGGTTGTC	120
CAAGCAGATG CAAGAAGACT CGCACCAGCG AGAGATGGAG AGCTTATAAC TAGTATCAAA	180
ACTAGGGCAA AAATGGACGG AGATAAGGCT ATAGGCGAAG TTTACACCAA CCTTAAATAC	240
GCTCCTTATG TTGAGTTTGG AACGGGACCA ATAGGACAAG CTAGCCATTC TGGTATTTCT	300
CCAGAGGTCA GCGTGAAGT CAAGTCTAGT CCGTGGTATG TACATGAAGA CCAAATCAAT	360
GTAGGACCGT ACCACTTTCA AAAAATCGGG GAGTTCTACA AGATGTATGG TCAACCTGCC	420
CAGCCTTATC TTTATCCAGC TTTGAGAGAC AATCAAGAGC GTGTGTCTAA GAATATTTTCG	480
AATTATGTCC GTAGAAAGAT AAGAGAACAA ATAAAATGA	519

(2) INFORMATION FOR SEQ ID NO:1837:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 651 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1837:

GAGAAGCCAG	GAAAAATAGT	AAAGAATTGG	CTAAAAACTA	TCGCTGACGT	GACTTCTAAA	60
ATTGTGGAAT	GGATCATCAA	TCTGGCTCCA	TTTGGAATCC	TTGGTCTTGT	TTTAAAAACC	120
ATTTCTGACA	AGGGAGTCGG	AAGCCTTGCC	AACTACGGTA	TTTTATTGGT	TCCATTAGTA	180
ACGACTATGC	TTTTTGTGTC	CCCTGTGGTC	AACCCTTTGA	TTGCCTTCTT	TTTTATGAGA	240
CGCAATCCTT	ACCCCTCTAGT	TTGGAAGTGC	CTCCGTGTCA	GCGGTGTGAC	AGCCTTTTTC	300
ACTCGTAGTT	CTGCGACTAA	CATTCCGTGC	AACATGAAAC	TCTGCCATGA	CCTTGGACTC	360
AACCCAGATA	CCTATTCTGT	TTCTATCCCA	CTCGGTTCTA	CTATCAATAT	GGCTGGAGTA	420
GCGATTACCA	TTAACCTTTT	GACCCTTGCT	GCAGTTAACA	CTCTTGGAAT	TCCTGTTGAC	480
TTTGCCACAG	CCTTTGTCCT	CAGTGTGGTA	GCAGCTATCT	CAGCCTGTGG	TGCTTCAGGT	540
ATTGCCGGAG	GTTCCCTCCT	TCTTATCCCA	GTTGCTTGTA	GCCTTTTCGG	TATTTCTAAC	600
GATATTGCCA	TACAAGTTGT	TGGGGTTGGT	TTTGTGATTG	GTGTCATCTA	A	651

(2) INFORMATION FOR SEQ ID NO:1838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 735 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1838:

ACGATAACAG	GAGGTGATTC	AGTGTTAAAA	ACAGAACGTA	AACAACATAAT	TTTAGAGGAG	60
TTAAATCAGC	ATCATGTAGT	TTCTCTAGAA	AAATTAGTTA	GTTTGCTAGA	AACGTCAGAA	120
TCAACGGTTC	GAAGAGACTT	GGATGAGTTG	GAAGCGGAAA	ACAAGCTTCG	TCGTGTGCAT	180
GGTGGAGCAG	AACTCCCCCA	CTCCTTACAG	GAAGAAGAAA	CCATTCAAGA	AAAATCTGTC	240
AAAAACCTTC	AAGAAAAGAA	ATTGCTGGCT	CAGAAAGCAG	CCTCTCTCAT	TAAAGAAAAA	300
GATGTCATCT	TTATCGATGC	TGGAACAACA	ACTGCTTTTT	TGATTCATGA	ATTGGTCAAT	360
AAGAATGTTA	CAGTTGTGAC	CAACTCCATT	CACCATGCCG	CTCAGTTGGT	TGAAAAGCAG	420
ATTCCAACCTG	TCATGGTTGG	AGGAAACGTC	AAGACGGCGA	CAGATGCTAG	TATCGGGGGC	480
GTTGCTCTTA	ACCAGATTAA	CCAATTGCAC	TTTGACCGTG	CCTTTATCGG	AATGAATGGT	540
GTTGACGATG	GCTATTATAC	GACTCCTGAT	ATGGAAGAGG	GAGCTGTGAA	AAAAGCTATT	600
TTGGAGAATG	CCAAGCAGAC	CTACGTCTTG	GTGGATTTCG	CAAAAATTGG	ACAAACTTGC	660
TTTGCCAAGG	TAGCCCCACT	CAAACGCGCT	ATCGTTATCA	CTAGTCAAGN	GCATGAGCTC	720
CTTGCAGGTT	ATTAA					735

(2) INFORMATION FOR SEQ ID NO:1839:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...288
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1839:

AAAAAACAG GCATCACAGT CATTGAACCA GATATGCTGA ATGAGAAAGA AAGCAAGCAA	60
CTACACTACC CAGGTCTGAA AGCAGGTTTG TTCTTTGGTC TATGGATGTT TTTTATAACT	120
CCTCTTCTCA GTATACTCAT AGATGAAGGT CAGGACTATT TTCATTCTCT TCTCACTATA	180
AGAAATGGTG TATCAAGTAT TCTCGGTTCT ATTTTCTTCG GAGCGAGCAT ACAGTTTCTC	240
ATCTCCCGTC GCATTGCAAA AACTAAGAAA AATCAAGATG AGGATTAG	288

(2) INFORMATION FOR SEQ ID NO:1840:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...213
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1840:

ACACCTGCAG GTGTGAGGGC GACACGGTTT TCGTTATTTT TAATTTCTTT TGGGATTCCG	60
ATTAACATTG AGATAACCTA CCTTTCAATT GACGGTCTTG TTTTGGTTGT CACATTCCAG	120
TTCATAAATC AAAAATGTGA CGGTTTCATT GTATATGAAA CCGCTTCAAA AATCAAGAAA	180
AACTTGTCAT CCAAATTTT TATGCTAGAC TAG	213

(2) INFORMATION FOR SEQ ID NO:1841:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...273
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1841:

CCATTGGCAG	GCATATTACT	TTGTACCGAA	CGAACAAC	TA CACCAGATGT	AACATTACTT	60
GGAATATTGA	GTCTTCTGAT	GTCGCTTGTA	CTCACATTAG	ATAAATTAAC	CATCTGGATT	120
CCCAAAGCTG	GACGCGTCAC	TTTTCCGTTT	TTTTCTAACT	GTTCAATAAT	ATTGATAGCA	180
TCATTTGCAG	GAATTGCGAA	ACCAAGACCT	TCTACAGATG	TTCTCTCCATT	TGTAGCAATT	240
TTACTTGAGG	TAATTCCGAT	AACCTGCCCT	TGA			273

(2) INFORMATION FOR SEQ ID NO:1842:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 945 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...945
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1842:

TTCTGGGCAG	GTCTTGCTAT	GACTATCACT	ATGGGAGGCT	TGGCCTTTGT	CCCAAATATC	60
TATTGGTTAA	TCTTCTTCG	TTTACTAAAC	GGTGTATTTG	CAGGTTTTGT	TCCTAATGCA	120
ACGGCACTGA	TAGCCAGTCA	GGTTCCAAAG	GAGAAATCAG	GCTCTGCCTT	AGGTACTTTG	180
TCTACAGGCG	TAGTTGCAGG	TACTCTAACT	GGTCCCTTTA	TTGGTGGCTT	TATCGCAGAA	240
TTATTTGGCA	TTCGTACAGT	TTTCTTACTG	GTTGGTAGTT	TTCTATTTTT	AGCTGCTATT	300
TTGACTATTT	GCTTTATCAA	GGAAGATTTT	CAACCAGTAG	CCAAGGAAAA	GGCTATTCCA	360
ACAAAGGAAT	TATTTACCTC	GGTTAAATAT	CCCTATCTTT	TGCTCAATCT	CTTTTTAACC	420
AGTTTTGTCA	TCCAATTTTC	AGCTCAATCG	ATCGGCCCTA	TTTTGGCTCT	TTATGTACGC	480
GACTTAGGGC	AGACAGAGAA	TCTTCTTTTT	GTCTCTGGTT	TGATTGTGTC	CAGTATGGGC	540
TTTCCAGTA	TGATGAGTGC	AGGAGTCATG	GGCAAGCTAG	GTGACAAGGT	GGGCAATCAT	600

CGTCTCTTGG	TTGTCGCCCCA	GTTTTATTCA	GTCATCATCT	ATCTCCTCTG	TGCCAATGCC	660
TCTAGCCCCC	TTCAACTAGG	ACTCTATCGT	TTCTCTTTG	GCTTGGAAC	CGGTGCCTTG	720
ATTCCCGGGG	TTAATGCCCT	ACTCAGCAAA	ATGACTCCCA	AAGCCGGCAT	TTCGAGGGTC	780
TTTGCCCTCA	ATCAGGTATT	CTTTTATCTG	GGAGGTGTTG	TTGGTCCCAT	GGCAGGTTCT	840
GCAGTAGCAG	GTCAATTTGG	CTACCATGCT	GTCTTTTATG	CGACAAGCCT	TTGTGTTGCC	900
TTTAGTTGTC	TCTTTAACCT	GATTCAATTA	TCGAACACTT	ATTAA		945

(2) INFORMATION FOR SEQ ID NO:1843:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...282
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1843:

TCATGGGCAG	GAAGTTGGAA	CATCAGTAAT	TCTGTGGCCC	ATGTTATCTT	CCGTGGAGCA	60
TTCAACGAGT	ATGCCAATTA	TATCCCGAAT	TACTACTATG	AANACTTACT	CCAAGCCATT	120
GAACGCTATG	AAACCATGGG	ACTTGAAATC	CTTTTATCCT	CATTAACACG	AACCATGATG	180
ACTCAGGCAA	GCAATATATG	GAGCAGATTC	GAATTGTTTCG	CCAGACCTTG	CAGAATCGTG	240
ATTGGAATGA	GAAAATTAAA	AAGACGGTTC	GAGGATTTAT	GA		282

(2) INFORMATION FOR SEQ ID NO:1844:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1844:

GGGGTTNCAG	GGAAGACAAA	GGATGGTTTC	CCTCTCCGGG	AAGTAAAGGG	AATTTCTCTCC	60
CTAATAATCC	GAAAAGGGAT	GGAGGGGACG	GAATTTATAT	GGAGATTTGG	GATTGTTTTA	120
TCAAGGGGCA	TGGTTCAAAA	CAATCGAGTC	TTTTGGATGG	ACAAACGCCA	TAATTCAGCT	180
TTTTCAGGGA	GGGACCTAGA	AATTGGTTTG	AGAGAGCGTA	GAGTGTTTAC	CCTTATCTTA	240
ACAGGTGTCT	GGACGGATAT	ATGTGTCCTA	CATACAGCTA	AAGAGGCCCTA	TAATGTAGGA	300
GATGACATAG	AGATTGTTAA	ACCAGCTGTA	GCTTCCATCT	GGCCTGAAAA	TCATCAATTT	360
GCCCTAGGTC	ATTTCAAAAA	TACACTCGGA	GGTAAGTCAG	TAGAAGAAAA	TTTAAATGAA	420
CTTCTGAGT	AA					432

(2) INFORMATION FOR SEQ ID NO:1845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1845:

CCTAATCAAG	GAGGATTTAT	GGCTACCTTA	AAAGACATTG	CACAGCTAGC	CTCTGTCTCT	60
ATCGCGACCG	TATCCCGCGT	CCTCAACCGC	GACCAGAGCC	TATCTGTTAC	AGAAGAAACC	120
AGACACCGTA	TTTTAACCGT	TGCTGAAGAG	CTGGGCTACA	CCAAGCACCT	CAAGACAGGC	180
GAGTCCCATA	AACCCAAGCA	AAAGATTGCC	ATTATTCAAT	GGGTCAGCGA	ACAAGGGGAG	240
CTAGACGACC	TCTACTACTA	CCAGATTTCG	CTAGGAATAG	AAAAAAGAGC	CCAAGAGTTG	300
GACTACGATA	TCTTGCGCTA	TTTTAATGAC	CATCCTTTTA	CCTTAAGCGA	GGAAGTGATT	360
GGGATTCTCT	GCATCGGAAA	ATTTAGCCGA	GCTCAGATTT	CTGCCTTTGA	AGAATACCAA	420
AAACCCCTGG	TCTTTCTAGA	CAGTGATACA	CTTTCCCTCG	GACATACCTG	CATTATTACG	480
GACTTTTACA	CTGCCATGAA	ACAGGTTGTC	GATTATTTCC	TCAGTCAAGG	GATGGACCGT	540
ATCGGGATTG	TAACAGGCCCT	TGAAGAAACA	ACTGACCAAG	AAGAAATCAT	TGAGGATAAG	600
CGGCTGGAAA	ATTTTCAGAAA	CTACAGTCAA	GCAAAAAGGAA	TCTATCATGA	TGAACTGGTC	660
TTTCAAGGAA	GATTTACTGC	CCAGTCTGGC	TATGACTTAA	TGAAGGAGGC	CATTTCAGAGC	720
TTGGGAGACC	AACTTCCGCC	AGCATTTTTT	GCAGCCAGCG	ATAGTTTAGC	TATCGGTGCC	780
CTCCGTGCCC	TCCAAGAAGC	TGGAATCAGC	CTGCCAGATC	GCGTCAGCCT	CATTTCTCTT	840
AACGACACTA	GTCTGACCAA	ACAGGTCCTAT	CCTCCCCTCT	CTAGTATTAC	AGTTTATACT	900
GAAGAAATGG	GCCGAGCAGG	TATGGATATT	CTTAACAAGG	AAGTCCTCCA	CGGTCGGAAA	960
ATCCCTAGCC	TGACCATGCT	GGGAACCAGA	CTGACATTAA	GAGAAAGTAC	CCTAAATCAA	1020
GAATAG						1026

(2) INFORMATION FOR SEQ ID NO:1846:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 897 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1846:

AAATTGCAAG	GAAGAGGTTG	GAGGCAGAAA	ATGAAACAAA	CTAGAAATTT	TGATGAGTGG	60
TTGTCAACGA	TGACCGACAC	AGTAGCTGAC	TGGACTTATT	ATACAGATTT	TCCTAAGGTT	120
TATAAAAATG	TATCTAGTAT	AAAAGTTGCT	CTAAATATTA	TGAATAGTCT	TATTGGTAGT	180
AAAAATATAC	AAGAGGATTT	TTTAGACTTA	TATCAAAATT	ATCCAGAAAT	TTTGAAAAGTT	240
GTGCTCTAC	TTATTGCTAA	ACGTTTGAGA	GATACGATTA	TTGTTAAGGA	TCCGATAAAA	300
GATTTCTATT	TTGATTTTAG	TAAACGAAAC	TATAGTATTG	AAGAATATAC	TATGTTTTTTG	360
GAAAAATCAG	GTATATTTGA	TTTATTGCAA	AATCATTTAG	TATCAAATTT	AGTTGACTAC	420
GTTACAGGTG	TTGAGGTTGG	TATGGATACT	AATGGGCGCA	AAAATCGGAC	TGGAGATGCG	480
ATGGAAAATA	TTGTTCAAAG	TTATCTTGAA	GCTGAAGGGT	ATATTTTAGG	AGAGAATTTA	540
TTTAAAGAGA	TTGAACAAAA	TGAAATAGAG	GAAATTTTTT	CTGTCGATTT	ATCTGCTATT	600
ACGAATGATG	GGAATACTGT	GAAACGTTTT	GATTTTGTCA	TAAAAAATGA	ACAAGTGCTT	660
TATCTGATTG	AGGTAAATTT	TTATTCAGGA	AGTGGTTCAA	AATTAAATGA	GACGGCTAGA	720
TCTTACAAAA	TGATTGCTGA	AGAAACTAAA	GCTATTCCCTA	ATGTTGAGTT	TATGTGGATT	780
ACTGATGGAC	AAGGTTGGTA	TAAGGCTAAG	AATAATTTAC	GAGAAACATT	TGATATTTTA	840
CCATTCTTAT	ATAATATTAA	CGATTTGGAA	CATAATATTT	TAAAGAATTT	GAAATAG	897

(2) INFORMATION FOR SEQ ID NO:1847:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 942 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1847:

AAAGTTAAAG	GAGTAGCCAT	GTCAGAAAAT	CAACAAGCAT	TGAACCATGT	GGTGTCCATG	60
GAAGACCTCA	CTGTCGATCA	AGTAATGAAA	TTGATCAAGC	GAGGAATTGA	GTTTAAAAAT	120
GGAGCCCAGC	TTCCCTATGA	AGACCATCCG	ATTGTTTCCA	ATCTCTTCTT	TGAGGATTCT	180
ACACGGACAC	ATAAGTCCTT	TGAAGTCGCA	GAGATTAAAC	TTGGATTGGA	ACGACTTGAC	240
TTTGATGTGA	AGACTAGTTC	GGTTAATAAG	GGTGAGACAC	TTTATGACAC	CATTTTGA	300
CTGTCTGCTT	TAGGAGTGGA	TGTCTGTGTG	ATTCGCCATC	CAGAGGTCGA	CTATTATAGA	360
GAATTGATTG	ATAGTCCAAC	GATTACGACT	TCCATCATCA	ATGGTGGAGA	TGGTTCGGGT	420
CAACACCCTA	GCCAGAGCTT	GCTTGATTTG	ATGACCATTT	ATGAGGAATT	TGGCCACTTT	480
GAGGGTCTTA	AAGTTGCTAT	TGCAGGTGAC	TTGGACCACT	CACGCGTTGC	CAAATCCAAT	540
ATGCAGATTT	TGAAACGCTT	GGGAGCTGAA	CTCTTTTTTCG	CTGGACCTGA	GGAATGGAGA	600
AGTCAAGAGT	TTGCAGACTA	TGGAAAGTTT	GTAACCATTG	ATGAAATCAT	TGATCAGGTT	660
GATGTCATGA	TGTTTCTCCG	TGTGCAACAC	GAACGCCATG	ATAGTGGAGC	TGTATTTTCA	720
AAAGAAGACT	ACCATGCCCA	ACATGGCTTG	ACTCAAGAAC	GTTACGATCG	TTTGAAAGAA	780
ACAGCAATCC	TCATGCACCC	AGCTCCAATC	AATCGTGATG	TAGAAATAGC	AGACCACTTG	840
GTTGAAGCAC	CAAAATCACG	GATTGTCCAA	CAAATGACCA	ATGGTGTCTT	TGTTCGAATG	900
GCAATCTTAG	AATCCGTACT	AGCGAGTAGA	AACGCCAACT	AA		942

(2) INFORMATION FOR SEQ ID NO:1848:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1848:

ATACCTAAAG	GAGAAATCAA	AATGGCAGTA	CCTGCACGTC	GCACTTCAAA	AGCGAAGAAA	60
AACAAACGTC	GTACACACTA	CAAAGTAACA	GCTCCATCTG	TAAACTTTGA	CGAAACTACT	120
GGAGATTACT	CACGTTCTCA	CCGTGTATCA	CTTAAAGGAT	ACTACAAAGG	ACGTAAAATC	180
ACTAAAGCTG	CATCAGCTGA	ATAA				204

(2) INFORMATION FOR SEQ ID NO:1849:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: *misc_feature*

(B) LOCATION 1...1281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1849:

ATTTATAAAG	GAGGCTTTCC	AATGAAATGG	TATAAAAAAA	TCGGACTTCT	TGCAACTACA	60
GGTTTAGCTT	TGGTTGGGCT	CGGCGCTTGC	TCCAACATATG	GTAAATCTGC	GGATGGCACA	120
GTGACCATCG	AGTATTTCAA	CCAGAAAAAA	GAAATGACCA	AAACCTTGGA	AGAAAATCACT	180
CGTGATTTTG	AGAAGGAAAA	CCCTAAGATC	AAGGTCAAAG	TCGTCAATGT	ACCAAATGCT	240
GGTGAAGTAT	TGAAGACACG	CGTTCTCGCA	GGAGATGTGC	CTGATGTGGT	CAATATTTAC	300
CCACAGTCCA	TGAACTGCA	AGAATGGGCA	AAAGCAGGTG	TCTTTGAAGA	TTTGAGCAAC	360
AAAGACTACC	TGAAACGCGT	GAAAAATGGC	TACGCTGAAA	AATATGCTGT	AAACGAAAAA	420
GTTTACAACG	TTCTTTTAC	AGCTAATGCT	TATGGAAATTT	ACTACAACAA	AGATAAAATTC	480
GAAGAACTGG	GCTTGAAGGT	TCCTGAAACC	TGGGATGAAT	TTGAACAGTT	AGTCAAAGAT	540
ATCGTTGCTA	AAGGACAAAC	ACCATTGGA	ATTGCAGGTG	CAGATGCTTG	GACACTCAAT	600
GTTTACAATC	AATTAGCCTT	TGCGACAGCA	ACAGGTGGAG	GAAAAGAAGC	AAATCAATAC	660
CTTCGTATT	CTCAACCAAA	TGCCATTAAA	TTGTCGGATC	CGATTATGAA	AGATGATATC	720
AAGGTCATGG	ACATCCTTCG	CATCAATGGC	TCTAAGCAAA	AGAACTGGGA	AGGTGCTGGC	780
TATACCGATG	TTATCGGAGC	CTTCGCACGT	GGGGATGTCC	TCATGACACC	AAATGGGTCT	840
TGGGCGATCA	CAGCGATTAA	TGAACAAAAA	CCGAACTTTA	AGATTGGGAC	CTTCATGATT	900
CCAGGAAAAAG	AAAAAGGACA	AAGCTTAACC	GTTGGTGCGG	GAGACTTGGC	ATGGTCTATC	960
TCAGCCACCA	CCAAACATCC	AAAAGAAGCC	AATGCCTTTG	TGGAATATAT	GACCCGTCCA	1020
GAAGTCATGC	AAAAATACTA	CGATGTGGAC	GGATCTCCAA	CAGCGATCGA	AGGGGTCAAA	1080
CAAGCAGGAG	AAGATTCACC	GCTTGCTGGT	ATGACCGAAT	ATGCCTTTAC	GGATCGTCAC	1140
TTGGTCTGGT	TGCAACAATA	CTGGACCAGT	GAAGCAGACT	TCCATACCTT	GACCATGAAC	1200
TATGTCTTGA	CCGGTGATAA	ACAAGGCATG	GTCAATGATT	TGAATGCCTT	CTTTAACCCG	1260
ATGAAAGCCG	ATGTGGATTA	G				1281

(2) INFORMATION FOR SEQ ID NO:1850:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 666 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: *misc_feature*

(B) LOCATION 1...666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1850:

CTTTGTAAAG	GCAGACTTTG	TAGATATTTT	GGAGGACATC	AAGTAATGAA	ACTCTACTTT	60
GTCCGCCACG	GTCGTACCCT	CTGGAACCAA	GAAGGTCGTT	TTCAAGGTGC	TAGCGGTGAT	120
TCTCCTCTTC	TTCCTGAATC	CATTGAAACC	CTAAAACGAC	TTGGCCAGTA	TCTCAAGGAA	180
ATTCTTTT	ATCAGATTTA	TTCAAGTGAT	TTACCTCGAG	CGGTCAAATC	TGCTGAGATT	240
ATCCAAAGTC	AACTCTATAC	CCCCTGTTCT	TTAGAAATCG	TTCCTAATCT	CCGTGAATGG	300
CAACTTGGGA	AGTTAGAAGG	TTTGAAAATT	GCAACCTTGG	AAGCTATTTA	CCCGCAACAA	360
ATCCAGGCTT	TTCGTTCAAA	TCTTGCTCAA	TTTGACACTC	GAATGTTCCG	AGCCGAATCC	420
CTCTATAGTA	CAACTCAGCG	GACCATCCAA	TTTATCAAAT	CATTAAAAGA	TAGTCCAGCT	480
GAGCGTATTC	TAATTGTCGG	ACACGGCGCC	AATCTTACTG	CCAGTCTTCG	TACTCTCCTA	540
GGCTATAAAG	AACCACTTCT	TCGTAAAGAT	GGCGGTCTAG	CAAATGCCAG	CCTGACCATT	600
ATAGAAACCC	ATGATTTTGA	AACATTCACT	CTCAATACTT	GGAATGATAC	TTCTTATCAA	660
TCATAA						666

(2) INFORMATION FOR SEQ ID NO:1851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1851:

TACTTCAAAG	GAGGAAATCA	GATGGTAGTA	AAAACAAGAA	AACAAGGAAA	TTCAATCACC	60
ATTACGATTC	CAAGTGAATT	TAATATTCCA	AGTGGTGTTA	AATACGAAGC	GAAATTGTTA	120
CAAAGTGGTG	AGATTATCTT	TACTCCTGAA	GAATTGGGGC	AGCAGGTTTC	TTATGTATCT	180
GATGATGCCT	TTGACTTAAA	TTTAGATAAA	ATATTTGACG	AATACGACGA	TGTTTTCAAA	240
GCTTTGGTGG	AAAAATGA					258

(2) INFORMATION FOR SEQ ID NO:1852:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1852:

GACCAAAAAG	GTCATATATA	TAAAGGAGTC	ACAAAAATCA	TGAACAAACG	TGTAAAGATC	60
GTTGCAACTT	TGGGTCCTGC	GGTAGAAATC	CGTGGTGGTA	AAAAATTCGG	TGAGGATGGA	120
TACTGGGGTG	AAAAACTTGA	TGTTGAAGCT	TCAGCTAAAA	ACATTGCTAA	ATTGATTGAA	180
GCTGGTGCTA	ACACATTCCG	ATTCAACTTC	TCACACGGCG	ACCACCAAGA	ACAAGGTGAG	240
CGTATGGCAA	CTGTTAAACT	TGCGGAAAAA	ATTGCAGGTA	AAAAAGTTGG	TTTCCTTCCTT	300
GATACAAAAG	GACCTGAAAT	CCGTACAGAA	TTGTTCGAAG	GTGAAGCTAA	AGAATATTCA	360
TATAAACTG	GTGAAAAAAT	TCGTGTTGCA	ACTAAACAAG	GAATCAAATC	AACTCGTGAA	420
GTGATTGCGT	TGAACGTTGC	TGGTGCTCTT	GATATCTATG	ATGATGTTGA	AGTTGGTCGT	480
CAAGTTTTTG	TTGACGATGG	TAAACTTGGT	CTTCGTGTGG	TTGCTAAAGA	TGATGCAACT	540
CGTGAATTTG	AAGTTGAAGT	TGAAAACGAT	GGTATCATCG	CTAAACAAAA	AGGTGTGAAC	600
ATCCCTAACA	CTAAAATTCC	TTTCCCAGCT	CTTGCTGAAC	GCGATAACGA	CGATATCCGT	660
TTCCGTCTTG	AACAAGGTAT	CAACTTCATC	GCAATTTTCAT	TCGTACGTAC	TGCAAAAGAA	720
TGTGAACGAA	GTTCGTGCAA	TCTGTGA				747

(2) INFORMATION FOR SEQ ID NO:1853:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1362 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1853:

AAAAGAAAAG	GAAAAATAAT	GACAAAACGT	GTAACGATTA	TTGACGTAAA	AGACTATGTT	60
GGTCAGGAAG	TGACGATTGG	CGCTTGGGTT	GCCAACAAAT	CAGGAAAAGG	AAAAATCGCT	120
TTCTTACAAT	TGCGTGATGG	AACAGCCTTC	TTTCAAGGTG	TGGCTTTTAA	ACCAAACCTTT	180
GTCGAAAAAT	TTGGTGAAGA	AGTGGGACTT	GAGAAGTTTG	ATGTTATCAA	ACGCTTGAGC	240
CAAGAAACGT	CTGTTTATGT	GACAGGTATT	GTCAAAGAGG	ACGAACGTTT	TAAATTTGGC	300
TATGAGTTGG	ACATCACAGA	CATCGAAGTG	ATCGGTGAAT	CTCAAGACTA	CCCAATCACA	360
CCAAAAGAAC	ACGGAACAGA	CTTTTGTGATG	GATAACCGTC	ACTTGTGGCT	ACGCTCTCGT	420
AAGCAAGTAG	CTGTGTTGCA	AATCCGTAAC	GCTATTATCT	ATGCAACTTA	TGAGTTCTTT	480
GACAAGAACG	GTTTATATGAA	GTTTGACAGC	CCAATTCTTT	CAGGAAATGC	GGCAGAAGAT	540

TCTACAGAAC	TCTTTGAAAC	TGACTACTTC	GGAACGCCAG	CCTACTTGAG	CCAATCAGGT	600
CAGCTTTACC	TAGAAGCAGG	GGCTATGGCT	CTTGGTCGTG	TCTTTGACTT	TGGTCCAGTT	660
TTCCGTGCTG	AAAAATCAAA	AACACGCCGT	CACCTTGACTG	AGTTCCTGGAT	GATGGATGCT	720
GAGTACTCAT	ACTTGACACA	TGATGAGTCG	CTTGACTTGC	AAGAAGCTTA	TGTGAAAGCT	780
CTTCTACAAG	GTGTTCTTGA	CCGCGCGCCT	CAAGCCTTGG	AAACCTTGGA	ACGTGATACA	840
GAACTCTTGA	AACGCTACAT	TGCAGAGCCA	TTCAAACGTA	TCACTTACGA	TCAAGCCATT	900
GACCTCTTGC	AAGAGCATGA	AAATGATGAA	GATGCTGACT	ACGAGCATCT	TGAGCATGGT	960
GATGACTTTG	GGTCACCACA	CGAAACTTGG	ATTTCAAACC	ACTTTGGTGT	GCCAACATTT	1020
GTCATGAACT	ATCCAGCAGC	CATCAAGGCC	TTCTACATGA	AACCAGTTCC	TGGAAATCCA	1080
GAGCGCGTGC	TTTGTGCAGA	CTTGCTTGCT	CCAGAAGGCT	ATGGAGAAAT	TATCGGTGGG	1140
TCTATGCGTG	AGGAAGATTA	CGATGCCCTT	GTCGCTAAGA	TGGATGAACT	TGGCATGGAT	1200
CGTACAGAAAT	ATGAATTCTA	CCTTGACCTT	CGTAAATACG	GTACAGTTCC	ACACGGAGGA	1260
TTTGGTATCG	GTATCGAACG	TATGGTAACC	TTCGCAGCAG	GAACAAAACA	TATCCGTGAA	1320
GCTATTCCAT	TCCCACGTAT	GTTGCACCGT	ATCAAACCAT	AA		1362

(2) INFORMATION FOR SEQ ID NO:1854:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...261
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1854:

AACCAGAAAG	GAGGTAATAT	TATGACTGAA	ATTCACGCAT	GTCTTTGCGG	AAATTGGGTG	60
AACCTATCAG	CCGACGACGA	TTGTGTAATG	GGACCAAATA	TGGCTAGTCC	TTACATTTGG	120
TGGGAAGAAA	ATGCAGAACT	CTACTCACCA	ATTTCTAAAC	CTGAAGCAAA	CTCGATGTAC	180
CATCAGGATT	ATATCTACAT	TCACTATCGT	GGCGCTGACT	ATCGTATCCA	TCCAATGTTC	240
ATTCAAATCG	TTTCTAGATA	A				261

(2) INFORMATION FOR SEQ ID NO:1855:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1855:

GTTAAGAAAG	GAAAAAACGA	AATGCATATT	GAACATCTTA	GCCACTGGAG	TGGTCATCTT	60
AACCGTGAAA	TGTACCTTAA	CCGTTATGGA	CATGGTGGA	TTCCAGTTGT	GGTCTTTGCT	120
TCATCAGGTG	GTAGTCACAA	CGAATACTAT	GATTTTGGCA	TGATTGATGC	CTGTGCTTCC	180
TTTATCGAGG	AAGGCCGTGT	CCAGTTCCTT	ACCCATATCTA	GTGTGGATAG	TGAGAGCTGG	240
TTGGCTACTT	GGAAAAATGC	TCATGACCAA	GCGGAAATGC	ACCGTGCCTA	CGAACGTTAT	300
GTGATTGAGG	AGGCCATTCT	TTTATCAAGC	ACAAGACAGG	TTGGTTTGAT	GGCATGA	357

(2) INFORMATION FOR SEQ ID NO:1856:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 624 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1856:

AAAGAGAAAG	GAAATCTCAT	GTTAAAACCTT	ATTGCTATTG	TTGGAACAAA	TTCAAAACGT	60
TCTACAAACC	GTCAATTGCT	TCAATACATG	CAAAAACACT	TTGCTGACAA	AGCTGAAATT	120
GAACTTGTTG	AAATCAAGGC	CATTCCGTGC	TTCAACAAAC	CAGCTGACAA	GCAAGTACCT	180
GCTGAAATAT	TGGAAATTGC	TGCTAAAATC	GAAGAGGCAG	ATGGCGTTAT	TATCGGTACT	240
CCTGAGTATG	ATCACTCTAT	TCCAGCTGTT	TTGATGAGCG	CTCTTGCTTG	GTTGTCTTAT	300
GGTATTTACC	CACTTTTGAA	CAAACCAATC	ATGATTACAG	GTGCTTCTTA	CGGTACGCTT	360
GGTTCATCTC	GTGCCCAATT	GCAACTTCGT	CAAATCTTGA	ATGCTCCTGA	AATCAAGGCA	420
AATGTTCTTC	CAGATGAATT	CTTGCTCTCA	CACTCTCTTC	AAGCATTTAA	CCCAAGTGGC	480
GACTTGTTG	ACCTTGATGT	TATCAAGAAA	TTGGATGCCA	TCTTTGATGA	CTTCCGTATC	540
TTCGTGAAGA	TACTGAGAA	ATTGCGCAAT	GCGCAAGAAT	TGCTTCGCAA	AGATGCTGAA	600
GACTTTGACT	GGGAAAATTT	GTAA				624

(2) INFORMATION FOR SEQ ID NO:1857:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1857:

TGTTTTGAAG	GGTGGTATAC	TAATCTCAAA	GATAACAATT	ATATCCAAAG	GAGGCAACAT	60
ATGCCAAACG	TCAAAGAAAT	TACAAGAGAG	TCATGGATTT	TAGCCACTTT	CCCAGAGTGG	120
GGAACATGGT	TGAACGAAGA	AATCGAAGAA	GAAGTCGTAC	CTGAAGGCAA	CTTTGCCATG	180
TGGTGGCTAG	GCAACTGTGG	TACTTGGATT	AAGACACCAG	CTGGTGCTAA	CGTTGTCATG	240
GACCTTTGGT	CAAACCGTGG	AAAATCAACC	AAAAAAGTGA	AAGATATGGT	TCGTGGGCAC	300
CAAATGGCAA	ATATGGCAGG	TGTTTCGTAAG	TTGCAACCAA	ACTTGCGTGT	TCAGCCAATG	360
GTTATCGATC	CATTTGCTAT	CAACGAACTA	GACTATTACT	TAGTTTCACA	CTTCCACAGT	420
GATCATATCG	ACCCATACAC	NGCTGCNGCA	TTTTTCACATT	TCCTAAGTTA	G	471

(2) INFORMATION FOR SEQ ID NO:1858:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1858:

ATTGTAGAAG	GTAAGGAATT	ATGCTATAAT	GGTACTATTC	TAAGGAAAGA	GGGTGTTAGA	60
ATGGGATTTA	CTGAAGAAAC	AGTACGTTTT	AAATTGACG	ATTCCAATAA	AAAAGAAATT	120
AGCGAAACTT	TGACAGATGT	TTATGCTTCG	TTGAACGATA	AGGGTTACAA	CCCAATTAAC	180
CAAATCGTAG	GTTACGTATT	GAGTGGAGAC	CCTGCCTACG	TTCCTCGTTA	TAATAATGCA	240
CGAAATCAAA	TCCGTAAGTA	TGAGCGTGAT	GAAATCGTTG	AGGAATTGGT	TCGCTACTAC	300
CTCAAAGGAC	AAGGAGTCGA	TCTATAA				327

(2) INFORMATION FOR SEQ ID NO:1859:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 516 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...516
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1859:

CCGCCAGAAG	GCAGTCGCAG	CGGTAAATCC	TTAATGATGA	AGAAGACTTA	TAATCATATT	60
TTGGTCTGGG	GAGTCATTTT	CTATAGCATT	TGCATTGTCT	ATTTTGTCTT	TACTCCTCAA	120
GAACAATCTA	CCGTGGGAGT	GGGAACTCCA	GATATTCAGC	ATCTTGGACG	CCTGGTTTTT	180
CTTTTGACTC	CTTTCAATTC	TCTCTGGAAA	CTGGGCGAAG	TGAGTGACAT	TGGACAATTA	240
TGTTGGATTT	TTTACAAAA	TATCCTCAAT	GTCTTCTTGT	TTTTTCCTCT	GATTTTCCAA	300
CTCCTTTATC	TATTTCCAAA	TTTGC GGAAA	ACAAAAAAGG	TCCTTCTTTT	TAGTTTCTTT	360
GTGAGTCTTG	GAATCGAGTG	TACGCAATTA	ATCTTGGACT	TTTTCTTTGA	TTTCAATCGC	420
GTCTTTGAGA	TTGATGATTT	GTGGACCAAC	ACTTTGGGTG	GCTATCTGGC	TTGGCTCCTT	480
TATAAACGAT	TACATAAAAA	CAAGATAAGG	AATTAA			516

(2) INFORMATION FOR SEQ ID NO:1860:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 486 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...486
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1860:

AATCAAGAAG	GAATCGAAAA	CTACGCTTAC	ACCACCAACA	GCAAGGGCGA	AAAGATTTAC	60
GCTTTTGAAG	TAGATGGCCT	AGGAAATGCC	AGCATCATGG	ATGATCCGAA	TGTGCCAAGT	120
CTACTAGCTG	CGCCCTATCT	GGGCTACTGT	TCGATCGATG	ATGAAGTGTA	TCAAGCCACT	180
CGCCGTACCA	TTCTGAGCTC	TGAAAATTCA	TACTTCTACC	AAGGAGAATA	CGCTAGCGGT	240
CTTGGAAGTT	CTCATACCTT	CTATCGCTAT	ATCTGGCCAA	TCGCCCTTTC	TATCCAAGGA	300
TTGACAACAA	GAGATAAGGC	AGAGAAAAAA	TTCTTGCTGG	ATCAGCTGGT	TGCCTGCGAT	360
GGTGGTACAG	GTGTCATGCA	CGAAAGCTTC	CACGTAGATG	ATCCGACCCT	CTACTCTCGT	420
GAATGGTTCT	CCTGGGCTAA	CATGATGTTT	TGTGAGTTGG	TCTTGGATTA	CTTGGATATT	480
CGCTAA						486

(2) INFORMATION FOR SEQ ID NO:1861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1083 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1083

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1861:

AAGAAAGAAG	GAAGTGAAT	GACAACATTA	TTTTCAAAAA	TTAAAGAAGT	AACAGAACTT	60
GCTGCAATCT	CAGGTCATGA	AGCGCCTGTC	CGTGCTTATC	TTCGTGAAAA	GTTGACACCG	120
CATGTGGATG	AAGTGGTGAC	AGATGGCTTG	GGTGGTATTT	TTGGTATCAA	ACATTCAGAA	180
GCTGTGGATG	CACCGCGCGT	CTTGGTCGCT	TCTCATATGG	ACGAAGTTGG	TTTTATGGTC	240
AGCGAAATCA	AGCCAGATGG	TACCTTCCGT	GTCTAGAAAA	TCGGTGGCTG	GAACCCCATG	300
GTGGTTAGCA	GCCAACGTTT	CAAACTCTTG	ACTCGTGATG	GTCATGAAAT	TCCTGTGATT	360
TCAGGTTCTG	TTCTCCGCA	TTTGACTCGT	GGAAAGGGGG	GACCAACCAT	GCCAGCCATT	420
GCCGATATCG	TTTTTGATGG	TGGTTTTGCG	GACAAGGCTG	AGGCAGAAAG	TTTTGGCATC	480
CGTCCTGGTG	ATACCATTTG	ACCAGATAGT	TCTGCAATTT	TGACAGCCAA	TGAAAAAAAT	540
ATCATCTCAA	AAGCTTGGGA	TAACCGCTAC	GGTGTCTTCA	TGGTAAGCGA	GCTAGCTGAA	600
GCTTTATCGG	GTTCAAAACT	CGGCAATGAA	CTCTATCTGG	GTTCTAACTT	CCAAGAAGAA	660
GTTGGTCTGC	GTGGCGCTCA	TACCTCTACA	ACCAAGTTTG	ACCCAGAAGT	CTTCCTCGCA	720
GTTGCTTGCT	CACCAGCAGG	TGATGTCTAC	GGTGGTCAAG	GCAAGATTGG	AGATGGAACC	780
TTGATTTCGTT	TCTATGATCC	AGGTCACCTG	CTTCTCCCAG	GGATGAAGGA	TTTCCTTTTG	840
ACAACGGCTG	AAGAAGCTGG	TATCAAGTAC	CAATACTACT	GTGGTAAAGG	CGGAACAGAT	900
GCAGGTGCAG	CTCATCTGAA	AAATGGTGGT	GTCCCATCAA	CAACTATCGG	TGCTCTGCCT	960
CGTTATATCC	ATTCTCACCA	AACCCTCTAT	GCAATGGATG	ACTTCCTAGA	AGCGCAAGCT	1020
TTCTTACAAG	CCTTGGTGAA	GAAATTGGAT	CGTTCAACGG	TTGATTTGAT	TAAACATTAT	1080
TAA						1083

(2) INFORMATION FOR SEQ ID NO:1862:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 282 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1862:

ACTAGGGAAG GAGAAATTTTC AATGGAACGC AATAATCGTA AAGTTCTTGT TGGACGTGTT	60
GTATCTGACA AAATGGACAA GACAATCACA GTTGTAGTTG AAACAAAACG TAACCACCCA	120
GTCTATGGTA AACGTATTAA CTACTCTAAA AAATACAAAG CTCATGATGA AAACAATGTT	180
GCCAAAGAAG GCGATATCGT ACGTATCATG GAAACTCGCC CGCTTTCAGC TACAAAACGT	240
TTCCGTCCTG TAGAAGTTGT TGAAGAAGCG GTCATCATCT AA	282

(2) INFORMATION FOR SEQ ID NO:1863:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1356 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1863:

AATCTTAGAG GTACAATCAA CTACGGAGGA ATAGAGATGC TCAGATTAGT TTACTATCAA	60
TTTTTACATA ATAAGAAACA ATGGTTAGGC GTTTCACCAG TAATTTTTTGT TTCGAGTTTA	120
GTTATGGGAT TGGCTGTTAA TGGGGTAATT AATGTTGAGA ATAATTCGCA AGTATTTGTC	180
GGACTTCCAG ATCCTAAACC AATTTTTTATG TTTCGGATAG TATTCGGAGG AGTAACATTA	240
TTCTTTGTGC TCTCTAACAT AATAAATATG TTGGTTGAAA TTTTITAGAGA TGATTACGAA	300
CTTCTGGAGG TGTTGGGAGC AAGTCGCCCTT CAACTATCAT TTCTTGTGGG GGGACAGATT	360
TTTATCATTT CCTCGATTAT TAGTTTTATT GCATATCTAT GCTCTATATT TGTTACGTCA	420

AATTATTATT	ATTTTTTACA	ATACTTTTTTC	GGGGAAAATA	TATTACCTGA	TATCCAATTT	480
CAAATGAGTG	CTGTTGGATG	TATCATTACA	GTAGTGTTGA	TTTCATTTTT	AGCCTTTCCTA	540
AGTGGTTGCT	TTTATACGTT	CAAGAAGATT	AGAAATAGGA	AGAGTTCCTAA	AATAAGGCAT	600
GTTCTTTCAA	TAGTAAAAAG	AATACTGCTA	TTGGCTGGTT	TTAGTGTTAT	CTGGTTGCCTT	660
TCTTTGCAAC	AAATTTTCCA	AGATAGCACA	ATTTTAGCGA	AGGCCCAGAT	AATATTCAAT	720
ATTGTAATCT	TAGATATTGT	GATTATTTAT	CAATTATCTC	CTTTTATACA	GTCATGTTTT	780
ATCAAACCTAC	TTTCTATAAT	TATATTTAGA	AATAATTTTA	TGTTCAATTGT	TTCGAAGTGG	840
AATTTACTAT	ATCGTAAGCC	TTATATAAAA	TCTATCAGTG	CTGCAATTAC	AGGAGCTATA	900
TTACTAATTT	CTAGTTTTCA	AATGATTTCT	CAGAAATATAC	TATCTCAATT	TCAAGATGAC	960
AGTGATTTAG	AGCTAAAAAGT	GGCATTATT	GTCTATGTAG	GAGCACCAAT	TTTGATAGTA	1020
CTTGCAAATA	TTATTTCAAT	TGCATTTTTG	TCATCGCATC	AAGAAAGGAT	TGAGATTCAG	1080
CAATTTGAAA	TTTTAGGAAC	TTCCAATTAC	CAGATGGTTA	AGATTAAAGT	TGGTGAGGCT	1140
ATATTTTTGA	CATTGTGTAC	TTCATTAAAT	GCATTTTTTAC	TTAACATTAA	AATTATGGTT	1200
TTAATATACT	ACTCTTTAGA	GGATATTTTA	ATAGATGATA	TGAATCTTTT	GGGGTTAATA	1260
CTTCCAAATT	TTATAGTGTC	TATTATTTTA	TTTATTTTAA	TATTTATTAC	TAAAAGTTCC	1320
TATTTTATCT	TTAAGAATGC	AAAAATTATT	TCTTAA			1356

(2) INFORMATION FOR SEQ ID NO:1864:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...378
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1864:

GAAAATAGAG	GATATTTATC	ACGTGGAGGG	ACTGCTATGA	GAGACGATAT	CAAAATCAAT	60
GACCGTGCTT	TGGCCTTGCA	AGACCAAATC	ATCGAAAAAC	TAGAGAAAGT	TTTTGATACA	120
GATGTGGAAT	TGGATGTTTA	CAATCTAGGT	CTGATTTATG	AAATCAATCT	GGATGAAACG	180
GGGCTCTGCA	AGATTGTCAT	GACCTTCACC	GATACTGCCT	GTGATTGCGC	CGAAAGCCTG	240
CCTATTGAAA	TCGTGGCAGG	TCTGAAACAA	ATCGAGGGTA	TCAAAGATAT	CAAGGTTGAA	300
GTTACCTGGT	CGCCTGCTTG	GAAAATCACA	CGAATCAGTC	GCTATGGCCG	TATTGCCCTT	360
GGACTACCAC	CTCGTTAA					378

(2) INFORMATION FOR SEQ ID NO:1865:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1455 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1865:

AGTAACAGAG	GATATTCATT	CATGAAAATT	TTATTTGTAG	CAGCAGAGGG	TGCACCCTTT	60
TCAAAAACAG	GTGGTTTGGG	AGACGTCATT	GGCGCTCTTC	CAAAATCACT	GGTAAAAGCT	120
GGGCACGAAG	TTGCAGTGAT	TTTACCCCTAC	TATGATATGG	TAGAGGCTAA	ATTTGGAAAT	180
CAGATTGAAG	ATGTGCTTCA	TTTTGAGGTG	AGCGTTGGTT	GGCGCAGACA	GTATTGTGGA	240
ATTAAGAAAA	CAGTATTTAA	TGGTGTAACC	TTCTACTTTA	TTGACAATCA	ATATTATTTT	300
TTCCGTGGTC	ATGTTTACGG	TGATTTTGAT	GACGGAGAAC	GCTTTGCCTT	TTTCCAACCTG	360
GCTGCCATTG	AGGCATATGA	AAGGATTGCC	TTTATTCCTG	ATCTTCTCCA	TGTTTCATGAC	420
TACCATACAG	CTATGATTCC	TTTCTTGTTG	AAGGAAAAAT	ACCGTTGGAT	TCAAGCCTAT	480
GAGGACATTG	AAACAGTTTT	AACCATTCAT	AATTTAGAAT	TCCAAGGACA	ATTTTCAGAA	540
GGAATGTTGG	GTGATTTGTT	TGGAGTTGGC	TTTGAACGTT	ACGCTGATGG	CACCCCTCGA	600
TGGAACAAC	GTCTGAACTG	GATGAAGGCA	GGTATTCTCT	ATGCGAACCG	TGTTTCAACT	660
GTTTCACCTA	GCTATGCTCA	TGAAATTATG	ACTAGTCAGT	TTGGATGTAA	TTTGGATCAG	720
ATTCTTAAAA	TGGAGTCTGG	TAAAGTATCT	GGTATCGTGA	ATGGGATTGA	TGCTGATCTT	780
TATAATCCTC	AGACGGATGC	TCTTTTAGAC	TATCATTTCA	ATCAGGAAGA	TTTGTCTGGG	840
AAAGCCAAAA	ATAAGGCAAA	ATTGCAAGAA	AGAGTTGGCT	TGCCTGTTAG	AGCTGACGTT	900
CCACTGGTGG	GAATTGTTTC	TCGTTTGACA	CGTCAAAAAG	GTTTTGATGT	GGTGGTCGAA	960
AGTCTTCACC	ATATCTTGCA	AGAAGATGTT	CAGATTGTTC	TTTTGGGAAC	TGGCGATCCA	1020
GCCTTTGAAG	GAGCTTTCTC	ATGGTTTGCT	CAGATTTACC	CAGACAAGCT	ATCAGCAAAT	1080
ATCACTTTTG	ATGTCAAAC	TGCTCAGGAA	ATCTACGCTG	CTTGTGACCT	CTTCCTCATG	1140
CCAAGTCGTT	TTGAACCGTG	TGGTTTGTCT	CAAATGATGG	CTATGCGTTA	TGGAACCTTG	1200
CCATTGGTCC	ATGAAGTTGG	AGGCTTGCGA	GATACAGTTT	GCGCTTTCAA	TCCAATCGAA	1260
GGAAGCGGTA	CTGGCTTTAG	CTTTGACAA	CTATCTCCTT	ATTGGTTAAA	TTGGACTTTT	1320
CAAACAGCAT	TGGACTTGTA	TAGAAACCAT	CCAGACATTT	GGAGAAACCT	ACAAAAACAA	1380
GCTATGGAGA	GTGACTTCTC	ATGGGATACA	GCCTGCAAGT	CATACCTTGA	CTTGTATCAT	1440
AGTTTAGTTA	ATTAA					1455

(2) INFORMATION FOR SEQ ID NO:1866:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1590 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1590

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1866:

AGAATAAGAG	GAAGAAAAAT	GGCATTGTGAA	AGTTTAAACAG	AACGTTTGCA	GAACGTCTTT	60
AAAAATCTAC	GTAAAAAAGG	AAAAATCTCT	GAATCTGATG	TCCAAGAGGC	AACCAAAGAA	120
ATTCGCTTGG	CCTTGCTCGA	GGCCGACGTT	GCCTTGCCTG	TTGTAAAGGA	CTTTATCAAG	180
AAAGTTTCGTG	AGCGTGCAGT	CGGGCATGAG	GTCATTGATA	CACTTAATCC	TGCGCAACAG	240
ATTATTAAAA	TCGTTGATGA	GGAAC TGACA	GCCGTTTTAG	GTTCTGATAC	GGCAGAAATT	300
ATCAAGTCAC	CTAAGATTCC	AACCATCATC	ATGATGGTTG	GTTTACAAGG	GGCTGGTAAA	360
ACAACCTTTG	CTGGTAAATT	GGCCAACAAA	CTCAAGAAAG	AAGAAAATGC	TCGTCCCTTG	420
ATGATTGCGG	CGGATATTTA	TCGTCCAGCT	GCCATTGACC	AGCTTAAGAC	CTTGGGACAA	480
CAGATTGATG	TGCCTGTCTT	TGCACTTGGA	ACAGAAGTAC	CAGCTGTTGA	GATTGTACGT	540
CAAGGTTTGG	AGCAAGCCCA	AACTAATCAT	AACGACTATG	TCTTGATTGA	TACTGCGGGT	600
CGTTTGACAGA	TTGATGAGCT	CCTCATGAAT	GAGCTTCGTG	ATGTGAAAAC	ATTGGCTCAA	660
CCAAATGAAA	TCTTGCTTGT	CGTTGATGCT	ATGATTGGTC	AGGAAGCAGC	CAATGTTGCG	720
CGTGAGTTTA	ATGCTCAGTT	GGAAGTGACT	GGGGTCATCC	TTACCAAGAT	TGATGGCGAT	780
ACTCGTGGTG	GTGCTGCTCT	GTCTGTTCTG	CACATTACTG	GAAAACCAAT	CAAGTTCACT	840
GGTACAGGTG	AAAAGATTAC	GGACATTGAA	ACCTTCACC	CAGACCGCAT	GTCTAGCCGT	900
ATCCTTGGTA	TGGGGGATAT	GCTCACTTTG	ATTGAGAAAG	CTTCTCAGGA	ATACGATGAA	960
CAAAAAGCCC	TTGAAATGGC	TGAGAAGATG	CGCGAAAACA	CCTTTGATTT	TAATGATTTT	1020
ATCGATCAAT	TAGATCAGGT	GCAAAATATG	GGGCCGATGG	AAGACTTGCT	CAAGATGATT	1080
CCAGGTATGG	CAAACAATCC	AGCCCTTCAA	AACATGAAGG	TGGATGAACG	CCAGATTGCT	1140
CGTAAACGTG	CCATTGTGTC	TTCGATGACA	CCTGAAGAGC	GTGAAAACCC	AGATTTGTTA	1200
AATCCAAGCC	GTCGCCGTCG	TATTGCTGCT	GGTCTGGAA	ATACATTCTG	CGAAGTCAAT	1260
AAATTCATCA	AGGACTTTAA	CCAGGCTAAA	CAGCTCATGC	AGGGTGTTAT	GTCTGGGGAT	1320
ATGAATAAAA	TGATGAAGCA	AATGGGGATT	AATCCAAATA	ACCTTCCTAA	AAATATGCCA	1380
AATATGGGAG	GAATGGATAT	GTCTGCCCTT	GAAGGAATGA	TGGGACAAGG	CGGTATGCCT	1440
GACTTATCAG	CTCTCGGAGG	AGCAGGAATG	CCAGATATGA	GCCAGATGTT	TGGTGGCGGT	1500
TTGAAAGGTA	AAATTGGTGA	ATTTGCTATG	AAACAGTCCA	TGAAACGTAT	GGCTAACAAA	1560
ATGAAGAAAG	CGAAGAAGAA	ACGCAAGTAA				1590

(2) INFORMATION FOR SEQ ID NO:1867:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1419 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1419

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1867:

ATTGAAAGAG	GTAGTGAGAT	GGACGCGAAA	TTAAGATACA	AGGCAAAGAA	GATCAAGATT	60
GTCCTTTTTT	ATATTGATGA	TACATTGCGG	AATTCAAAGA	CAGGGTTTAT	TCCAACCTACA	120
ATTCCCACCTG	TTTTTAAACA	GTTGCGTGAA	AAAGGAATTT	TAACAGGAAT	CGCCTCTGGA	180
CGTGGCATT	TTGGTGTGTT	TCCAGAGATT	CGTGATCTCA	AGCCTGACTT	TTTTGTAAC	240
TTGAAATGGGG	CTTATATCGA	AGATAAAAAA	GGTCAGGTCA	TTTATCAGCA	TCAGATTGAA	300
AAGTCATATG	TTGAGGAGTA	TATCTCTTGG	GCTAAGCAAG	AAGGAATTGA	GTATGGCTTG	360
GTTGGGAGTC	ATGATGCCAA	GTTGTCTGACT	CGCACCGATA	TGATGAGTGA	AGCTATCAAT	420
CCAATTTTATC	CCGACTTAGA	TGTAGATCCC	GATTTCCATG	AAAAAGAAGA	TATCTATCAG	480
ATGTGGACTT	TTGAAGATAA	GGGAGATGAC	TTGCACCTGC	CTGACAGTCT	CTCAGACAAA	540
CTTCGCATGG	TTCGTTGGCA	TCAACATTCG	TCTGATATTG	TGCCGATTTC	AGGCTCCAAA	600
GCGACGGGGG	TGGAAGAGT	TGTGGAACAC	CTTGGCTTGA	AACCAGAGAA	GGTCATGGTT	660
TTTGGAGATG	GTCTCAACGA	CTTGGAACTC	TTTGATTATG	CTGGAATCAG	CGTTGCCATG	720
GGAATTTCTC	ATGATAAAAT	CAAAGAAAAA	GCAGATTATA	TTACACAAAC	ATTAGAAGAA	780
GATGTCATTT	TTGATGCCTT	AGAAGTATTT	GGTATGGTAG	AAAAAGAATT	GCATTTTCCA	840
CAAGTAGACA	TTGAAACAGT	AGAAGGTCCT	CTTGCGACTA	TTAAGACCAA	TCACGGAGAC	900
TTACGTATCA	AGCTTTTCCC	TGAACATGCT	CCTAAAACAG	TGGCTAACTT	TGTATCTCTT	960
TCAAAAGATG	GCTACTATGA	TGGTGTCAAT	TTCCACCGTA	TTATCAAGGA	CTTTATGATC	1020
CAAGGTGGAG	ACCCAACCTG	AACTGGTATG	GGTGGCGAGT	CAATCTACGG	CGAATCTTTT	1080
GAGGATGAAT	TCTCAGAAGA	GCTTTACAAT	ATCCGTGGTG	CTCTTTCCAT	GGCAAATGCT	1140
GGTCCAAATA	CCAACGGCAG	CCAGTTCCTT	ATCGTGCAAA	ACCAACACCT	ACCTTATTCT	1200
AAGAAAGAAA	TTACTCGTGG	TGGTTGGCCA	GAACCGATTG	CAGAAATCTA	TGCCAATCAA	1260
GGTGGGACAC	CTCACCTAGA	CCGCCGTCAC	ACGGTTTTTG	GTCAGTTAGC	TGATGAAGCA	1320
TCTTACGCTG	TCTTGATGT	CATTGCTGCT	GTTGAGACAG	GAGCTATGGA	CAAGCCAGTT	1380
GAAGATGTTG	TAAATGAAAC	TATTGAAATC	GAGGACTAA			1419

(2) INFORMATION FOR SEQ ID NO:1868:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1868:

TCTAAGAGAG	GAGAAAATAT	GGAAGCAATT	ATCGAGAAAA	TCAAAGAGTA	TAAAATCATC	60
GTCATCTGTA	CTGGTCTGGG	CTTGCTTGTA	GGAGGATTTT	TCCTGCTAAA	ACCAGCTCCA	120
CAAACACCTG	TCAAAGAGAC	GAATTTGCAG	GCTGAAGTCG	CAGCTGTTTC	CAAGGATTTG	180
GTATCCGAAA	AGGAAGTGAA	CAAGGAAGAA	AAGGAAGAAC	CCCTTGAACA	AGATCTAATC	240
ACAGTAGATG	TCAAAGGTGC	TGTCAAATCG	CCAGGGATTT	ATGACTTGCC	TGTAGGTAGT	300
CGAGTCAATG	ATGCTGTTCA	GAAGGCTGGT	GGCTTGACAG	AGCAAGCAGA	CAGCAAGTCG	360
CTCAATCTAG	CTCAGAAAGT	TAGTGATGAG	GCTCTGGTTT	ACGTTCTTAC	TAAGGGAGAA	420
GAAGCAGTTA	GCCAACAGAC	TGGTTTGGGG	ACAGCTTCTT	CAATAAGCAA	GGAAAAGAAG	480

GTCAATCTCA	ACAAGGCCAG	TCTGGAAGAA	CTCAAGCAGG	TCAAGGGACT	GGGAGGAAAA	540
CGAGCTCAGG	ACATTATCGA	CCATCGTGAG	GCAAATGGCA	AGTTCAAGTC	AGTAGACGAG	600
CTCAAGAAGG	TCTCTGGCAT	TGGTGGCAAA	ACAATAGAAA	AGCTTAAAGA	CTATGTTACA	660
GTGGATTAA						669

(2) INFORMATION FOR SEQ ID NO:1869:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1677 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1677

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1869:

GATTTTGGAG	GAAAAATGAG	TAATATCAGT	TTAACAACAC	TTGGTGGTGT	GCGTGAGAAT	60
GGAAAAAATA	TGTACATTGC	TGAAATTGGA	GAGTCCATTT	TTGTTTTGAA	TGTAGGGTTA	120
AAATATCCTG	AAAATGAACA	ATTAGGGGTC	GATGTGGTGA	TTCCAAACAT	GGATTACCTT	180
TTTGAAAATA	GCGACCGTAT	TGCTGGGGTT	TTCTTGACCC	ACGGGCATGC	GGATGCGATT	240
GGTGCTCTAC	CTTATCTCTT	GGCAGAGGCT	AAAGTTCCTG	TATTTGGGTC	TGAGTTGACC	300
ATTGAGTTGG	CAAAGCTCTT	TGTCAAAGGA	AATGATGCCG	TTAAGAAATT	TAATGATTTT	360
CATGTCATTG	ATGAGAATAC	GGAGATTGAT	TTTGGTGGGA	CAGTGGTTTC	CTTCTTCCCT	420
ACGACTTACT	CCGTTCCAGA	GAGTCTGGGA	ATTGTCCTTGA	AGACATCGGA	AGGAAGCATC	480
GTTTATACAG	GTGACTTCAA	ATTTGACCAA	ACGGCTAGTG	AATCTTATGC	AACTGATTTT	540
GCTCGTTTGG	CAGAGATTGG	TCGTGACGGC	GTCTGGGCTC	TCCTCAGTGA	TTCGGCCAAT	600
GCAGACAGCA	ATATTACAGT	GGCTAGTGAA	AGTGAAGTTA	GGGATGAAAT	TACCCAAACT	660
ATTGCTGACT	GGGAAGGTCG	TATCATCGTT	GCAGCTGTTT	CCAGTAATCT	TTCTCGTATT	720
CAGCAGATTT	TTGACGCTGC	GGATAAAACA	GGTCGACGTA	TCGTCTTGAC	AGGATTTGAT	780
ATTGAAAATA	TCGTCCGCAC	AGCGATTTCG	CTTAAGAAGT	TGTCTTTAGC	CAACGAAATT	840
CTCTTGATTA	AGCCTAAAGA	TATGTCTCGC	TTTGAAGACC	ATGAGTTGAT	TATTCTTGAG	900
ACAGGTCGTA	TGGGTGAACC	TATCAATGGA	CTTCGTAAGA	TGTCGATTGG	TCGCCATCGT	960
TATGTAGAAA	TCAAGGATGG	GGACCTGGTC	TATATTGCTA	CGGCTCCGTC	TATTGCTAAA	1020
GAAGCCTTTG	TTGCGCGTGT	AGAAAATATG	ATTTATCAGG	CAGGTGGGGT	TGTCAAATTG	1080
ATTACCCAAA	GTTTACATGT	ATCAGGGCAC	GGAAATGTGC	GTGATTTGCA	GCTGATGATC	1140
AATCTTTTGC	AACCTAAGTA	CCTCTTCCCT	GTCCAAGGGG	AGTATCGTGA	GTTGGATGCT	1200
CACGCTAAGG	CTGCCATGGC	AGTTGGGATG	TTGCCAGAAC	GCATCTTCAT	TCCTAAAAAG	1260
GGGACGACCA	TGGCTTACGA	GAATGGAGAC	TTTGTTCAG	CTGGATCGGT	TTCAGCAGGA	1320
GATATCTTAA	TTGATGGGAA	TGCCATTGGT	GATGTTGGAA	ATGTTGTTCT	TCGTGACCGT	1380
AAGGTCTTGT	CAGAGGATGG	AATTTTCATC	GTGGCTATTA	CAGTCAACCG	TCGTGAGAAG	1440
AAAATTGTGG	CTAGAGCTCG	TGTTCACACG	CGTGGATTTG	TTTATCTCAA	GAAGAGTCGC	1500
GATATTCTCC	GTGAAAGTTC	AGAATTGATT	AACCAAACGG	TAGAAGATTA	TCTTCAAGGA	1560
GATGACTTTG	ACTGGGCAGA	TCTTAAAGGG	AAGGTTTCGAG	ATAATTTGAC	CAAGTATCTC	1620
TTTGACCAAA	CCAAGCGTCG	TCCAGCTATT	TTACCAGTAG	TCATGGAAGC	AAAATAA	1677

(2) INFORMATION FOR SEQ ID NO:1870:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1870:

GTGATTGGAG GCAAGAATAT GGATAAAGAT TATATATTAA AAGTGATAGG GCTGTATCAT	60
CAATTTTTTAC TGGGAAACAA TAAAACGTTG CAAGTGCTGA AAAATGTTTC TCTTCTGCT	120
TCGAGAGGAG AATTTATAAG TATTCTAGGA ATTACGTGGT TCTGGAAAGT CAACTTTATT	180
AAAATGTATT TCTAG	195

(2) INFORMATION FOR SEQ ID NO:1871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1871:

AAAATCGGAG GAAATATTAT GAAGCTTATC AATACGACAA ACTCACACTC GCAACTTGTA	60
AAAAGTCAAC TAGAAAGTAC CGATGCAACC CTTGTTGAGG TTTATTCTGC AGGGAATACA	120
GATGTTATTT TTACCCAAGC TCCGCTTCAC TATGAAATCC TCATCTCAA CAAACACCGT	180
GCTATTCGTG AGCCTGAAAT CGAAACCATT CAAGAATTTT TCTTGAAACG TAAAATTGAT	240
AAGGCCTCTG TTGATGAAGC CAATATCAAG AACTCTACT CAGAGAAATT AATTGGAATT	300

(2) INFORMATION FOR SEQ ID NO:1872:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1872:

AAAAACGGAG	TTTTTGTCAT	GAACAAAAAA	AGTCTTTTGA	AATGCGCTGT	TATCGGGTTA	60
GTAGCTACCT	TTGGTTTAGC	AGCTTGTGGA	ACATCTAAGG	ATGCAAGCGG	TGGAAGTTCT	120
TCTGGTAAAG	AAGTATTAGA	ATTTTATCAT	GGGTATCATC	ATAGTGAAGA	TGAATGGCCT	180
GTAGCGAAGA	CTATGCGAGA	TTTATATGAT	AAATTTGCAG	AAGAACATAA	AGATAGTGGT	240
GTAGAATTTA	AACCAACCCC	TGTAAATGGT	GATTTGAAGG	ATATAATGAA	TAACAAGGTT	300
GCTAGTGGTG	AGTTTCCTGA	TGTGATTGAC	CTAGCAGGTA	ATGCAGTATC	ATTAGCTGCG	360
ATTGAACAAA	AACCTGTTTT	AGATTTGAAA	CCATATATCG	ATTCAAATAA	GCTTGAAAAA	420
AATGTTGGTT	TGAACTATAA	GCAAAACCAA	AAAGATGGAA	AAATTTATAC	AGTTCACGAA	480
CAGTTATTTA	CAATGGGTTT	GTGGTACAAC	AAGGACATAT	TTGCAAAAGC	GGGTGCTAAG	540
ACACCTGATC	AGTGGAATAC	TTGGGATGAT	TTCCTCAGG	CAATGGCAAG	CATTAGAAAA	600
CAAGATGGAG	TGTATGCATT	TGGTGCTGGA	GAACCATCTA	TTCGCTTGTT	TAATACAGTA	660
TTAGGAACCA	CAGAAAATGG	ACGTAAATTA	TTAGACAAGC	CATTAACAAA	AGAAGGAATT	720
GAATCTAAAG	AATTTGCAGA	TGCTTTGAAA	ATGGTTATGA	AAGAAATTC	AGCTAATGGT	780
TCTAAGAATG	CTGGTGCCGA	TGCCAATGCT	TATTCCAAAG	ATTTCCAAGA	AGGTAAATCT	840
GCAGTCTTCT	TTAATGGTGT	GTGGGCTTCT	GGTGAGATGT	CTAAGAACCC	AAGTCTTGCA	900
CCTGGAATCT	ATCCTGCAGG	TGTAGCAATT	AGTTCCTCTG	GAGGTGGTAT	CACTATCTCA	960
AGTAAGATGT	CTGAAGCTAA	ACAAAACTA	GCTCTTGAGT	TTTTGAAATA	TATGACTAGC	1020
GATGATGTAC	AAAAAGTAAT	TTTTGAAAAA	GTAGGAGCAA	ATCCTTCTAA	TGAAAAATGA	1080
AATGTAAAAG	AACTTTCAGA	AAAGAGTTCA	GAAAGCTACTA	CTAAAATTTT	AGGACAAGCA	1140
ATCACTCAAG	TTAAGAATGC	AAAAGCAGTT	GTTCCAAGTG	TAAGTGATGT	TTGGGGTGGC	1200
GATGTACACA	CAGCTATTAT	CAATGCATTG	ACAGAAAGTG	CTGCTGAAAA	TGTAGATGTT	1260
GATCAAAAAG	TAAAATCTAC	TCAAGATGTG	TTGAAATCAT	TGATTGGTTA	A	1311

(2) INFORMATION FOR SEQ ID NO:1873:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1873:

ACTTTAGGAG	GTCTTATGAA	ATTATTAGAA	GATCGCATCC	TCAAGGATGG	GCATATCTTG	60
GGTGATAACA	TCCTCAAGGT	AGATTCCTTT	TTAACCCACC	AAGTTGACTT	TAGCTTGATG	120
CGAGAGATTG	GTAAGGTTTT	TGCGGAAAAA	TTTGCTGCTG	CCGGCATTAC	CAAGGTCGTA	180
ACCATTGAAG	CGTCGGGTAT	TGCCCCAGCC	GTTTTTACAG	CTGAAGCCTT	AAATGTTCCC	240
ATGATTTTTG	CCAAAAAGGC	TAAAAACATC	ACCATGAACG	AAGGTATCCT	AACTGCCCAA	300
GTCTACTCCT	TTACCAAGCA	AGTGACCAGC	ACCGTTTCTA	TCGCTGGAAA	ATTCCTCTCA	360
CCAGAGGACA	AGGTCTTGAT	TATCGACGAT	TTCTTGCTA	ATGGCCAAGC	TGCTAAAGGC	420
TTGATTCAAA	TCATCGAACA	GGCCGGTGCC	ACAGTCCAAG	CTATCGGTAT	CGTGATTGAG	480
AAATCCTTCC	AAGATGGTCG	TGATTTGCTT	GAAAAAGCAG	GCTACCCTGT	CCTATCACTT	540
GCTCGCTTGG	ATCGTTTTGA	AAATGGTCAG	GTCGTATTTA	AGGAGGCAGA	TCTCTAA	597

(2) INFORMATION FOR SEQ ID NO:1874:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 432 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1874:

AGAATAGGAG	GTTGTATGCA	AATTGAATTT	TTCAATTTTC	TAAGAAGTGT	CGTACAGACT	60
GAAGATGGTT	TGGTTTTGTA	CGCTCTAGCA	CTGATTGTCT	CAATGGAAAT	CATTGATTTT	120
GTGACAGGGA	CGATTGCGGC	GATTATCAAT	CCTGACATCG	AGTACAAGAG	CAAAATCGGC	180
ATTAACGGGC	TCCTTCGTAA	GATTTCAAGG	GTTCTCTTAC	TGATGATCCT	CATTCCGGCG	240
TCCGTTTTGT	TGCCTGAAAA	GACAGGTTTT	GTATTCCTTG	ACTCAATCTA	TCTCGGGTAC	300
ATCGCATTTA	CTTTTCAATC	TCTCATTGAA	AATTATCGCA	AATTAAAAGG	AAATGTTACT	360
CTTTTTCAGC	CGATTGTAAA	AGTATTTTCA	CGATTACTTG	AAAAAGATGA	TGACACGAAA	420
AAAGGAGAA	AA					432

(2) INFORMATION FOR SEQ ID NO:1875:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1500 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1500
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1875:

TCAAAAGGAG	GCTCTATAGT	GATCTTAGTA	GATAAAATTTG	TAACACATGT	CATTTCTGAA	60
AGTTCATTTG	AGGAAATGGA	TCGAATCTAC	CTGACCAACC	GTGTTTGGC	ACGAGTGGGA	120
GAAGGTGTTT	TGGAAGTTGA	GACCAATCTG	GATAAAATTTG	TTGACCTCAA	GGACCAGCTA	180
GTTGAGGAAG	CCGTTTCGATT	AGAGATGATT	GAGGATAGTC	AGACTGCGCG	TGAAATCCTT	240
GGTACTGAAC	TGATGGACTT	GGTGACTCCT	TATCCGAGTC	AGGTCAATCG	TGACTTCTGG	300
GAAGCCTATG	TCCACTCTCC	TGAGCAAGCG	ATAGAGGATT	TTTATCAACT	CAGTCAGAAA	360
AATGACTACA	TCAAACCTCAA	GGCCATTGCT	AAAAATATCG	CTTATCGTGT	TCCATCTGAT	420
TATGGAGAAC	TTGAAATTAC	CATCAATCTC	TCTAAGCCTG	AAAAGGATCC	GAAAGAGATT	480
GCGGTAGCCA	AGTTGGTGCA	AGCTAGTAAT	TATCCTCAGT	GTCAACTTTG	TTTAGAGAAT	540
GAGGGTTACC	ATGGTCGGGT	CAACCACCCA	GCTCGCAGCA	ACCACCGGAT	TATCCGTTTT	600
GAAATGGTTG	GTCAGGAATG	GGGGTTCCAG	TATTCGCCCT	ATGCTTACTT	TAATGAGCAT	660
TGTATTTTTT	TAGATGGCCA	GCATCGTCCC	ATGGCCATTA	GTCGTCAGAG	TTTTGAACGT	720
CTGTTGGCTA	TCGTAGAGCA	GTTTCCAGGA	TATTTTGCTG	GATCTAATGC	CGACCTGCCG	780
ATTGTGGGGG	GCTCTATTCT	AACTCACGAT	CATTATCAGG	GAGGCCGTCA	CGTATTTCCCT	840
ATGGAATTGG	CTCCCTTGCA	AAAGACCTTC	CGATTTGCTG	GTTTTGAGCA	GGTCAAGGCT	900
GGAATTATCA	AGTGGCCAAT	GTCTGTCCTA	CGCTTGACTT	CGGATTCCAA	AGAGGATTTG	960
ATTAACCTAG	CTGATAAGAT	TTTCCAGGAA	TGGCGTCAGT	ATTCAGATTC	TAGTGTGCAG	1020
ATTTTAGCAG	AGACAGACGG	GACACCGCAT	CACACCATCA	CACCAATAGC	GCGTAAGCGT	1080
GATGGACAGT	TTGAGTTGGA	CTTGGTCTTG	CGAGACAATC	AGACTTCAGC	AGAGCATCCT	1140
GATGGCATCT	ATCATCCCCA	CAAGGATGTC	CAACATATCA	AGAAGGAAAA	TATCGGCTTG	1200
ATTGAGGTCA	TGGGCTTGGC	AATCTTGCCA	CCACGTCTGA	AAGAAGAAGT	GGAGCAAGTC	1260
GCTAGCTATC	TTGTAGGAGA	AGCTGTTACA	GTTGCCGATT	ATCATCAGGA	GTGGGCAGAC	1320
CAACTCAAAT	CCCAACATCC	AGACCTAACG	GATAAAGAAA	AAGCCCTTGC	AATCGTCAAG	1380
GACTCTGTGG	GTGCTATCTT	TGTGCGTGTA	CTTGAGGATG	CAGGAGTCTA	CAAGCAGACA	1440
GAACAAGGGC	AGACAGCCTT	TATGCGCTTT	GTGGAACAGG	TCGGAATTTT	ACTAGACTAG	1500

(2) INFORMATION FOR SEQ ID NO:1876:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 717 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1876:

GAAAAAGGAG	GAAAAAGGAT	GTCACAGATT	AGCAAAGAAG	CCTTGATTGA	GCAAATCAAA	60
GATGGAATCA	TCGTTTCTTG	TCAGGCTCTT	CCTCATGAAC	CGCTTTTATAC	AGAAGCGGGA	120
GGGGTGATTG	CCTTGCTGGT	CAAAGCGGCT	GAGCAAGGTG	GAGCAGTCGG	TATCCGAGCA	180
AACAGTGTTG	GCGATATCAA	GGAAATTAAG	GAAGTCACTA	AACTTCCAAT	CATTGGGATT	240
ATCAAACGTG	ATTATCCACC	TCAGGAACCC	TTCATCACGG	CTACTATGAA	AGAAGTTGAT	300
GAATTGGCAG	AACTGGACAT	CGAGGTGATT	GCTCTGGATT	GTACCAAGCG	TGAACGCTAC	360
GATGGTTTGG	AAATTCAAGA	GTTCAATTCGT	CAGGTTAAGG	AGAAATATCC	TAATCAGCTT	420
TTGATGGCTG	ATACTAGTAT	CTTCGAAGAA	GGGCTAGCAG	CTGTAGAAGC	AGGAATTGAC	480
TTTGTCGGAA	CAACCTTATC	AGGCTACACA	TCCTACAGTC	CAAAAGTAGA	TGGTCCAGAT	540
TTTGAATTGA	TTAAGAAACT	CTGTGATGCC	GGTGTAGATG	TCATTGCAGA	AGGAAAAATT	600
CATACACCAG	AACAAGCCAA	ACAAATCCTT	GAATATGGAG	TGCGAGGCAT	CGTTGTTGGT	660
GGCGCTATTA	CTAGACCAAA	AGAGATTACA	GAACGTTTTG	TAGCGGGATT	AAAATAG	717

(2) INFORMATION FOR SEQ ID NO:1877:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 606 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1877:

GAAAAAGGAG	GGCTAGATAT	GTTGCAGCTT	ACTCATGTGA	CCTTAAAAAC	GCGACAAGTC	60
ATCTTGCAAG	ATGCGGATTT	CACCTTTAAA	AAGGGTAGGT	TTTATGGTCT	TCTTGCTATC	120
AATGGCTCTG	GAAAGACGAC	CCTGTTCCGT	GCCATTAGCA	ATTTAATTCC	CATAAGTAGT	180
GGAAATATCG	CAGCCCCTCC	TTCTTTATTT	TATTATGAGA	GTATTGAATG	GCTGGATGGA	240

AACTTAAGTG	GGATGGACTA	CCTTCGTCTT	ATCAAAAACA	TCTGGAAGTC	AGACCTAAAC	300
TTGAGAGATG	AAATCGCCTA	CTGGGAAATG	GCTGACTATA	TCAGTCTTCC	CATCCGCAAG	360
TATTCCTTAG	GCATGAAGCA	ACGCTTGGTG	ATTGCTATGT	ATTTTCTCAG	TCAGGCAAAA	420
TGCTGGCTCA	TGGATGAGAT	TACAAATGGC	TTAGACGAGT	ATTATCGACA	GAAGTTTTTT	480
GATAGGCTAG	CACAAATCGA	TAGACAAGAA	CAGCTGGTTC	TTTTAAGTTC	CCACTATAAG	540
GAAGAGTTGG	TTGATATCTG	CGATAGAGTA	GTAACCATTC	ATCAGGGGCA	GATAGAAGAG	600
GTTTAG						606

(2) INFORMATION FOR SEQ ID NO:1878:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...234
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1878:

CAGAAAGGAG	GTAGGAACGT	GCAGTGGACT	TTAGAAGCTA	TGAGAATCAA	CAAAGGACTT	60
ACTCAAGCAG	AGTTGGCAGA	AAAATTTGAA	GTTTCAAGTC	AAACAATTGC	TAGATTAGAA	120
AAAGATAGCT	CTGATATCGG	TTATCAGCTA	TTGAAAAAAT	ACATGTTTTT	TTTCAATGTG	180
AAATTCGATG	ATATTTTTTT	AGGGAAAAAA	TACGAAAATT	TCGTAAATAA	CTAG	234

(2) INFORMATION FOR SEQ ID NO:1879:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1879:

ATTGAAGGAG	GAGGTCATAA	ATTGAAACGA	TTCATAGCTA	TCTGGATTCT	GCTATCTGCT	60
GGATTGAATA	TCTGGCAGAG	TATCTACATT	AAAAAGTTAG	AAGAAAAGCG	CCCTATTGTC	120
GTCTATAAAG	CTGATAACGC	AGGCGCTGAG	ATATTCCGTA	AAGTCGTCGA	GAAAGGACGG	180
CATGGCAAGC	TATACACGCT	TACCATTTCGT	GACTACGGGG	TGTTTCGTGGT	TACGAAGGAC	240
GTGTATGAGA	AAGTGAAAGT	AGGGGATGAG	GTGTTACTCT	AA		282

(2) INFORMATION FOR SEQ ID NO:1880:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 639 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1880:

AGACGAGGAG	GGCTAAGAGC	AGAACAGACA	GCCAAAGCTG	ATGGAACAGT	CGGAAGTAAG	60
TCTCAAGGAG	CTGCCCAGAA	GAAAGCAGAA	GTGGTCAATA	AAGGTGATTA	CTACAGCATT	120
CAAGGCANAT	ACGATGAAAT	CATCGTAGCC	AACAAACACT	ATCCATTGTC	TAAAGACTAT	180
AATCCAGGGG	AAAATCCAAC	AGCTAAGGCA	GAGTTGGTCA	AACTCATCAA	AGCGATGCAA	240
GAGGCAGGTT	TCCCCATTAG	CGACCATTAC	AGTGGCTTTA	GAAGTTATGA	AACTCAGACC	300
AAGCTCTATC	AAGATTATGT	CAACCAAGAT	GGGAAGGCAG	CAGCTGACCG	CTACTCTGCT	360
CGACCTGGTT	ATAGCGAACA	CCAGACAGGC	TTGGCCTTTG	ATGTGATTGG	GACTGATGGT	420
GATTTGGTGA	CAGAAGAAAA	AGCAGCCCAA	TGGCTTTTGG	ACCATGCAGC	TGATTATGGC	480
TTTGTGTGCC	GTTATCTCAA	AGGCAAGGAA	AAGGAAACAG	GCTATATGGC	TGAAGAATGG	540
CACTTGCGTT	ATGTAGGAAA	AGAAGCTAAA	GAAATTGCTG	AGAGTGGTCT	CAGTTTGGAA	600
GAATACTATG	GCTTTGAAGG	CGGAGATTAC	GTCGATTAA			639

(2) INFORMATION FOR SEQ ID NO:1881:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2415 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2415

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1881:

CAAGGAGGAG	GTGAGAAGAT	GGCCCTAGCT	AAGATTATCG	TAGATGTGCC	CTTGATGCAG	60
ACGGACCAGC	CCTATAGTTA	CAGGATTCCG	GAGGAATTTG	AGGGAATGCT	GGAAGTTGGG	120
ATGCGGGTTC	ATGTGCCTTT	TGGTAAGGGT	AATCGCCTGA	TTCAAGGGAT	TGTTCTTGGT	180
TTGAAGTCCC	AATCAGATGG	AGAAGAGATG	GAGCAAGATT	TAAAAGATAT	TGCAGAGGTG	240
CTGGATTTTT	CTCCTGTTCT	CACGCCAGAA	CAACTCTGGC	TGGCTGAGGA	GTTACGCAAA	300
TCTGTCTTCT	CCTACAAAAT	CTCTATCCTC	AAGGCCATGC	TTCCAGGGTT	TCTGAATTCT	360
AGCTATGACA	AGATTCTCTA	TCCTCTGGAA	GGCTTGAGTC	AGGAAGAACG	AGTACGCCTG	420
TTTGGTTCAG	AAGATTCGCT	AGCCTTTTCT	TCACTAGACC	TTGCCAAGCA	AGCTGAAATG	480
ATGCGTTTGA	CTAGAAAAGG	CCTGCTTGCT	CTGGAATATC	AGGCAGTCGA	TCAAAAAGAAG	540
GTCAAGACCC	AGTCTTG GTA	TGAGGTTGAC	CATGCCCAAT	TAGAAGGTGT	TGAGATTTCT	600
ACACGTGCCA	AGAAAAAGTT	GGAAC TGAGA	GATTATCTGC	TGTCTCATCC	AGAGAGCGCT	660
TCCTTG GCTA	GCTTGTTAGA	GTCCTACTCG	CGAGAGCAAG	TCAACTTCTT	TGTGGATCAA	720
GGTGCTGTTA	CCATAGTCCA	AAAGGAAGTT	CAACGCTCGG	CTGCTTATTT	TGAAGGAATT	780
GAAGCAAGTA	GACCTTTGGA	GTTAAATCCA	GAACAAAGAC	AGGCGCGTGA	TGCGGTTGTG	840
AGTTCTATTG	GCAGTTCTCA	ACCTCCCTTT	CTACTTCAAG	GGATTACAGG	AAGTG GGAAG	900
ACCGAGGTTT	ACTTG CAGAT	TATCCAAGGT	GCCCTGGATA	AGGGCAAGAC	AGCTATTTTG	960
CTGGTACCTG	AGATTTCTCT	GACTCCTCAG	ATGACCGAGC	GTTTTATAGC	ACGTTTTTGGG	1020
GACAAGG TAG	CCATTCTTCA	CTCAGGATTA	TCCAATGGCG	AAAAGTATGA	TGAATGGCGC	1080
AAGGTGGAGC	GTGGCGATGC	CCAAGTTGTT	GTTGGTGCCA	GATCTGCTAT	CTTTGCTCCT	1140
CTGAAAAATC	TGGGTGTCAT	GATTATTGAT	GAAGAGCATG	AAGCGGCTTA	TAAGCAGGAC	1200
AGCAATCCCC	GTTACCATGC	CAGAGAGGTA	GCTATTTTAC	GGGCTCAGTA	TAATCAAGCA	1260
ACTCTGGTAC	TTGGATCTGC	AACGCCGAGC	TTAGAGAGCC	GGGCACGTGC	TGGCAAAGGC	1320
GTCTATCAAC	ACTTACGTCT	AACCCAACGT	GCCAATCCTT	TGGCTACAAT	CCCTGAGGTT	1380
CAAGTGATTG	ACTTTCGAGA	CTATATCGGA	CAAAATGAGA	CGTCAAACCT	TACGCCTCCT	1440
TTGCTAGAGG	CTATCCAAGA	CCGTCTGGTT	AAAAAAGAGC	AGGTGGTTCT	CATGCTCAAT	1500
CGCCGTGGTT	ATTCTAGCTT	TGTCATGTGT	CGGGAGTGTG	GGACGGTGGA	TACTTGTCCC	1560
AACTGCGATA	TTTCTCTGAC	CTTG CATATG	GATACCAAGA	CTATGAACTG	CCATTATTGT	1620
GGTTTCTCGA	AGGATATTCC	TCAGGTCTGT	CCTAACTGTA	AGAGCCACAG	TATTCGTTAC	1680
TATGGAACGG	GAACTCAGAA	GGCTTATGAT	GAGCTAGCAG	AACTCTTTCC	CCAAGCTCGC	1740
ATTCTGAGGA	TGGATGTGGA	TACGACTCGA	AAGAAAGGCA	GTCACCAAGC	CTTGCTTGAC	1800
CAGTTTGGGC	GAGGGGAAGC	GGATATTTTA	CTTGGTACTC	AGATGATTGC	AAAGGGTTTG	1860
GATTTTCCCA	ATGTTACCCT	AGTCGGAGTT	CTAAATGCGG	ATACGGCCTT	GAATCTGCCT	1920
GATTTCCGTT	CTTCTGAGAG	AACCTTCCAG	CTCTTGACTC	AGGTGGCAGG	TCGATCAGGT	1980
CGGGCTGAAA	AGGCAGGTCA	AGTCTTGATA	CAGTCTTACA	ATCCGCAGCA	CTATGCTATT	2040
CGATTTGCCA	AGGATCAAGA	TTACGAAGGC	TTTTATGCCCT	ATGAAATGGG	AATCAGACGA	2100
CAACTCGGCT	ATCCACCTTA	CTATTTT CACG	ATTGGTATTA	CCCTTTCTCA	CAAGAAAGAA	2160
GAAGAGGTTT	TCAAACGTGC	CTATGAAGTC	ATGAACATTT	TGCGGTCAGG	CTTGTCAGAG	2220
ACCAGTCCCA	TTCTGGGGCC	AACGCCAAAA	CCGATTGCCC	GTACCCACAA	CCTCTATCAT	2280
TACCAGATTT	TAATTAAATA	CCGTTTAGAA	GATGAGCTGG	GGCCGACCCCT	CAACCAGGTT	2340
TTAGCCTTGA	CTCAAGAACG	GGAAAATAGT	GAGCTCCGTC	TCAGCATTGA	CCATGAGCCC	2400
CAGCAATTTT	TATAA					2415

(2) INFORMATION FOR SEQ ID NO:1882:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 201 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...201
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1882:

GTTAAGGGAG GATATATTAT TAAGGTAGAT GGAAAGTATT ATGTTTACCT TAAAGATCAA	60
GCTCATGCAG AAAATGTACG AACAAAAGAT GAAATCAATC GCCAAAAACA AGAACATGGT	120
AAAGACGATA AAGGAGCTAG TGCAGAAGTA TCTGTAGCAA AATTACAGGG ACGTTATACT	180
ACCGATGATG GTTATATATA G	201

(2) INFORMATION FOR SEQ ID NO:1883:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1176 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1176
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1883:

AGGTGTCTGG GTAGACAGGT CACTAACGAC AAAGCGTCTG GTCGTTGCTG GATGTTTGCG	60
GCTCTCAACA CCTTCCGCCA CAACTCATC TCGCAATACA AATTGGAGAA CTTTGAGTTG	120
TCACAAGCCC AACTTTCTT CTGGGATAAG TATGAGAAAT CAACTGGTT CTTGGAGCAA	180
GTCATTGCGA CTTCAGACCA AGAATTGACT AGCCGCAAGG TTAGCTTCTT ACTTCAAACA	240
CCTCAACAAG ATGGTGGTCA ATGGGATATG GTCGTTTCCC TCTTTGAAAA ATACGGTGTC	300
GTGCCTAAGT CAGTTTATCC TGAGTCTGTT TCATCTAGCA GCAGTCGTGA GCTAAATGCG	360
ATCCTTAATA AATTGCTTCG TCAAGATGCT CAAATCTTGC GTGACTTGCT TGTTCCTGGT	420
GCAGATCAAG CGACTGTTCA AGCTAAGAAA GAAGACCTCT TGCAAGAAAT CTTTAACTTT	480
CTTGCTATGT CATTAGGACT TCCACCACGC AAGTTTGACT TTGCTTATCG CGATAAAGAT	540
AACAACCTACA AAAGTGAAAA AGGAATCACA CCACAAGAGT TTTACAAGAA ATATGTCAAT	600
CTTCCTTTAG AAGACTACGT TTCTGTTATC AATGCTCCAA CTGCTGATAA ACCTTACGGA	660
AAATCTTACA CAGTTGAGAT GTTGGGGAAT GTGGTTGGTA GCCGTGCAGT TCGTTACATC	720

AACGTTCCAA	TGGAGCGCTT	GAAAGAATTG	GCGATTGCCC	AAATGCAAGC	AGGTGAGACT	780
GTTTGGTTTG	GTTCTGATGT	CGGCCAGCTC	AGTAACCGTA	AGGCTGGCAT	CCTTGCGACA	840
GATGTTTATG	ACTTTGAATC	AAGCATGGAC	ATTAAACTTA	CTCAAGACAA	GGCTGGACGT	900
TTGGACTATA	GCGAAAGCTT	GATGACCCAC	GCCATGGTCT	TGACAGGTGT	TGACTTGGAC	960
GAAATGGTA	AATCAACCAA	GTGGAAGGTT	GAAAACTCAT	GGGAGACAA	GGTCGGTACA	1020
GATGGTTACT	TTGTTGCCTC	AGACGCTTGG	ATGGACGAAT	ACACATACCA	AATCGTTGTT	1080
CGTAAGGAAT	TGCTGACAGC	AGAAGAACAA	GCTGCCTATG	GAGCAGAACC	AATTGTACTT	1140
GCACCATGGG	ATCCAATGGG	AGCCTTGGCT	GAATAA			1176

(2) INFORMATION FOR SEQ ID NO:1884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1884:

AACAGTCTGG	GGAGTGACTG	TTTCAATCGG	GAGATAGAGA	TGAGCTTTAT	TGCTCAGGAC	60
TTTGATAAGC	TCAATATCAT	AACTGTTCTT	GAGAGCAGAA	CACAAGCCAT	CATCCGAAAT	120
CCCATGAATA	CAAGGCTATC	AAGCGATACT	GAAAGCTCAT	TCAACAAGAT	AGTCAGAAAC	180
TGA						183

(2) INFORMATION FOR SEQ ID NO:1885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1885:

AACATCCTGG	GGGTAGGCGA	AATTAAGGAA	ATTATTGAGA	AGGAGGGGGT	GGGAGGGAAT	60
TTTCGAATGC	AAACAGATGT	TGCAGCTCGC	AACAGAGTTA	TTGAGTTGAA	GCCAATTGGA	120
GACGTAGTAG	AGAAACTTGG	TATTTCTTAC	GACGATTTGG	AGTTGTACGG	AAAGTACAAG	180
GCTAAACTCA	GC'TTTGATAA	AA'TTCGGGCA	G'TTGAGAGCA	ATCCAGTCGG	TAAATTGATC	240
TTGGTTACTG	CCATCAACCC	AACACCTGCA	GGTGAAGGAA	AGTCGACGCT	TACCATTGGT	300
CTTGCGGATG	CCTTGAACAA	GATTGGCAAG	AAAACCATGA	TTGCTATCCG	CGAACCGTCT	360
CTTGGTCCAG	TCATGGGGAT	CAAGGGTGGT	GCTGCTGGTG	GTGGGTATGC	ACAAGTTCTG	420
CCAATGGAAG	ACATCAACCT	CCACTTTACT	GGAGATATGC	ATGCTATTAC	AACTGCCAAC	480
AATGCCCTTT	CTGCCTTGAT	TGACAACCAC	TTGCACCAAG	GGAATGAGCT	GGGAATTGAT	540
CAACGTCGTA	TCCTCTGGAA	ACGCGTTGTG	GACTTGAACG	ACCGTGCGCT	CCGCCATGTG	600
ACTGTTGGTC	TTGGTGGTCC	TCTAAACGGT	ATTCCACGTG	AGGATGGTTT	TGATATTACA	660
GTTGCTTTCAG	AAATCATGGC	AATTC'TTTGC	TTGGCAACGG	ACATCGAGGA	CTTGAAACGT	720
CGTTTGGCGA	ATATCGTTAT	TGGTTATCGC	TATGACCGTA	CGCCTGTTTC	TGTAGGTGAT	780
TTGCAGGTTG	AGGGTGCCTT	GGCTTTGATT	TTGATGGATG	CTATTAAGCC	AAACTTGGTT	840
CAGACAATTT	ACGGTACACC	TGCCTTTGTA	CACGGTGGTC	CATTTGCCAA	TATCGCTCAT	900
GGCTGTAACT	CTGTTTGGC	GACGACAACA	GCCCTTCACT	TGGCTGATTA	CACTGTTACT	960
GAAGCTGGTT	TTGGTGCGGA	CCTTGGTGC	GAGAAATTC	TTGATATCAA	GACACCAAAC	1020
TTGCCAACAT	CTCCAGATGC	AGTTGTTATT	GTCGCAACCC	TTCGTGCCCT	TAAGATGAAT	1080
GGTGGTGTGG	CTAAAGACGC	TCTGACTGAA	GAAAATGTAG	AGGCAGTTCG	TGCAGGTTTT	1140
GCTAACTTGA	AACGCCACGT	TGAAAAATATC	CGTAAGTTTCG	GTATTCCAGC	AGTTGTAGCT	1200
ATTAACGAAT	TTGTATCTGA	TACAGAAGCT	GAAATTGCAG	TCTTAAAAGA	ACTCTGTGCC	1260
TCAATCGATG	TACCAGTTGA	ATTGGCTAGT	GTCTGGGCTG	ATGGAGCAGA	AGGTGGAGTA	1320
GCACTTGCCG	AAACAGTTGT	TAAGACAATT	GCTGAAAATC	CAGCTAACTA	TAAACGTTTG	1380
TACGATAATG	ACCTTTCTGT	CCAAGAAAAG	ATTGAAAAAA	TTGTCACTGA	AATCTATCGT	1440
GGTAGCAAAG	TGAAC'TTTGA	GAAGAAATCT	CAAACACAAA	TTGCTCAAAT	CGTTCAAAAC	1500
GGTTGGGACA	AATTGCCAAT	CTGTATGGCT	AAAAC'TCAAT	ACAGTTTCTC	AGACAATCCA	1560
AATGCGCTTG	GAGCACCAGA	AAACTTTGAA	ATTACCATTTC	GTGAATTGGT	ACCAAAATTA	1620
GGTGCAGGCT	TCATCGTTGC	CTTAACTGGT	GATGTTATGA	CCATGCCAGG	TCTTCCAAAA	1680
CGTCCAGCAG	CTCTCAACAT	GGATGTTGAA	AGCGATGGAA	CTGTACTAGG	CTTGTTCTAG	1740

(2) INFORMATION FOR SEQ ID NO:1886:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1886:

TACAAATATGG	GTATGATTTT	AATGAAATTA	GCATCTATTT	TATTATTGAT	ACTGACCTTA	60
GTCGTCTGCA	TTATCCTAAC	CAAACTTTTT	AGATTAAAAA	AACTAGGACG	AAACTTTGCG	120
GATTTGGCTT	TTCCAGTCTT	GGTATTTGAG	TATTACTTGA	TTACAGCTAA	AACCTTTACC	180
CATAATTTCC	TCCCTAGACT	GGGGCTAGCC	CTCTCGTTCC	TAGCCATTAT	TCTCGTCTTT	240
TTCTTCCTTT	TGAAAAAACG	CAGCTTTTAC	TATCCTAAAT	TCATCAAATT	CTTCTGGCGT	300
GCAGGATTCT	TATTAACCCT	TATCATGTAT	ATAGAAATGA	TTGTTGAATT	GTTCTTAATG	360
AAATAG						366

(2) INFORMATION FOR SEQ ID NO:1887:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 189 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...189
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1887:

CTAGATATGG	GTATTAAAAAT	GGAAAAAATT	TTTGTTATTA	TTTTTTTTGT	ATGTCTATTT	60
ATATCATCCA	TAACTTTTTT	AGCCTATGAT	TTTGTTAGCG	AAGAAATAAA	AAAATTGATT	120
ATTTGGATCA	ATGTCGTTTT	TTTGATTTTA	ATCATAGCAA	TGATGATTTA	TCCAAAATTA	180
AGAAAAATGA						189

(2) INFORMATION FOR SEQ ID NO:1888:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1888:

AGACCCATGG	GAATGAAGCA	GGAAGAGGCT	GAGAAGAAGG	CGAGTGGACT	CTTGGAACAG	60
TTAGGACTAG	GAGGACACGC	AGAGGCCTAT	CCTTTCTCAC	TATCTGGTGG	GCAAAAGCAG	120
CGGGTGGCTT	TGGCGCGTGC	TATGATGATT	GACCCAGAAA	TCATTGGCTA	CGATGAACCA	180
ACTTCTGCCC	TGGATCCAGA	ATTACGTTTG	GAAGTGGAGA	AGCTAATCTT	GCAAAATAGG	240
GAAC TTGGGA	TGACCCAGAT	TGTGGTTACC	CATGATTGTC	AGTTTGCTGA	AAATATCGCA	300
GATGTATTAT	TGAAAGTAGA	ACCTAAATAG				330

(2) INFORMATION FOR SEQ ID NO:1889:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1889:

CCCAAAATGG	GCAGAAATTC	AAACATTGAC	CTCTATCTGG	ACCAGGTTTT	GCTCTATGTC	60
AATCAGGTCT	GCGCCCTAT	CTCTCCTAAT	AAAGACAAGG	GCCTAACAGC	ATCTATGGTC	120
AACAATTATG	TGAAAAATGG	TTACCTGACA	AAGCCTGACA	AAAAAAATA	CCAACGCCAA	180
CAGATTGCCC	GTTTGATTGC	TATCACAACC	CTCAAGTCTG	TATTTTCTAT	TCAAGAAATA	240
GCCCAGACAC	TTAATACTCT	ACAAACTCAA	GCAAGTTCAG	ACCAACTCTA	CGATGCTTTT	300
GTGGACTACA	TGAACCAAGG	AATTGACCCA	GCTAACCCTA	TTATCCAAAC	CAGCTGCCAA	360
ACCGTTAAAC	TCTATCATCA	AACTCTAGAC	TTAATCGATC	ATACTCAAGA	GGAGGTAATC	420
CAATGA						426

(2) INFORMATION FOR SEQ ID NO:1890:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1890:

TATGAAATGG	GGGAAGAAGA	GATGAGAAAT	AAAATGATTA	TCGCAGTAAG	TTAGTAGTA	60
GCAGGAGTTA	TGACCTATCT	CATGTTTTCG	GGATTGGATG	AGGATTTCTA	CCATTTTCCT	120
TGGAAGGTCT	TTGCTGGCTT	TGGAATCATG	TCTTGGCTTG	TTAGAGAAGG	TTTGAAATTA	180
GTCAGAGATG	TGAAAAAGGA	GTTTGAAGAA	TGA			213

(2) INFORMATION FOR SEQ ID NO:1891:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 873 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1891:

GTAGAGGTGG	GCTCATGCCT	GCTTCTTGTT	TTTACAGAAG	GAGGACTTAT	GCCTGAATTA	60
CCTGAGGTTG	AAACCGTTTG	TCGTGGTTTA	GAAAAATTGA	TTATAGGAAA	GAAGATTTTCG	120
AGTATAGAAA	TTCGCTACCC	CAAGATGATT	AAGACGGATT	TGGAAGAGTT	TCAAAGGGAA	180
TTGCCTAGTC	AGATTATCGA	GTCAATGGGA	CGTCGTGGAA	AATATTTGCT	TTTTTATCTG	240
ACAGACAAGG	TCTTGATTTC	CCATTTGCGG	ATGGAGGGCA	AGTATTTTAA	CTATCCAGAC	300
CAAGGACCTG	AACGCAAGCA	TGCCCATGTT	TTCTTTCATT	TTGAAGATGG	TGGCACGCTT	360
GTTTATGAGG	ATGTTTCGCA	GTTTGGAAAC	ATGGAACCTC	TGGTGCCTGA	CCTTTTAGAC	420
GCCTACTTTA	TTTCTAAAAA	ATTAGGTCCT	GAACCAAGCG	AACAAGACTT	TGATTTACAG	480
GTCTTTCAAT	CTGCCCTTGC	CAAGTCCAAA	AAGCCTATCA	AATCCCATCT	CCTAGACCAG	540
ACCTTGGTAG	CTGGACTTGG	CAATATCTAT	GTGGATGAGG	TTCTCTGGCG	AGCTCAGGTT	600
CATCCAGCTA	GACCTTCCCA	GACTTTGACA	GCAGAAGAAG	CGACTGCCAT	TCATGACCAG	660
ACCATTGCTG	TTTTGGGCCA	GGCTGTTGAA	AAAGGTGGCT	CCACCATTCG	GACTTATACC	720
AATGCCTTTG	GGGAAGATGG	AAGCATGCAG	GACTTTCATC	AGGTCTATGA	TAAGACTGGT	780
CAAGAATGTG	TACGCTGTGG	TACCATCATT	GAGAAAATTC	AACTAGGCGG	ACGTGGAACC	840
CACTTTTGTC	CAAACTGTCA	AAGGGGGGAC	TGA			873

(2) INFORMATION FOR SEQ ID NO:1892:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...327
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1892:

AACAGTCCGG	GGAGTGACTG	TTTCAATCGG	GAGATGGAGA	TGAGCTTCAT	TGCGCAAGAT	60
TTTAACAATC	TCAATATCAT	CACTGTTCTT	GAGGGAAGAA	CACAAGCTAT	CATTTCGAAAT	120
CACTTTCTTC	GCTACGATAG	AGCCGTCCGA	TGTCGCGTCA	AAATCATTAC	TATGGATATG	180
TTTAGCCCTT	ACTATGGCTT	GGCTAAACAG	CTTCGCTTTC	AAATTTCTAG	GCTCAGGCTG	240
AAACAGTCTC	CCAGACTGTT	TCACTCCCGA	ATGCTAAAAAT	CGTTCTTGAT	CGCTTTCACA	300
TTGTGCAACA	TCTTAGCCGT	GCTATGA				327

(2) INFORMATION FOR SEQ ID NO:1893:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...327
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1893:

AACAGTCCGG	GGAGTGACTG	TTTCAATCGG	GAGATGGAGA	TGAGCTTTAT	TGCGCAAAAT	60
TTTGAAAAGC	TCGATATCAT	CACTGTTCTT	GAAGGTAGAA	CACAAGCTGT	CATCCGAGAT	120
CACTTTCTTA	AATATGATAG	AGCCGTCCGA	TGTCGCGTCA	AAATCATTAC	TATGGATATG	180
TTTAGCCCTT	ACTATGACTT	GGCTAAACAG	CTTCGCTTTC	AAATTTCTAG	GCTCAGGCTG	240
AAACAGTCTC	CTAGACTGTT	TCACTCCCGA	ATGCTAAAAAT	CGTTCTTGAT	CGCTTTCACA	300
TTGTACAACA	TCTTAGCCGT	GCTATGA				327

(2) INFORMATION FOR SEQ ID NO:1894:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...327
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1894:

AACAGTCCGG	GGAGTGACTG	TTTCAATCGG	GAGATGGAGA	TGAGCTTCAT	TGCGCAAGAT	60
TTTAACAATC	TCAATATCAT	CACTGTTCTT	GAGGGAAGAA	CACAAGCTAT	CATTCGAAAT	120
CACTTTCTTC	GCTACGATAG	AGCTGTCCGA	TGTCGCGTCA	AAATTATTAC	TATGGATATG	180
TTTAGCCCTT	ACTATGACTT	GGCTAAACAG	CTTCGCTTTC	AAATTTCTAG	GCTCAGGCTG	240
AAACAGTCTC	CCAGACTGTT	TCACTCCCGA	ATGCTAAAAT	CGTTCTTGAT	CGCTTTCACA	300
TTGTACAACA	TCTTAGCCGT	GCTATGA				327

(2) INFORMATION FOR SEQ ID NO:1895:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...327
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1895:

AACAGTCCGG	GTAGTGACTG	TTTCAATCGG	GAGATGGAGA	TGAGCTTTAT	TGCGCAAGAT	60
TTTGACAAGC	TCAATATCAT	CACTGTTCTT	GAGGGAAGAA	CACAAGCTAT	CATTCGAAAT	120
CACTTTCTTC	GCTACGATAG	AGCCGTCCGA	TGTCGCGTCA	AAATCATTAC	TATGGATATG	180
TTTAGCCCTT	ACTATGGCTT	GGCTAAACAG	CTTCGCTTTC	AAATTTCTAG	GCTCAGGCTG	240
AAACAGTCTC	CCAGACTGTT	TCACTCCCGA	ATGCTAAAAT	CGTTCTTGAT	CGCTTTCACA	300
TTGTACAACA	TCTTAGCCGT	GCTATGA				327

(2) INFORMATION FOR SEQ ID NO:1896:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 801 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...801
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1896:

AACAGTCCGG	GGAGTGACTG	TTTCAATCGG	GAGATGGAGA	TGAGCTTTAT	TGCGCAAGAT	60
TTTGAAAAGC	TCGATATCAT	CACTGTTCTT	GAAGGTAGAA	CACAAGCTGT	CATCCGAGAT	120
CACTTTTCTTA	AATATGATAG	AGCCGTCCGA	TGTCGCGTCA	AAATCATTAC	TATGGATATG	180
TTTAGTCCTT	ACTATGACTT	AGCTAGACAA	CTTTTCCCGT	GTGCTAAAAT	CGTTCTTGAT	240
CGCTTTCACA	TTGTACAACA	TCTTAGCCGT	GCTATGAGTC	GTGTGCATGT	CCAAATCATG	300
AATCAGTTTC	ATCGAAAATC	CCATGAATAC	AAGGCTATCA	AGCGCTACTG	GAAACTCATT	360
CAACAGGATA	GCTGTAAACT	GAGTGATAAG	CGATTTTATC	GTCCTATTTT	TCGTATGCAC	420
TTAACCAATA	AAGAGATTTT	AAACAAGCTT	TTGAGCTATT	CGGAAGACTT	GAAACACCAC	480
TATCAACTCT	ATCAGCTCTT	GCTTTTTTCA	TTCCAGAATA	AGGAACCAGA	GAAATTTTTC	540
GGACTTATTG	AGGACAATCT	TAAGCAGGTT	CATCCTATTT	TTCAGACTGT	CTTTAAAACC	600
TTCTTCAAAG	ATAAAGAAAA	GATTATCAAC	GCCCTTCAAC	TACACTATTG	TAATGCCAAA	660
CTGGAAGCGA	CCAATAATCT	CATCAAACTT	ATCAAGCGCA	ATGCCTTTGG	TTTTTCGAAAC	720
TTTGAAAAC	TCAAAAAACG	GATTTTATATC	GCTCTGAATA	TCAAAAAAGA	AAGGACAAAA	780
TTTGTCTTTT	CTCGAGCTTA	G				801

(2) INFORMATION FOR SEQ ID NO:1897:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1897:

AACAGTCCGG	GGAGTGACTG	TTTCAATCGG	GAGATGGAGA	TGAGCTTTAT	TGCGCAAGAT	60
TTTGAAGAGC	TCGATATCAT	CACTGTTCTT	GAAGGTAGAA	CACAAGCTGT	CATCCGAGAT	120
CACTTTCTTA	AATATGATAG	AGCCGTCCGA	TGTCGCGTCA	AAATCATTAC	TATGGATATG	180
TTTAGCCCTT	ACTATGACTT	GGCTAAACAG	CTTCGCTTTC	AAATTTCTAG	GCTCAGGCTG	240
AAACAGTCTC	CCAGACTGTT	TCACTCCCGA	ATGCTAAAT	CGTTCTTGAT	CGCTTTCACA	300
TTGTGCAACA	TCTTAGCCGT	GCTATGA				327

(2) INFORMATION FOR SEQ ID NO:1898:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1898:

GAGGACACGG	GCTTGTTCCT	GTATAAACTA	TTTTGGAGGA	TTACCCAAGT	CCGGCTGAAG	60
GGAACGGTCT	TGAAAACCGT	CAGGCGTGTA	AAAGCGTGCG	TGGGTTCGAA	TCCCACATCC	120
TCCTTTTATA	TTAACGCGGG	ATGGAGCAGC	TCGGTAGCTC	GTCGGGCTCA	TAACCCGAAG	180
GTCGTAGGTT	CAAATCCTGC	TCCC GCAATA	AGGCTCGGTA	GCTCAGTTGG	TAGAGCAATG	240
GATTGA						246

(2) INFORMATION FOR SEQ ID NO:1899:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1899:

GCTGGAACGG	GATGCTGCGT	GAAAAAGATA	AAACTCCTTG	TATTCGTCGA	ATACTGCGTC	60
AGTTTTTTTCT	CCTACATCCC	AATCTTCGAA	GCCGAGTTGG	AGAGGATATT	ACGACCGTAT	120
GATGTTTTTTG	AAAAAGTATC	GTGGCAATTT	TTAAAGAAGA	TGAGTGTCTT	TCTTCAAACA	180
AAGGGAAGCA	ATCAAAAAGA	GTATTGA				207

(2) INFORMATION FOR SEQ ID NO:1900:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2178 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1900:

TTAGATAAGG	GAAATTTTAT	GGGATTAAAA	CATCTTGAAG	ACGTGACTTA	CTTCCGTCTT	60
AATAACGAAA	TTAACCGTCC	TGTTAATGGA	CAAAATCATGC	TTCATAAAGA	TAAGGAAGCC	120
TTGGATGCTT	TCTTTAAAAGA	AAATGTAGTT	CCAAACACTA	TGGTTTTTTGA	TTCAATCAAA	180
GACAAAATCA	ATTACCTCAT	TGAACACAAC	TACATCGAAA	CAGCCTTTAT	CAAGAAATAC	240
CGTCCAGAGT	TCTTGGAAGA	ATTGGCTCAA	TTTATCAAAG	ACCAAAACTT	CCAATTCAAG	300
TCATTTCATGG	CAGCTTATAA	ATTTTACAAT	CAATATGCCT	TAAAGACTAA	TGACGGTGAA	360
TACTATCTTG	AAAATATGGA	AGACCGTGTC	TTCTTCAACG	CCCTTTTATTT	CGCTGATGGG	420
AATGAAGCTG	TTGCAATCGA	TATTGCCAAT	GAAATCATCC	ACCAACGCTA	CCAACCTGCT	480
ACTCCTTCCT	TCTTGAATGC	TGGACGTGCT	CGTCGTGGGG	AGTTGGTATC	TTGTTTCCTA	540
ATCCAAGTGA	CGGATGATAT	GAACTCTATC	GGACGTTCTA	TCAACTCAGC	TCTTCAACTT	600
TCACGTATTG	GTGGTGGTGT	GGGAATTACC	CTCAGCAACC	TTCGTGAAGC	TGGTGCACCT	660
ATCAAAGGCT	ATGAAGGAGC	TGCTTCAGGT	GTCGTTCCCTG	TTATGAAGCT	TTTTGAAGAC	720
AGCTTCTCTT	ACTCCAACCA	ATTGGGGCAA	CGTCAAGGTG	CTGGTGTTGT	CTACCTCAAC	780
GTCTTTCACC	CAGATATCAT	CGCTTTCCTT	TCAACTAAGA	AAGAAAACGC	TGATGAAAAA	840
GTACGTGTCA	AGACTCTGTC	ACTTGGTGTT	GTAGTACCTG	ATAAATTCTA	CGAATTGGCT	900
CGTAAAAATG	AAGAAATGTA	CCTCTTCAGC	CCTTACTCTG	TAGAAAAAGA	ATACGGTGTG	960
CCATTCAATT	ACATCGACAT	TACTGAAAAA	TACGATGAAT	TGGTCGCAAA	TCCAAATATT	1020
CGCAAGACAA	AAATCAAGGC	GCGGGATTTG	GAAACTGAAA	TCTCTAAATT	GCAACAAGAG	1080
TCTGGCTATC	CTTATGTAGT	CAACATCGAT	ACGGCTAACC	GTGCAAATCC	TGTTGATGGA	1140
AAGATTATCA	TGAGTAACTT	GTGCTCTGAG	ATTCTTCAAG	TTCAAGAACC	AAGCTTGATC	1200
AACGATGCTC	AAGAATTCCT	TCAAATGGGA	ACAGATGTTT	CATGTAACCT	GGGTTCAACC	1260
AACGTGGTTA	ACATGATGAC	TTCACCTGAT	TTTGGTCGTT	CTATCCGTGC	TATGGTTTCGT	1320

GCCCTTACTT	TCGTTACAGA	TAGTTCACAT	ATCGTAGCTG	TACCAACGAT	TGACCATGGA	1380
AATAGCCAAAG	CCCACACCTT	TGGTCTCGGT	GCCATGGGAC	TGCACAGCTA	CCTTGCCCAA	1440
CAACTCATTG	AATATGGTTC	ACCTGAGTCT	GTTGAAATTA	CAAGCATCTA	CTTTATGCTT	1500
ATGAACTACT	GGACCTTGGT	AGAGTCAAAAC	AATATTGCGC	GTGAACGTGG	TATTACCTTC	1560
CACAACTTTG	AAAAATCAGA	CTATGCTAAC	GGAAGTTACT	TTGACAAGTA	TGTAACCTGGT	1620
GAATTTGTTT	CAACATCAGA	CCGTGTTAAA	GAACCTTCA	AAAATGTTTT	TATCCCTGGT	1680
GTTGCTGATT	GGGCTGAACT	TCGCGACAAG	GTTCAAGAAG	ATGGTCTTTA	CCACCAAAAT	1740
CGCCTTGCTG	TAGCGCCAAA	TGGTCTTATC	AGCTATATCA	ACGACGTTTC	TGCTTCTATC	1800
CACCCGATTA	CGCAACGTAT	CGAAGAACGC	CAAGAGAAGA	AAATTGGTAA	AATCTACTAC	1860
CCTGCTGCTG	GCTTGTCTAC	AGAAAACCATT	CCTTACTACA	CTTCTGCCTA	CGATATGGAT	1920
ATGCGTAAAG	TCATCGATGT	TTACGCTGCT	GCGACTGAAC	ACGTGGATCA	AGGACTTTCA	1980
CTCACCTCT	TCATGCGTAG	TGACATTCCA	AAAGGCCCTT	ACGAATGGAA	GAGGGAAAAT	2040
AAACAAACGA	CACGTGACTT	GTCCATCCTT	CGTAACTATG	CCTTTAACAA	GGGAATCAAG	2100
TCTATCTACT	ACGTCCGTAC	CTTTACAGAT	GACGGTGGAG	AAGTCGGCGC	CAACCAATGT	2160
GAAAGCTGTG	TGATTTAG					2178

(2) INFORMATION FOR SEQ ID NO:1901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1901:

ATAGAAAAGG	GAAGTAAGAT	GAACATTCA	AAAGCATTGA	ATGAATGTAT	CGAAAGTGCC	60
TACATGGTTG	CTGGACATTT	TGGAGCTCGT	TATCTAGAGT	CTTGGCACTT	GTTGATTGCC	120
ATGTCTAATC	ACAGTTATAG	TGTAGCAGGG	GCAACTTTAA	ATGATTATCC	GTATGAGATG	180
GACCGTTTAG	AAGAGGTGGC	TTTGGAACTG	ACTGAAACGG	ACTATAGCCA	GGATGAAACC	240
TTTACGGAAT	TGCCGTTCTC	CCGTCGTTTG	CAGTTTCTTT	TTGACGAAGC	AGAGTATGTA	300
GCGTCAGTGG	TCCATGCTAA	GGTGCTAGGG	ACAGAGCACG	TCTTCTATGC	GATTTTGCAT	360
GATGGCAATG	CCTTGGCAAC	TCGTATCTTG	GAGAGGGCTG	GTTTTTCTTA	TGAAGACAAG	420
AAAGATCAGG	TCAAGATTGC	TGCCCTTCGT	CGAAATTTAG	AAGAACGGGC	AGGCTGGACT	480
CGTGAAGACC	TCAAGGCTTT	ACGCCAACGC	CATCGTACAG	TAGCTGACAA	GCAAAATTCT	540
ATGGCCAATA	TGATGGGCAT	GCCGCAGACT	CCTAGTGGTG	GTCTTGAGGA	CTATACGCAT	600
GATTTGACAG	AGCAAGCGCG	TTCTGGCAAG	TTAGAACCAG	TCATCGGTCG	GGACAAGGAA	660
ATCTCACGTA	TGATTCAAAT	CTTGAGCCGT	AAGACTAAGA	ACAACCCTGT	CTTGGTTGGG	720
GATGCTGGTG	TCGGGAAAAC	AGCTCTGGCC	CTTGGTCTTG	CCCAGCGTAT	TGCTAGTGGT	780
GACGTGCCTG	CGGAAATGGC	TAAGATGCCG	GTGTTACAAC	TTGATTTGAT	GAATGTCGTT	840
GCAGGGACAC	GCTTCCGTGG	TGACTTTGAA	GAACGCATGA	ATAATATCAT	CAAGGATATT	900
GAAGAAGATG	GCCAAGTCAT	CCTCTTTATC	GATGAACTCC	ACACCATCAT	GGGTTCTGGT	960
AGCGGGATTG	ATTGCACTCT	GGATGCGGCC	AATATCTTGA	AACCAGCCTT	GGCGCGTGGA	1020
ACTTTGAGAA	CGGTTGGTGC	CACCACTCAG	GAAGAATATC	AAAAACATAT	CGAAAAAGAT	1080

GCGGCTCTTT	CTCGTCGTTT	CGCTAAAAGTG	ACGATTGAAG	AACCAAGTGT	GGCAGATAGT	1140
ATGACTATTT	TACAAGGTTT	GAAGGCGACT	TATGAGAAAC	ATCACCGTGT	ACAAATCACA	1200
GATGAAGCGG	TTGAAACAGC	GGTTAAGATG	GCTCATCGTT	ATTTAACCAG	TCGTCACTTG	1260
CCAGACTCTG	CTATCGACCT	CTTGGACGAA	GCAGCAGCAA	CAGTGCAAAA	TAAGGCAAAG	1320
CATGTAAAAG	CAGACGATTC	AGATTTGAGT	CCAGCTGACA	AGGCCCTGAT	GGATGGCAAG	1380
TGGAAACAGG	CAGCCCAGCT	AATCGCAAAA	GAAGAGGAAG	TACCTGTCTA	CAAAGACTTG	1440
GTGACAGAGT	CTGATATTTT	GACCACCTTG	AGTCGCTTGT	CAGGAATCCC	AGTTCAAAAA	1500
CTGACTCAAA	CGGATGCTAA	GAAGTATTTA	AATCTTGAAG	CAGAACTCCA	TAAACGTGTC	1560
ATCGGTCAAG	ATCAAGCTGT	TTCAAGCATT	AGCCGTGCCA	TTCGCCGTAA	TCAGTCAGGA	1620
ATTCGCAGTC	ACAAGCGTCC	GATCGGTTCC	TTTATGTTCC	TAGGACCCAC	AGGTGTCGGT	1680
AAGACCGAGT	TGGCCAAGGC	TTTGGCAGAA	GTTCTCTTTG	ATGACGAATC	AGCCCTTATC	1740
CGCTTTGATA	TGAGTGAGTA	TATGGAGAAA	TTTCGCAGCCA	GCCGTCTAAA	TGGAGCTCCT	1800
CCAGGCTATG	TGGGTTACGA	AGAAGGTGGG	GAGTTGACAG	AGAAGGTTCC	CAATAAACCC	1860
TATTCCGTTT	TCCTCTTTGA	TGAGGTAGAG	AAGGCCACC	CAGATATCTT	TAATGTTCTC	1920
TTGCAGGTTT	TGGATGACGG	TGTCTTGACA	GATAGCAAGG	GACGCAAGGT	CGATTTTTTCA	1980
AATACCATTA	TCATTATGAC	ATCGAACCTA	GGTGCAGACT	CCTTTCGTGA	TGATAAGACT	2040
GTGGTTTTTG	GGGCTAAGGA	TATTCTTTTT	GACCAGGAAA	ATATGGAAAA	ACGCATGTTT	2100
GAAGAACTGA	AAAAAGCTTA	TAGACCGGAA	TTCATCAACC	GTATTGATGA	GAAGGTGGTC	2160
TTCCATAGCC	TATCTAGTGA	CCATATGCAG	GAAGTGGTGA	AGATTATGGT	CAAGCCTTTA	2220
GTGGCAAAGT	TGGCTGAAAA	AGGCATTGAC	TTGAAATTAC	AAGCTTCAGC	TCTGAAATTG	2280
TTAGCAAATC	AAGGATATGA	CCCAGAGATG	GGAGCTCGCC	CACTTCGCAG	AACCCTGCAA	2340
ACAGAAAGTG	AGGACAAAGT	GGCAGAACTT	CTTCTTAAGG	GAGATTTAGT	GGCAGGCAGC	2400
ACACTTAAGA	TTGGTGTCAA	AGCAGGCCAG	TTAAATTTTG	ATATTGCATA	A	2451

(2) INFORMATION FOR SEQ ID NO:1902:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 768 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...768
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1902:

ATTGTAGAGG	GAATGGTTAT	GAGTAACAAT	ACTAAGTATA	TCTTTTTATC	TCCACATTTA	60
GATGACGCAA	TTTTTTCCTG	TGGTGATTAT	ATTTCAAAAT	TAACTTCAGA	AGGAGAAAAT	120
GTACTTGTTA	TTACTATATT	TTCTGGTTAC	CCTTTGAGCC	AACAGCTACA	GCCCTCTGCT	180
AAGCAATTTT	ATAAGTTGTG	TAACCTTGGG	AAATATCCGA	TTGAAGAAAG	GAAGAAAGAA	240
GACAGGTTAG	CTTGTGAACG	TCTACAGTGT	GATTTTAGAC	ACTTATCGTA	CTATGAATGT	300
CTCTATAGGA	AAGATAGAAA	TGGCAATTTT	CTATACCGTC	ATATCTATAG	TGAATTAAAA	360
AATGAGGACA	CATTAAAGAA	TGATATCATA	AAAGAGCTGT	TAATGCATTT	AGACGACAAA	420
TGTGTCGTAT	ATTGTCCGCT	TTCACTTGGT	GACCATATTG	ATCATGTTTT	TGTGAATAGT	480
ATTGGAAGGG	CGCTTGAATT	TATGCGTTAT	AAAGTAATAT	ATTATGAGGA	CTTCCCATAT	540
GTAAGTGATA	GTAGTATGGT	TAGTTATATG	GGAAAACTA	AAGAATTAAA	AATGTATCAA	600

GAGGAACTTG	ATGAAAAACA	TTATATTGAT	AGAATATCAT	CAATATTGTG	CTATAAATCT	660
CAGATTTTGA	TAATCTGGAA	ATCAGTTGAA	AAACTTTTAA	ACAATATTAA	AGAGTTGTAT	720
TTAAGGAATG	GGGCAGCTTA	TTCTATTAGA	TTTTGGATTA	AGAAATAA		768

(2) INFORMATION FOR SEQ ID NO:1903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...6717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1903:

TATAAGGAGG	GTTTTATGGG	GAAAGGCCAT	TGGAATCGGA	AAAGAGTTTA	TAGCATTCGT	60
AAGTTTGCTG	TGGGAGCTTG	CTCAGTAATG	ATTGGGACTT	GTGCAGTTCT	ATTAGGAGGA	120
AATATAGCTG	GAGAATCTGT	AGTTTATGCG	GATGAAACAC	TTATTACTCA	TACTGCTGAG	180
AAACCTAAAG	AGGAAAAAAT	GATAGTAGAA	GAAAAGGCTG	ATAAAGCTTT	GGAAACTAAA	240
AATGTAGTTG	AAAGGACAGA	ACAAAGTGAA	CCTAGTTCAA	CTGAGGCTAT	TGCATCTGAG	300
AAGAAAGAAG	ATGAAGCCGT	AACTCCAAAA	GAGGAAAAAG	TGTCTGCTAA	ACCGGAAGAA	360
AAAGCTCCAA	GGATAGAATC	ACAAGCTTCA	AGTCAAGAAA	AACCGCTCAA	GGAAGATGCT	420
AAAGCTGTAA	CAAAATGAAGA	AGTGAATCAA	ATGATTGAAG	ACAGGAAAAGT	GGATTTTAAT	480
CAAAATTGGT	ACTTTAAACT	CAATGCAAAT	TCTAAGGAAG	CCATTAAACC	TGATGCAGAC	540
GTATCTACGT	GGAAAAAATT	AGATTTACCG	TATGACTGGA	GTATCTTTAA	CGATTTTCGAT	600
CATGAATCTC	CTGCACAAAA	TGAAGGTGGA	CAGCTCAACG	GTGGGGAAGC	TTGGTATCGC	660
AAGACTTTCA	AACTAGATGA	AAAAGACCTC	AAGAAAAATG	TTCGCCTTAC	TTTTGATGGC	720
GTCTATATGG	ATTCTCAAGT	TTATGTCAAT	GGTCAGTTAG	TGGGGCATT	TCCAAATGGT	780
TATAACCAGT	TCTCATACGA	TATCACCAAA	TACCTTCACA	AAGATGGTCG	TGAGAATGTG	840
ATTGCTGTCC	ATGCAGTCAA	CAAACAGCCA	AGTAGCCGTT	GGTATTCAGG	AAGTGGTATC	900
TATCGTGATG	TGACTTTACA	AGTGACAGAT	AAGGTGCATG	TTGAGAAAAA	TGGGACAAC	960
ATTTTAACAC	CAAAACTTGA	AGAACAACAA	CATGGCAAGG	TTGAAACTCA	TGTGACCAGC	1020
AAAATCGTCA	ATACGGACGA	CAAAGACCAT	GAACTTGTAG	CCGAATATCA	AATCGTTGAA	1080
CGAGGTGGTC	ATGCTGTAAC	AGGCTTAGTT	CGTACAGCGA	GTCGTACCTT	AAAAGCACAT	1140
GAATCAACAA	GCCTAGATGC	GATTTTAGAA	GTTGAAAGAC	CAAACTCTG	GACCGTTTTA	1200
AATGACAAAC	CTGCCTTGTA	CGAATTGATT	ACGCGTGT	ACCGTGACGG	TCAATTGGTT	1260
GATGCTAAGA	AGGATTGT	TGGTTACCGT	TACTATCACT	GGACTCCAAA	TGAAGGTTTC	1320
TCTTTGAATG	GTGAACGTAT	TAAATCCAT	GGAGTATCCT	TGCACCACGA	CCATGGGGCG	1380
CTTGGAGCAG	AAGAAACTA	TAAAGCAGAA	TATCGCCGTC	TCAAACAAAT	GAAGGAGATG	1440
GGAGTTAACT	CCATCCGTAC	AACCCACAAC	CCTGCTAGTG	AGCAAACCTT	GCAAATCGCA	1500
GCAGAACTAG	GTTTACTCGT	TCAGGAAGAG	GCCTTTGATA	CGTGGTATGG	TGGCAAGAAA	1560
CCTTATGACT	ATGGACGTTT	CTTTGAAAAA	GATGCCACTC	ACCCAGAAGC	TCGAAAAGGT	1620
GAAAAATGGT	CTGATTTTGA	CCTACGTACC	ATGGTCGAAA	GAGGCCAAAA	CAACCTTGCT	1680
ATCTTCATGT	GGTCAATTGG	TAATGAAATA	GGTGAAGCTA	ATGGTGATGC	CCACTCTTTA	1740
GCAACTGTTA	AACGTTTGGT	TAAGGTTATC	AAGGATGTTG	ATAAGACTCG	CTATGTTACC	1800

ATGGGAGCAG	ATAAATTCCG	TTTCGGTAAT	GGTAGCGGAG	GGCATGAGAA	AATTGCTGAT	1860
GAACCTGATG	CTGTTGGATT	TAACATTTCT	GAAGATAATT	ACAAAGCCCT	TAGAGCTAAG	1920
CATCCAAAAT	GGTTGATTTA	TGGATCAGAA	ACATCTTCAG	CTACCCGTAC	ACGTGGAAGT	1980
TACTATCGCC	CTGAACGTGA	ATTGAAACAT	AGCAATGGAC	CTGAGCGTAA	TTATGAACAG	2040
TCAGATTATG	GAAATGATCG	TGTGGGTTGG	GGGAAAACAG	CAACCGCTTC	ATGGACTTTT	2100
GACCGTGACA	ACGCTGGCTA	TGCTGGACAG	TTTATCTGGA	CAGGTACGGA	CTATATTGGT	2160
GAACCTACAC	CATGGCACAA	CCAAAATCAA	ACTCCTGTTA	AGAGCTCTTA	CTTTGGTATC	2220
GTAGATACAG	CCGGCATTCC	AAAACATGAC	TTCTATCTCT	ACCAAAGCCA	ATGGGTTTCT	2280
GTTAAGAAGA	AACCGATGGT	ACACCTTCTT	CCTCACTGGA	ACTGGGAAAA	CAAAGAATT	2340
GCATCCAAAG	TAGCTGACTC	AGAAGGTAAG	ATTCCAGTTC	GTGCTTATTC	GAATGCTTCT	2400
AGTGTAGAAT	TGTTCTTGAA	TGGAAAATCT	CTTGGTCTTA	AGACTTTCAA	TAAAAACAA	2460
ACCAGCGATG	GGCGGACTTA	CCAAGAAGGT	GCAAATGCTA	ATGAACTTTA	TCTTGAATGG	2520
AAAGTTGCCT	ATCAACCAGG	TACCTTGGAA	GCAATTGCTC	GTGATGAATC	TGGCAAGGAA	2580
ATTGCTCGAG	ATAAGATTAC	GACTGCTGGT	AAGCCAGCGG	CAGTTCGTCT	TATTAAGGAA	2640
GACCATGCGA	TTGCAGCAGA	TGGAAAAGAC	TTGACTTACA	TCTACTATGA	AATTGTTGAC	2700
AGCCATGGGA	ATGTGGTTCC	AACTGCTAAT	AATCTGGTTC	GCTTCCAATT	GCATGGCCAA	2760
GGTCAACTGG	TCGGTGTAGA	TAACGGAGAA	CAAGCCAGTC	GTGAACGCTA	TAAGGCGCAA	2820
GCAGATGGTT	CTTGGATTCT	TAAAGCATTT	AATGGTAAAG	GTGTTGCCAT	TGTCAAATCA	2880
ACTGAACAAG	CAGGGAAAAT	CACCCTTACT	GCCCCACTCT	ATCTCTTGAA	ATCGAACC	2940
GTCACGTCT	TTACTGGTAA	GAAAGAAGGA	CAAGAGAAGA	CTGTTTTGGG	GACAGAAGTG	3000
CCAAAAGTAC	AGACCATTAT	TGGAGAGGCA	CCTGAAATGC	CTACCACTGT	TCCGTTTGTA	3060
TACAGTGATG	GTAGCCGTGC	AGAACGTCTT	GTAACCTGGT	CTTCAGTAGA	TGTGAGCAAG	3120
CCTGGTATTG	TAACGGTGAA	AGGTATGGCT	GACGGACGAG	AAGTAGAAGC	TCGTGTAGAA	3180
GTGATTGCTC	TTAAATCAGA	GCTACCAGTT	TGAAACGTA	TTGCTCCAAA	TACTGACTTG	3240
AATTCTGTAG	ACAAATCTGT	TTCTTATGTT	TTGACTGATG	GAAAGTGTGA	AGAGTATGAA	3300
GTGGACAAGT	GGGAGATTGC	CGAAGAAGAT	AAAGCTAAGT	TAGCAATTCC	AGGTTCTCGT	3360
ATTCAAGCGA	CCGGTTATTT	AGAAGGTCAA	CCAATTCATG	CAACCCTTGT	GGTAGAAGAA	3420
GGCAATCCTG	CGGCACCTGC	AGTACCAACT	GTAACGGTTG	GTGGTGAAGC	TGTCACAGGT	3480
CTTACTAGTC	AAAAACCAAT	GCAATACCGC	ACTCTTGCTT	ATGGAGCTAA	GTTGCCAGAA	3540
GTCACAGCAA	GTGCTAAAAA	TGCAGCTGTT	ACAGTTCTTC	AAGCAAGCGC	AGCAAACGGC	3600
ATGCGTGCGA	GCATCTTTAT	TCAGCCTAAA	GATGGTGGCC	CTCTTCAAAC	CTATGCAATT	3660
CAATTCCTTG	AAGAAGCGCC	AAAAATTGCT	CACCTTGAGCT	TGCAAGTGGA	AAAAGCTGAC	3720
AGTCTCAAAG	AAGACCAAAC	TGTCAAATTG	TCGGTTCGAG	CTCACTATCA	AGATGGAACG	3780
CAAGCTGTAT	TACCAGCTGA	TAAAGTAACC	TTCTCTACAA	GTGGTGAAGG	GGAAGTCGCA	3840
ATTCGTAAAG	GAATGCTTGA	GTTGCATAAG	CCAGGAGCAG	TCACCTTGAA	CGCTGAATAT	3900
GAGGGAGCTA	AAGGCCAAGT	TGAACTCACT	ATCCAAGCCA	ATACTGAGAA	GAAGATTGCG	3960
CAATCCATCC	GTCCTGTAAA	TGTAGTGACA	GATTTGCATC	AGGAACCAAG	TCTTCCAGCA	4020
ACAGTAACAG	TTGAGTATGA	CAAAGGTTTC	CCTAAAACTC	ATAAAGTCAC	TTGGCAAGCT	4080
ATTCCGAAAG	AAAAACTAGA	CTCCTATCAA	ACATTTGAAG	TACTAGGTAA	AGTTGAAGGA	4140
ATTGACCTTG	AAGCGCGTGC	AAAAGTCTCT	GTAGAAGGTA	TCGTTTCAGT	TGAAGAAGTC	4200
AGTGTGACAA	CTCCAATCGC	AGAAGCACCA	CAATTACCAG	AAAGTGTTCC	GACATATGAT	4260
TCAAATGGTG	ACGTTTCATC	AGCTAAGGTT	GCAATGGGATG	CGATTCTGCC	AGAGCAATAC	4320
GCTAAGGAAG	GTGTCTTTAC	AGTTAATGGT	CGCTTAGAAG	GTACTCAATT	AACAACATAA	4380
CTTCATGTTT	GCGTATCTGC	TCAAACTGAG	CAAGGTGCAA	ACATTTCTGA	CCAATGGACC	4440
GGTTCAGAAT	TGCCACTTGC	CTTTGCTTCA	GATTCAAATC	CAAGCGACCC	AGTTTCAAAT	4500
GTTAATGACA	AGCTCATTTT	CTACAATAAC	CAACCAGCCA	ATCGTTGGAC	AAACTGGAAT	4560
CGTAGTAATC	CAGAAGCTTC	AGTCGGTGTC	CTATTCCGAG	ATTCAGGTAT	TTTGAGCAAA	4620
CGTTCAGTTG	ATAACTTAAG	CGTTGGCTTC	CATGAAGACC	ATGGAGTTGG	TGCACCGAAG	4680
TCTTATGTGA	TTGAGTATTA	TGTTGGTAAG	ACTGTCCCAA	CAGCTCCTAA	AAACCCTAGT	4740
TTTGTGGTGA	ATGAGGACCA	TGTCTTTAAT	GATTCTGCCA	ACTGGAAACC	AGTTACTAAT	4800
CTAAAAGCCC	CTGCTCAACT	CAAGGCTGGA	GAAATGAACC	ACTTTAGCTT	TGATAAAGTT	4860
GAAACCTATG	CTGTTTCGTAT	TCGCATGGTG	AGAGCAGACA	ACAAACTAGG	AACGTCTATC	4920
ACAGAGGTAC	AAATCTTTGC	GAAACAAGTT	GCGGCAGCCA	AGCAAGGACA	AACAAGAATC	4980
CAAGTTGACG	GTAAAGACTT	AGCAAACTTC	AACCCGTGATC	TGACAGACTA	CTACCTTGAG	5040
TCTGTAGATG	GAAAAGTTCC	GGCAGTCACA	GCAAGTGTTA	GCAACAAATG	TCTCGCTACC	5100
GTCGTTCCAA	GCGTTCGTGA	AGGTGAGCCA	GTTGCTGTCA	TCGCGAAAGC	TGAAAATGGC	5160
GACATCTTAG	GAGAATACCG	TCTGCACTTC	ACTAAGGATA	AGAACTTACT	TTCTCATAAA	5220

CCAGTTGCTG	CGGTTAAACA	AGCTCGCTTG	CTACAAGTAG	GTCAAGCACT	TGAATTGCCG	5280
ACTAAGGTTT	CAGTTTACTT	CACAGGTAAA	GACGGCTACG	AAACAAAAGA	TTTGTCAGTT	5340
GAATGGGAAG	AAGTTCCAGC	AGAAAATCTG	ACAAAAGCAG	GTCAATTTAC	CGTTCGAGGC	5400
CATGTCCTTG	GTAAGTATCT	TGTTGCTGAG	GTCACGTGAC	GAGTGACAGA	CAAAC TAGGC	5460
GAAGCTCTTT	CAGATAACCC	TAACATATGAT	GAAAACAGTA	ACCAGGCCTT	TGCTTCAGCA	5520
ACCAATGATA	TTGACAAAAA	CTCTCATGAC	CGCGTTGACT	ATCTCAATGA	CGGAGATCAT	5580
TCAGAAAAATC	GTCGTTGGAC	AAACTGGTCT	CCAACACCAT	CTTCTAATCC	AGAAGTATCA	5640
GCGGGTGTGA	TCTTCCGTGA	AAATGGTAAG	ATTGTAGAAC	GGACTGTTGC	GCAAGCCAAA	5700
CTTCACTTCT	TTGCAGATAG	TGGTACGGAT	GCACCAACTA	AACTCGTTTT	AGAACGCTAT	5760
GTCGGTCCAG	AGTTTGAAGT	GCCAACCTAC	TATTCAAAC	ACCAAGCCTA	CGACGCAGAC	5820
CATCCATTCA	ACAATCCAGA	AAATGGGAA	GCTGTGCCTT	ATCGTGCGGA	TAAAGACATC	5880
GCAGCTGGTG	ATGAAATCAA	CGTAACATTT	AAAGCTGTCA	AAGCCAAAGC	TATGAGATGG	5940
CGTATGGAGC	GTAAAGCAGA	TAAGAGCGGT	GTTGCGATGA	TTGAGATGAC	CTTCCTTGCA	6000
CCAAGTGAAT	TGCCCTAAGA	AAGCACGCAA	TCGAAGATTC	TTGTAGATGG	AAAAGAACTT	6060
GCTGATTTTCG	CTGAAAATCG	TCAAGACTAT	CAAATTACCT	ATAAAGGTCA	ACGGCCAAAA	6120
GTCTCAGTTG	AAGAAAACAA	TCAAGTAGCT	TCAACTGTGG	TAGATAGTGG	AGAAGATAGC	6180
CTTCCAGTAC	TTGTTGCGCT	CGTTTCAGAA	AGTGGAAAAC	AAGTCAAGGA	ATACCGTATC	6240
CACTTGACTA	AGGAAAAACC	AGTTTCTGAG	AAGACAGTTG	CTGCTGTACA	AGAAGATCTT	6300
CCAAAACCTCG	AATTTGTTGA	AAAAGATTTG	GCCTACAAGA	CAGTTGAGAA	AAAAGATTCA	6360
ACACTGTATC	TAGGTGAAAC	TCGTGTAGAA	CAAGAAGGAA	AAACTGGTAA	AGAACGTATC	6420
TTTACAGCGA	TTAATCCTGA	TGGAAGTAAG	GAAGAAAAAC	TCCGTGAAGT	GGTAGAAGCT	6480
CCGACAGACC	GCATCGTCTT	GGTTGGAACC	AAACCAGTAG	CTCAAGAAGC	TAAAAAACCA	6540
CAAGTGTGAG	AAAAAGCAGA	TACAAAACCA	ATTGATTCAA	GTGAAGCTAG	TCAAAC TAAT	6600
AAAGCCCAGT	TACCAAATAC	AGGTAGTGCG	GCAAGCCAAG	CAGCAGTAGC	AGCAGGTTTA	6660
GCTCTTCTAG	GTTTGAGTGC	AGGATTAGTA	GTTACTAAAG	GTAAAAAAGA	AGACTAG	6717

(2) INFORMATION FOR SEQ ID NO:1904:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1904:

GGGGGCGGGG	GAATTCANAC	CGTGGTCAAG	ATGCTCTATC	TGCATGCTCT	GGATCAGGTG	60
CAAGCACTAA	AGGTGAGAAG	ACATTCTCAT	ACATTTATGA	GACAGACCCT	GATAACCTCA	120
ACTATTTGAC	AACTGCTAAG	GCTGCGACAG	CAAATATTAC	CAGTAACGTG	GTTGATGGTT	180
TGCTAGAAAA	TGATCGCTAC	GGGAACTTTG	TGCCGTCTAT	GGCTGAGGAT	TGGTCTGTAT	240
CCAAGGATGG	ATTGACTTAC	ACTTATACTA	TCCGTAAGGA	TGCAAAATGG	TATACTTCTG	300
AAGGTGAAGA	ATACGCGGCA	GTCAAAGCTC	AAGACTTTGT	AACAGGACTA	AAATATGCTG	360
CTGATAAAAA	ATCAGATGCT	CTTTACCTTG	TTCAAGAATC	AATCAAAGGG	TTGGATGCCT	420
ATGTAAGAGG	GGAAATCAAA	GATTTCTCAC	AAGTAGGAAT	TAAGGCTTTG	GATGATCAGA	480

CAGTTCAGTA	CACTTTGAAC	AAACCAGAAA	GCTTCTGGAA	TTCTAAGACA	ACCATGGGTG	540
TGCTTGCGCC	AGTTAATGAA	GAGTTTTTGA	ATTCAAAAGG	AGATGATTTT	GCCAAAGCTA	600
CGGATCCAAG	TAGTCTCTTG	TATAATGGAC	CTTATTTGTT	GAAATCCATT	GTGACCAAAT	660
CTTCTGTTGA	ATTTGCGAAA	AATCCGAAC	ACTGGGATAA	GGACAATGTG	CATATTGACA	720
AAGTTAAATT	GTCATTCTGG	GATGGTCAAG	ATACCAGCAA	ACCTGCAGAA	AACTTTAAAG	780
ATGGTAGCCT	TACAGCAGCT	CGTCTCTATC	CAACAAGTGC	AAGTTTCGCA	GAGCTTGAGA	840
AGAGTATGAA	GGACAATATT	GTCATATCTC	AACAAGACTC	TATTACGTAT	CTAGTTGGTA	900
CAAATATTGA	CCGTCAGTCC	TATAAATACA	CATCTAAGAC	CAGCGACGAA	CAAAAGGCAT	960
CGACTAAAAA	GGCTCTCTTA	AACAAGGATT	TCCGTCAGGC	TATTGCCTTT	GGTTTTGATC	1020
GTACAGCCTA	TGCCTCTCAG	TTGAATGGAC	AAACTGGAGC	AAGTAAAATC	TTGCGTAATC	1080
TCTTTGTGCC	ACCAACATTT	GTTCAAGCAG	ATGGTAAAAA	CTTTGGCGAT	ATGGTCAAAG	1140
AGAAATTGGT	CACTTATGGG	GATGAATGGA	AGGATGTTAA	TCTTGCAGAT	TCTCAGGATG	1200
GTCTTTACAA	TACAGAAAAA	GGCAAGGCTG	AGATTTGCTA	A		1241

(2) INFORMATION FOR SEQ ID NO:1905:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...276
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1905:

ACCATTAGGG	GACCGTGTGC	TCTTAAAAAT	AGAAGACAAA	GAACAAACCG	TTGGGGGGCTT	60
TGTCCTTGCA	GGCTCAGCCA	AGAAAAAACC	AAAACAGCTC	AAGTTGTGGC	TACTGGACAA	120
GGTGTTCGTA	CCTTGAACGG	TGACTTGGTT	GCTCCAAGTG	TTAAAACTGG	AGATCGTGTC	180
TTAGTTGAAG	CCCACGCAGG	TCTTGATGTC	AAAGATGGCG	ATGAAAAGTA	CATCATCGTA	240
GGCGAAGCTA	ACATTTTGGC	AATCATTGAG	GAATAG			276

(2) INFORMATION FOR SEQ ID NO:1906:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1906:

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CAGAAATAGGG GAGAAAACAT GTCAAAGACA TATCATTTTA TCGGAATTAA GGGATCAGGG      60
ATGAGTGCCT TGGCCTTGAT GTTGCACCAG ATGGGGCACA AGGTTTCAGGG ATCAGATGTT      120
GAAAAGTACT ACTTTACCCA ACGCGGTCTT GAGCAGGCAG GAATTACCAT TCTTCCTTTT      180
GATGAAAAGA ATCTAGACGG TGATATGGAA ATTATCGCTG GAAATGCCTT TCGTCCAGAT      240
AACACGTCG AAATTGCCTA TGC GGACCAA AATGGTATCA GCTACAAACG TTACCATGAG      300
TTTCTAGGTA GCTTTATGCG TGACTTTGTT AGCATGGGAG TAGCAGGAGC ACATGGAAAA      360
ACTTCAACGA CAGGTATGTT GTCTCATGTC TTGTCTCACA TTACAGATAC CAGCTTCTTG      420
ATTGGAGATG GGACAGGTCG TGGTTCGGCT AATGCCAAAT ATTTTGTCCT TGAATCTGAC      480
GAATATGAGC GTCACCTTCAT GCCTTACCAC CCAGAATACT CTATTATCAC CAACATTGAC      540
TTTGACCATC CAGATTATTT CACAAGTCTC GAGGATGTTT TCAATGCCTT TAACGACTAT      600
GCCAAACAAA TTACCAAGGG TCTTTTGTGTC TATGGTGAAG ATGCTGAATT GCGTAAGATT      660
ACGTCTGATG CACCAATTTA TTATTATGGT TTTGAAGCTG AAGGCAATGA CTTTGTAGCT      720
AGTGATCTTC TTCGTTCAAC AACTGGTTCA ACCTTCACCG TTCATTTCCG TGGACAAAAC      780
TTGGGGCAAT TCCACATTCC AACCTTTGGT CGTCACAATA TCATGAATGC GACAGCCGTT      840
ATTGGTCTTC TTTACACAGC AGGATTTGAT TTGAACTTGG TCGGTGAGCA CTTGAAAACA      900
TTTGCCGGTG TTAAACGTCG TTTCACTGAG AAAATTGTCA ATGATACAGT GATTATCGAT      960
GACTTTGCCC ACCATCCAAC AGAAATTATT GCGACCTTGG ATGCGGCTCG TCAGAAATAC     1020
CCAAGCAAGG AAATTGTAGC AGTCTTTCAA CCGCATACCT TTACAAGAAC CATTGCCTTG     1080
TTGGACGACT TTGCCCATGC TTTAAACCAA GCAGATGCTG TTTATCTAGC GCAAATTTAT     1140
GGCTCGGCTC GTGAAGTAGA TCATGGTGAC GTTAAGGTAG AAGACCTAGC CAATAAAATC     1200
AACAAAAAAC ACCAAGTGAT TACTGTTGAA AATGTTTCTC CACTCCTAGA CCATGACAAT     1260
GCTGTTTACG TCTTTATGGG AGCAGGAGAC ATCCAAACCT ATGAATACTC ATTTGAGCGT     1320
CTCTTGCTTA ACTTGACAAG CAATGTTCAA TAG                                     1353
```

(2) INFORMATION FOR SEQ ID NO:1907:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1907:

```
AAAAACAGGG GTAAAATCAA AATGACAGTA TTAAAAGGAG ATAACTTAGA AATATTAAAA      60
```

ACTATTGAAT	CCTCAAGTAT	TGATTTAATC	TATATGGACC	CTCCTTTCTT	TACACAGAAA	120
ACCCAAAAAT	TATCTAATAA	CAAAAATATT	ATGTATTTCAT	TCGAAGATAC	GTGGACTTCG	180
ATTGAGGATT	ACAAAGAAAT	TTTGTCTGTA	AGATTAGAAG	AATGCAAAAG	AGTGCTAAAA	240
AATAGTGGA	GTATTTTCGT	TCATTGTGAT	AAAATTGCAA	ATCATCATAT	TAGATTAATT	300
TTAGATAATA	TCTTTGGAGC	AGATATGTTT	CAAAGCGAAA	TTATATGGAA	CTATAAGCGG	360
TGGTCTAATT	CAAAAAAGGG	ATTATTGAAC	AATCATCAAA	ACATTTACTT	TTATTCAAAG	420
TCAAAAAGATT	TTAAATTTAA	TACAATTTTT	ACAGAGTATT	CTTCTACTAC	AAATATCGAC	480
CAAATACTAG	TGGAACGAAA	ACGAGATGGA	AACCTCTAAA	CTATATATAA	AGTTGATAAT	540
AATGGTAACT	ATATTCTAGC	AAAAGAGAAA	AATGGAGTTC	CCCTTTCAGA	TGTTTGGAAT	600
ATACCATTTT	TTAATCCAAA	AGCTAAAGAA	AGAGTAGGTT	ATCCTACACA	AAAACCTATT	660
CTGTTATTAG	AACAAATTAT	AAAGATTGCT	ACTGATAAAA	ATGATATAGT	TTTAGACCCG	720
TTCTGTGGAA	GTGGAACACT	TTTAGTAGCC	TCCAAGATTT	TGAATAGAAA	TTATATGGGG	780
ATTGATTTAT	CTGAGGAAGC	TATCAATATA	ACTCAGCAAC	GTCTGGAAAA	TGTTATAAAA	840
ACAAGTTCAA	ATTTATTGAA	TAAAGGAATC	GAAGCATATA	GAACCAAAAC	TGAGGAAGAG	900
GAAAACATTC	TTAAATTTAT	ACAGGCAAAA	ATTGTTCAAA	GAAATAAAGG	AATTGATGGT	960
TTTTTACCTA	AACATTTTCA	AAAAAAACCG	ATACCTATAA	TAATTCCAAA	AAATAATGAA	1020
TGCTCTGAATG	AGAGTATCTC	TTTATTACAG	AAGGCTATAA	ACTCCAAAAG	AATTGAATTG	1080
TGGAGTATTA	TAAAAAACCC	TTCCGATAAT	TTATTATGTG	ATTTTGAAAC	CATTCCCTGA	1140

(2) INFORMATION FOR SEQ ID NO:1908:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1908:

AGGTCAAGGG	GTTCAAGAGC	TGGAAGAAAT	GAAATCCAAC	CATCATCTTC	GCCCTACTGT	60
AGAGGAGAGA	CAAAATGTTAA	CTTCAGTTGT	AGAAAGATTA	AGTCAGGAAT	TGGAGGAAAC	120
AGAATGATGA	GAAGTACGAA	AGAATTACGG	CATGTATATA	GAGACTTCCT	TTTAGAGGCT	180
AATCAAAGTT	ATTCTGATAT	AGTAGCTTGA	GAAGCCGATT	TGTCAAGTTC	GATGGCTACT	240
CATAATCTTG	AAAAGGACTT	CGGAGACCGT	TATGTGAATG	TTGGGATTAT	GGAAGCAGAA	300
ATGGTCGGCC	TTGCAGCAGG	CTTGTCTATT	CAGGGGTTTA	GACCTTATCT	TCATACATTT	360
GGTCCTTTTG	CTTCACGAAG	AGTATTTGAT	CAATTATTTA	TTTCTCTTGG	ATACGCACAA	420
TTGGATGCCA	CTGTGATTGG	ATCAGATGCA	GGAGTAACTG	CAGAAATGAA	TGGTGGGACA	480
CATATGCCAT	TTGAAGAAAT	TGGATTGTTA	CGTTTAATTC	CTAAATCGAT	CATTTTTTGAA	540
GCAACTGATG	ATATCCAATT	TCGTGAAATA	TTGAACCAGA	CATTAGACTT	AAAAGGACTA	600
AAATATATTC	GAACAATTAG	AAAAGCTCCA	GTTCTGTGTG	ATCAAGGTGG	AGAAGATTTT	660
TCTAAAGGCT	ACATTGAGTT	AAGGCATGGT	GAAGATCTTG	TAATCGTTGC	TTCTGGTATA	720
ATGGTTGCTC	CAAGTATTCG	AGTTGCAGAT	GAAGTGCTTA	AATTAGGTTA	TTCAAGTAAGT	780
GTGATAGATT	TATTTAGAAT	CAAACCGATA	CCAGAACAGA	TAAAAACAAT	GTTAAGTGGA	840
AAAACATATAT	TTACTGTAGA	AAATCACAAAT	CAGATAGGTG	GAATTGGCAG	TGCTTTATGT	900

GAATTATTCT CTGATGATGG AATAACAAAA ATTCATCGGA TGGGTGTTCA AGAAAGATTC	960
GGTCAAGTAG GGAAAAATGGA TTATCTTCTT AATGAGTATG GTTTGAGTGA ATCGAATATA	1020
AAAGAGAAGG TTCTAGAAAT TTATAATGCA AGATAG	1056

(2) INFORMATION FOR SEQ ID NO:1909:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...432
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1909:

GAGAAAAGGG GGTGCTCTTG CTTGATTAAAG AGAGGAGATG TTGTAGCTCT TTATTTGCCT	60
TTTCCGACTA TTAGTAGCGA TTTGGCTGTG AAGAATCATA TGTATATCTG TATTGACAAC	120
AGCATGACTA AAAACAAAGA GCTGGTTAAA AATCAGACCT TCAAACCAGC TCTCTTGACC	180
AGACGTTTGG TCAAGAACTT TATGATAGAA GAGCCGGATC TAGCTCGTAA TCCTTTTACA	240
AGACCAACCT TGATTGACTT AGATAAGGTA TTTATGTTGG ATAATACGGT CATTCCGACT	300
TCTTATTTAG CCAGACGGCG ACGCAATGTC TCAGAAGAAT TGTACGAGGA AATTTTGGAT	360
TACTTAGTCC AACCACGGCT GATTTCGCTG AACAAGTCTG AGTTTATGCA ACTCAATCCA	420
GGAACCTATT AG	432

(2) INFORMATION FOR SEQ ID NO:1910:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1910:

AATGGAAGGG	GAGGGATTCG	AACCCCCGAA	CCCGAAGGAG	CGGATTTACA	GTCCGCCGCG	60
TTTAGCCTCT	TCGCTACCCT	TCCAAAATAT	ATAAATGGCG	CGAGACGGAA	TCGAACCGCC	120
GACACATGGA	GCTTCAATCC	ATTGCTCTAC	CAACTGAGCT	ACCGAGCCTT	ATTGCGGGAG	180
CAGGATTTGA	ACCTACGACC	TTCGGGTTAT	GAGCCCACG	AGCTACCGAG	CTGCTCCATC	240
CCGCGTTAA						249

(2) INFORMATION FOR SEQ ID NO:1911:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1536 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1536

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1911:

GATGTGAGGG	GGAGTTTTAT	GTTTAAAGTT	TTACAAAAAG	TTGGAAAAGC	TTTTATGTTA	60
CCTATAGCTA	TACTTCCTGC	AGCAGGTCTA	CTTTTGGGGA	TTGGTGGTGC	ACTTTCAAAC	120
CCAACCACGA	TAGCAACTTA	TCCAATACTA	GACAATAGTA	TTTTTCAATC	AATATTCCAA	180
GTAATGAGCT	CTGCAGGAGA	GGTTGTATTTC	AGTAATTTGT	CACTACTTCT	CTGTGTGGGA	240
TTATGTATTG	GCTTAGCGAA	ACGAGATAAA	GGAACCGCTG	CGTTAGCAGG	AGTAACTGGT	300
TACTTAGTTA	TGACTGCAAC	GATCAAAGCT	TTAGTAAAAC	TTTTTATGGC	AGAAGGATCT	360
GCAATTGATA	CTGGAGTTAT	TGGAGCATT	GTTGTCCGAA	TAGTTGCCGT	ATATTTGCAC	420
AACCGATATA	ACAATATTCA	ATTACCTTCC	GCTTTAGGAT	TCTTTGGAGG	TTCACGCTTC	480
GTTCCATTG	TTACATCGTT	CTCTTCTATC	TTGATTGGCT	TTGTCTTCTT	TGTTATTTGG	540
CCACCTTTCC	AACAACTTCT	TGTTTCTACA	GGTGGATATA	TTTCTCAGGC	GGGTCCAATT	600
GGAACTTTTC	TATATGGATT	TTTAATGAGA	CTTTCTGGAG	CAGTAGGCTT	ACATCATATA	660
ATTTACCCTA	TGTTTTGGTA	TACTGAACTT	GGTGGTGTTG	AAACTATTGC	AGGACAAACA	720
GTGGTTGGAG	CTCAAAAAAT	ATTTTTTGCT	CAATTAGCCG	ATCCGGCCCA	TTCTGGATTA	780
TTTACAGAAG	GAACAAGGTT	TTTTGCAGGT	CGTTTCTCAA	CAATGATGTT	CGGTTTACCG	840
GCTGCCTGTT	TAGCGATGTA	CCATAGTGTT	CCTAAAAATC	GTCGTAAAAA	ATACGCGGGT	900
TTGTTTTTTG	GAGTTGCTTT	AACATCTTTT	ATTACCGGTA	TTACAGAACC	AATTGAATTT	960
ATGTTTCTAT	TCGTCAGTCC	GGTTCATAT	GTTGTTACG	CATTCCCTGA	TGGTGTTAGC	1020
TTCTTTATTG	CAGACGTCTT	AAATATTTCA	ATAGGAAACA	CATTTTCAGG	AGGTGTAATC	1080
GATTTCACTT	TATTTGGAAT	TTTGCAGGGG	AACGCTAAGA	CGAATTGGGT	TC TTCAGATT	1140
CCAATTGGAC	TTATTTGGAG	TGTTTTGTAT	TATATTATTT	TTAGATGGTT	CATTACTCAA	1200
TTCAACGTTT	TAACGCCAGG	ACGAGGAGAA	GAAGTAGATT	CTAAAGAAAT	TTCTGAATCC	1260
GCAGATTCAA	CTTCAAATAC	TGCAGATTAT	TTAAACAGG	ATAGCCTACA	AATTATCAGA	1320
GCGTTGGGTG	GATCAAATAA	TATAGAAGAT	GTAGATGCTT	GTGTGACACG	TTTACGTGTA	1380
GCTGTAAAAA	AAGTTAATCA	AGTTGATAAA	GCACTTTTAA	AACAAATTGG	TGCAGTTGAT	1440
GTCTTAGAAG	TGAAGGGTGG	CATTCAAGCA	ATCTATGGAG	CAAAAGCAAT	CTTATATAAA	1500
AATAGTATTA	ATGAAATTTT	AGGTGTAGAT	GATTAA			1536

(2) INFORMATION FOR SEQ ID NO:1912:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 639 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...639
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1912:

TATAAAATTT	TGAATATAGA	GAGTTTTCTG	ACAATGAATC	AATCCTACTT	TTATCTAAAA	60
ATGAAAGAAC	ACAAACTCAA	GGTTCATTAT	ACAGGTAAGG	AGCGCCGTGT	ACGTATTCTT	120
CTTCCTAAAG	ATTATGAGAA	AGATACAGAC	CGTTCCTATC	CTGTTGTATA	CTTTCATGAC	180
GGGCAAAATG	TTTTTAATAG	CAAAGAGTCT	TTCATTGGAC	ATTCATGGAA	GATTATCCCA	240
GCTATCAAAC	GAAATCCGGA	TATCAGTCGC	ATGATTGTCT	TTGCTATTGA	CAATGATGGT	300
ATGGGGCGGA	TGAATGAGTA	TGCGGCTTGG	AAGTTCCAAG	AATCTCCTAT	CCCAGGGCAG	360
CAGTTTGGTG	GTAAGGGTGT	GGAGTATGCT	GAGTTTGTCA	TGGAGGTGGT	CAAGCCTTTT	420
ATCGATGAGA	CCTATCGTAC	AAAAGCAGAC	TGCCAGCATA	CGGCTATGAT	TGGTTCCTCA	480
CTAGGAGGCA	ATATACCCAG	TTTATCGGTT	TGGAATACCA	AGACCAAATT	GGTTGCCTGG	540
GCGTTTTTTC	ATCTGCAAAC	TGGCTCCACC	AAGAAGCCTT	TAACCGCTAT	ATCGAGTGCC	600
AGAAACTATC	GCCTGACCAG	CGCATCTTCA	TCTATGTAG			639

(2) INFORMATION FOR SEQ ID NO:1913:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 942 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1913:

TTATTTTTTA	TTAAGGAGTA	TTCAATGTCT	AAGAAATTAA	CATTTCAAGA	AATTATTTTG	60
ACTTTGCAAC	AATTTTGGAA	TGACCAAGGT	TGTATGCTTA	TGCAGGCTTA	TGATAATGAA	120
AAAGGTGCGG	GAACAATGAG	TCCTTACACT	TTCCTTCGTG	CTATCGGACC	TGAGCCATGG	180
AATGCAGCTT	ATGTAGAGCC	ATCACGTCGT	CCTGCTGACG	GTCTTTATGG	GGAAAACCCCT	240
AACCGTCTCT	ACCAACACCA	CCAATTCCAG	GTGGTCATGA	AGCCTTCTCC	ATCAAATATC	300
CAAGAACTTT	ACCTTGAGTC	TTTGGAAAAA	TTGGGAATCA	ATCCTTTGGA	GCACGATATT	360
CGTTTTGTTG	AGGACAACCTG	GGAAAACCCA	TCAACTGGTT	CAGCTGGTCT	TGGTTGGGAA	420
GTTTGGCTTG	ACGGAATGGA	AATCACTCAG	TTCACCTATT	TCCAACAAGT	CGGTGGATTG	480
GCAACTGGCC	CTGTGACTGC	GGAAGTTACC	TATGGTTTGG	AGCGCTTGGC	TTCTTACATT	540
CAAGAAGTAG	ACTCTGTCTA	TGATATCGAG	TGGGCTAATG	GTGTAAAATA	CGGAGAAATC	600
TTTATCCAGC	CTGAGTATGA	GCACTCAAAA	TATTCATTTG	AAATTTTCGA	CCAAGAAATG	660
TTGCTTGAAA	ACTTTGATAA	GTTTGAAAAA	GAAGCTGGTC	GTGCATTAGA	AGAAGGCTTG	720
GTACACCCTG	CCTATGACTA	TGTTCTCAAA	TGTTACACATA	CCTTTAATCT	GCTTGACGCG	780
CGTGGTGCCG	TATCTGTAAC	AGAGCGTGCA	GGCTATATCG	CTCGTATCCG	TAACCTGGCC	840
CGTGTGTAG	CCAAAACCTT	TGTTGCAGAA	CGCAAACGCC	TAGGTTACCC	ACTTTTGGAT	900
GAAGAAACAC	GAGTTAAACT	TTTAGCAGAA	GACGCAGAAT	AG		942

(2) INFORMATION FOR SEQ ID NO:1914:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1914:

GAAAAAATTT	TGGAGGGTAT	CCGTATGAAA	ATTGTTGGTG	TTGCAGCTTG	TACTGTGGAA	60
ATTGCCCAACA	CTTATATTGC	ACAGGAAAAA	TTAGAGAATG	CCGCAAAGGT	AGCTGGACAT	120
GTGATTCATG	TTGAGACTCA	GGGGACAATA	GGGGTAGAAA	ATGAATTGAG	TCAAGAGCAG	180
ATTGATGCAG	CGGATGTAGT	TATTTTAGCA	GTTGATGTTA	AGATTTCTGG	TATGGAACGC	240
TTTGAGGGTA	AAAAGATTAT	CAAGGTTCCA	ACAGAAAGTG	CAGTCAAATC	TCCCAATAAA	300
CTGATTGCTA	AAGCTGTTGA	GATTGTTACG	AAATAA			336

(2) INFORMATION FOR SEQ ID NO:1915:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1915:

ATTATTTT	TGAATATT	GG GTTAACATTT	GAACATTATT	CAAGTAAGCG	TTCACATATT	60
GAATAATAA	AACGTGGGGA	TTATAATAAA	GTAAATCAAG	GACGAAGAGA	GAAGAAAAAT	120
GGAAGCGGT	TTAGCAATAG	ATTTAGGTGC	GACTTCTGGA	AGAGCAATCG	TTGGTTACCT	180
TTCTGA						186

(2) INFORMATION FOR SEQ ID NO:1916:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 888 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1916:

GGAGTTTT	TGAAAAACAA	ATTTTTTCTA	ATAGCTATTT	TAGCTATGTG	TATAGTTTTT	60
AGCGCTTG	TTCTAATTC	TGTTAAAAAT	GAAGAAAAATA	CTTCTAAAGA	GCATGCGCCT	120
GATAAAATAG	TTTGTAGATCA	TGCTTTCGGT	CAAACTATAT	TAGATAAAAA	ACCTGAAAGA	180
GTTGCAACTA	TTGCTTGGGG	AAATCATGAT	GTAGCATTAG	CTTTAGGAAT	AGTTCCTGTT	240
GGATTTTCAA	AAGCAAATTA	CGGTGTAAGT	GCTGATAAAG	GAGTTTACC	ATGGACAGAA	300
GAATAATCA	AAGAACTAAA	TGGTAAAGCT	AACCTATTTG	ACGATTTGGA	TGGACTTAAC	360
TTTGAAGCAA	TATCAAATTC	TAAACCAGAT	GTTATCTTAG	CAGGTTATTC	TGGTATAACT	420
AAAGAAGATT	ATGACACTCT	ATCAAAAAAT	GCTCCTGTAG	CAGCATACAA	ATCTAAACCT	480
TGGCAAACTT	TATGGAGAGA	TATGATTAAA	ATTGATTCAA	AAGCCTTAGG	TATGGAAAAA	540
GAAGGTGATG	AGTTAATCAA	AAATACTGAA	GCTCGTATAT	CCAAAGAATT	AGAAAAACAT	600
CCAGAAATCA	AAGGAAAAAT	CAAAGGAAAA	AAAGTATTAT	TTACTATGAT	TAATGCTGCA	660
GATACATCAA	AATTCTGGAT	TTATACTAGC	AAAGATCCAA	GAGCAAATTA	TTTAACAGAT	720

TTAGGTCTAG TTTTCCCTGA ATCATTAAAA GAATTTGAGA GTGAAGATAG TTTTGCAAAG	780
GAAATTTCTG CAGAAGAAGC AAATAAGATA AATGATGCTG ATGTAATCAT AACTTATGGT	840
GATGATAAAA CTCTTGAAGC TTTACAAAAA GGATCCTCTT TTAGGTAA	888

(2) INFORMATION FOR SEQ ID NO:1917:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...267
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1917:

AATCCTTTTA TCCTCATTA CACGAACCAT GATGACTCAG GCAAGCAATA TATGGAGCAG	60
ATTCGAATTG TTCGCCAGAC CTTGCAGAAAT CGTGATTGGA ATGAGAAAAAT TAAAAAGACG	120
GTTTCGAGGAT TTATGATTGA ATCTTACCTA GCAGATGGTC GTCAAAACCA ACCAGAGGTC	180
TTTGGTTGCT CTATTACTGA CCCTTGCCTA GGTGTTGGAAA ATACAGAGGC CTTGGTAGAA	240
GAGATTTATG TTACCTTGAC AAAATAA	267

(2) INFORMATION FOR SEQ ID NO:1918:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...327
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1918:

CTCACTTTTA TCAACTGGTT CTTTAGTACC AATACCCTTT ATTTTATCTT CTGGTTTCGG	60
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TGTTTCCTCT	ACAGCCTTCT	CTTCAGGAGC	TTCTGGTTGC	TTTTCTGGAG	AGACTGGTGC	120
CTTTTCGTCT	TCACTTGGCT	CGACTGGTTC	ACCTACTTGT	TCAACTTTTG	GTTCCGTTTG	180
TTTTTCTACA	GCAGGCGTTT	CAACTTTTGG	TTCTTCAACA	GGTTGATTAG	CAGCCTCATC	240
TTTTGTTTCT	ACTACTTCTG	GCTGTGTATC	TTCTTGTTTC	GGTGTATCTT	CCGCTCCCCT	300
ATCTTCTTTA	GGATCTTCTG	GTTGTGA				327

(2) INFORMATION FOR SEQ ID NO:1919:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...336
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1919:

AGGTTTTTCT	TTTTTTTAAA	AGGAAAACGA	GAACAGGAGG	TTCTTATGAA	AGCAAGCATT	60
GCCTTGCAAG	TTTTACCCCT	AGCACAGGGG	ATTGATCGGA	TAGCTGTTAT	TGATCAGGTC	120
ATTGCTTATC	TGCAAACTCA	AGAAGTGACG	ATGGTAGTGA	CACCATTTGA	AACGGTCTTG	180
GAAGGGGAGT	TTGATGAGCT	TATGCGCATT	CTAAAAGAAG	CGCTGGAAGT	GGCAGGGCAG	240
GAGGCAGACA	ATGTCTTTGC	CAATGTCAAA	ATAAATGTAG	GAGAGATTTT	AAGTATTGAT	300
GAGAAACTTG	AAAAGTATAC	TGAGACGACA	CATTAG			336

(2) INFORMATION FOR SEQ ID NO:1920:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 207 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1920:

AATCATTTTA	TACTCTTCGA	AAATCTCTTC	AAACCACGTC	AGCTTCACCT	TGCAGTATAT	60
ATGTTACTGA	CTTCGTCAGT	TCTATCCACA	ACCTCAAAAC	GGTGTTTTGA	GCTGACTTCG	120
TCAGTTCTAT	CCACAACCTC	AAAACACTGT	TTTAAGCAAC	CTGCGGCTAG	CTTCCTAGTT	180
TGCTCTTTGA	TTTTCATTGA	GTATTAG				207

(2) INFORMATION FOR SEQ ID NO:1921:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1921:

AAGAATTTTA	TGACTGATAT	TAAAACTTTG	GCTCTAAAGT	ATGGAGGTTA	TACAAGTCTG	60
GACAAGGTCT	ATCTGGATCA	GCTTCTAGCT	GGTAAAACAG	ATCAGGAGCA	GTTAACTACT	120
ATTACACCTC	CGCCAAGTGT	TGTTAATGCC	TACTTTGCAG	AACTCTATCA	GAAAAAGAGT	180
CCTCAGGCTG	CGACGGATTA	TTTTCAGAG	CTCAGTCAGG	AACTGAATCT	TTACAATACT	240
GAGCCAAGTT	TCACCCTAGA	AAATAAGCCT	TTTATTCGGC	TTAATCTGTC	TGGTAAATCC	300
TTTGGTTTTT	GTTATGAGAG	TGACGGCCCT	GGTCGGATTT	TCTTTGAAAA	TGAGGAGAAA	360
ATCTCGGATG	ACTTGCTCTT	TGAAATTGCG	CAAAATTTCC	CCCATCAATT	AGTCTTTGAA	420
GAGTCTGGTA	AGATTTACAT	GAAGCCTGTC	GAGGACGAGG	AAGTTATCAG	CCTAGAAAGT	480
CTCACAGCTT	TGACTGATTT	GGAAAGATTG	GCTGATGGTC	GAAAACGTCT	CAAAGGCTAC	540
AGCCAAGAGG	ATTTATTGCA	AGAAGCTGCT	GCTTTTCTG	GCAAACGCTA	TTTCCGATCG	600
GAAAACCGCA	CAGCCATGTT	ATATATTGAT	TAA			633

(2) INFORMATION FOR SEQ ID NO:1922:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1922:

AAGGTTTTCT	TACTCATATC	AAAGGCACGA	ACCACTCCTA	AAAGATTATT	GGTTGTCAAC	60
ACCAAATCTG	CTGACTCGAT	GGCGATATCT	GTTCCAGCTC	CCATAGCAAT	CCCCACATCT	120
GCTACACTAA	GGGCAGGAGC	GTCATTGATA	CCGTCCCCAA	CAAAGGCTAC	TTTCCCTGAC	180
TGTTGCAGTT	TATGGATTTT	ATGGGCTTTT	TCTTCTGGCA	AGACGCCTGC	AATGACCTCT	240
TCAATTCGGA	TTTGA					255

(2) INFORMATION FOR SEQ ID NO:1923:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1923:

GGAGTATTTA	TGAAATTAAA	ATTATTAAGA	GTAATACTA	AGGTGATTAT	GGGGAGTTTC	60
TTACTTGTTT	TGTCTAGTCT	ACTTGCTTTG	TTGCTTCCCC	TTATCTTAAA	GGGTTTAATA	120
GATGGGAGTT	CTATTGAAAA	TATAGGTTCC	AAAGTATTTT	AATCGTTTTT	GATTTTTATT	180
GGTCAAGCCT	TGTTTTCTTC	TATTGGTTAC	TATCTGTTTA	GTCAATCGGG	TGAAAAAAG	240
ATAGCAAAAA	TCAGGAAAAA	AGTGATAGAG	GGGTTGATTT	ATGCAGAGAA	ATCCTTCCTT	300
GATAAGAGCC	AAAGTGGGGA	GTTGACTTCT	GCCATTGTCA	ATGACATGAG	TGTCATTCTG	360
GAGTTTTTAA	TTACGACTTT	CCCAAATATT	ATTCTGAGTT	TAGTTATGGT	ACTTGGTTCC	420
ATTGTAGTCT	TATTTAGTCT	TGATTGGAAT	CTTTCTCTAC	TTTTATTTCAT	CACCTTCCT	480
TGTATGATGT	TTATTATCTT	GCCCCCTTCC	AATATCAGTG	AAAAGTATAG	TCGTCGTTTA	540
CAGGAGGAAA	TTTAA					555

(2) INFORMATION FOR SEQ ID NO:1924:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1029 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1924:

AAAAGATTTA	TTTTTAAAC	AAAAATGAAA	CGTTTCAAAA	AAGAAATAAA	GAGACAGCGC	60
CAAGCGCTAT	CTTTTCTAGA	AAAAATGAAA	CGTTTCAAAA	AGGAGGTTGC	TATGAATAGC	120
AAAGCGAAGC	AAGTTTCTCT	TTGGGAAAGA	ATCAAGAAAC	AAAAACTCTT	GTTATTGATG	180
ACTGTCCCCG	GTTTAGTTTT	AACCTTTTATC	TTTAAATACA	TCCCTATGTA	TGGGGTTTTA	240
ATCGCATTTA	AAGATTACAA	TCCTTTAAAA	GGAATTTTAG	GGAGTGATTG	GATTGGTTTT	300
TCTGAGTTTA	CAAAATTCAT	ATCCTCTCCC	AACCTTTGGTA	TCTTGTTAGC	CAACACATTA	360
AAATTAAGTA	TCTATGGTTT	ATTGCTTGGC	TTTTTACCAC	CAATCATTTCT	TGCTATTATG	420
CTCAATCAAC	TCTTGAGTGA	AAAAGTCAAA	AAACGAATTC	AGCTCATTTT	ATACGCACCA	480
AACCTTATCT	CAGTCGTTGT	TATTGTCGGT	ATGATTTTCC	TCTTCTTTTC	AGTGGGAGGA	540
CCAATCAACA	ATTTTCTTTC	TATGTTTGGA	ATGAAGGCTG	ACTTCTTGAC	AAATCCAGAC	600
TTCTTTAGAC	CCTTATACAT	CTTTAGTGGT	ATCTGGCAAG	GAATGGGCTG	GGCTTCAACG	660
CTCTACACGG	CAACATTTGGT	AAATGTAGAT	CCAGCCTTAG	TAGAAGCAGC	CCGACTGGAT	720
GGAGCCAATA	TCTTCCAACG	AATCTGGCAC	ATTGATATTC	CAGCTCTTAA	GCCTATTATG	780
GTTATCCAAT	TTGTTTTAGC	TGCAGGTGGA	ATTATGAATG	TCGGATATGA	AAAAGCATTC	840
TTGATGCAGA	CATCGTTAAA	TTTGCCAACT	TCTGAAATTA	TCTCGACATA	TGTCTATAAA	900
GTTGGTCTTG	TATCAGGAGA	CTATTCTTAC	TCAACAGCGG	TTGGTTTGTT	TAATGCAGTG	960
ATTCACGTAG	TATTGCTTGT	TGCAGTTAAC	CAAATCGTTA	AACGCATGAA	TAATGGTGAA	1020
GGAATTTAA						1029

(2) INFORMATION FOR SEQ ID NO:1925:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1925:

AAAGGATTTA	TGAAACACCT	ATTATCTTAC	TTCAAACCCT	ACATCAAGGA	ATCAATTTTA	60
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GCCCCCTTGT	TCAAGCTGTT	AGAAGCTGTT	TTTGAGCTCT	TGGTTCCCAT	GGTGATTGCT	120
GGGATTGTTG	ACCAATCTTT	ACCTCAGGGA	GATCAAGGTC	ATCTCTGGAT	GCAGATTGGC	180
CTGCTCCTTA	TCTTTGCAGT	AATTGGCGTT	TTAGTGGCCT	TGATAGCTCA	ATTTTACTCA	240
GCAAAGGCAG	CAGTAGGCTT	GGCTATAGGA	ATTGACAAAC	GATCTTTATC	GTCATATTCT	300
TTCTTGCCC	AAGCATAG					318

(2) INFORMATION FOR SEQ ID NO:1926:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...315
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1926:

AGCCATTTCT	TTGGGGGGAA	AAAAAGGGGG	GAATTGAGTG	ATTTTTTTGA	GGAAGAAGGA	60
GGTTTCCACC	CACCCTTAAT	TTTTGGACAC	CATGTACCCC	ATTTGAAAAC	GAACTTTTTT	120
AGAGGGGATT	TTGGGGGGGG	CAACACCTTT	TTTTTCAAAG	AAGGGGAATT	AGAGGGGGTT	180
TTGAAAAAAA	ATTTTTTTTT	TAAAGAAACT	CCACAACGAG	GAACAGGGGG	GTTTTTCGTC	240
CCCCGGGGGG	GGGATTCCTC	CGGGGTCTCC	CTCCTGGAGG	GAGGATGTAA	AAAGTGGGGA	300
TGTGAGGTTC	TTTAA					315

(2) INFORMATION FOR SEQ ID NO:1927:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 546 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1927:

TGGCTTCTTA	TCATCTGCTT	GTGGCTTGCT	ATTATCTGGT	TTTGGTTTTT	CTGGTTGCGG	60
TTTAACCTCT	GGTTTTGGTT	TTTCTGGTTG	CGGTTTAACC	TCTGGTTTTG	GTTTTTCCGG	120
CTGCGGTTTA	ACCTCTGGTT	TTGGTTTTTC	CGGCTGCGGT	TTAACCTCTG	GTTTTGGTTT	180
TTCCGGCTGC	GGTTTAACCT	CTGGTTTTGG	TTTTTCCGGC	TGCGGTTTAA	CCTCTGGTTT	240
TGGTTTTTCC	GGCTGCGGTT	TAACCTCTGG	TTTTTGGTTTT	TCCGGCTGCG	GTTTAACCTC	300
TGGTTTTGGT	TTTTCCGGCT	GCGGTTTAAC	CTCTGGTTTT	GGTTTTTCCG	GCTGCGGTTT	360
AACCTCTGGT	TTTGGTTTTT	CCGGCTGCGG	TTTAACCTCT	GGTTTTGGTT	TTTCTGGTTG	420
CGGTTTAACC	TCTGGTTTTG	GTTTTTCCAG	CTGCGGTTTA	ACCTCTGGTT	GAGGACTTGG	480
TTGCATACCT	GGTTTTGGAG	CAGATGGTTT	TTTGTTACCT	GGTTCTTTTT	GTGTGTCCTG	540
AGTTAA						546

(2) INFORMATION FOR SEQ ID NO:1928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 963 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1928:

GAAATTCTTA	TGTCTATTAG	CCAACGTACG	ACCAAGCTCA	TCTTAGCTAC	CTGTCTTGCC	60
TGCCTGCTTG	CTTATTTTCT	CAATCTTTCG	TCAGCAGTTT	CGGCTGGAAT	TATCGCTCTC	120
TTGAGCCTAT	CTGATACGCG	TAGAAGTACT	TTAAAACTGG	CTCGCAATCG	TCTTTTTTCT	180
ATGCTTCTAG	CTCTGGCTAT	CGGTGTTCTA	GCTTTTCACT	TGAGCGGATT	TCATATCTGG	240
AGTCTCGGCC	TCTATCTGGC	CTTCTACGTT	CCTTTAGCCT	ACAAGATGGG	CTGGGAAATT	300
GGCATCACAC	CAAGCACTGT	TTTGGTTAGC	CATCTCTTGG	TTCAAGAGTC	AACCTCTCCA	360
GACCTTCTAG	TCAATGAATT	CCTTCTCTTT	GCTATTGGTA	CAGGATTTGC	CTTGCTTGTT	420
AATCTCTATA	TGCCTTCACG	AGAAGAGGAA	ATCCAGCACT	ACCACACGCT	GGTGGGAAGAA	480
AAGTTAAAAG	ATATCCTCCA	GCGCTTCAAA	TACTATTTAT	CCAGAGGAGA	CGGACGCAAC	540
CGAGCACAGC	TGGTAGCAGA	ATTAGACACG	CTTTTGAAAG	AAGCCCTCAG	ACTGGTCTAT	600
TTGGATCACT	CTGACCACCT	CTTTCACCAG	ACCGACTACC	ATATCCACTA	CTTTGAGATG	660
AGACAGCGAC	AAAGTCGTAT	CCTGAGAAAC	ATGGCCCAAC	AGATTAAACAC	TTGTCACCTT	720
GCCGCCAGTG	AAAGCCTGAT	CTTAGCGCAA	CTCTTTTCAA	AAATTGCAGG	TCAACTGAGC	780
CAGACCAATC	CTGCTTCTGA	TTTGCTAGAT	GAAATTGAAC	GTTATCTGGA	AGTCTTCCGG	840
AACCGCAGTC	TGCCCAAAAC	AAGAGAAGAG	TTTGAAACCC	GCGCCACCCT	TCTTCAACTC	900
CTACGTGAAG	CCAAAACCTT	CATCCAAGTA	AAAGTTGATT	TTTACCAAAA	ATATAGACAG	960
TAA						963

(2) INFORMATION FOR SEQ ID NO:1929:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 954 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...954
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1929:

AGATATCTTA	TACAAAGAGG	TATTCATATG	TCTATTTATA	ACAACATTAC	TGAATTAATC	60
GGTCAAACAC	CGATTGTTAA	ACTTAACAAC	ATCGTGCCAG	AAGGTGCTGC	AGACGTCTAT	120
ATAAAGCTTG	AAGCATTTAA	TCCTGGTTCA	TCTGTAAAAG	ACCGTATTGC	CCTTAGCATG	180
ATTGAAAAAG	CTGAACAAGA	TGGTATTCTG	AAACCTGGTT	CTACTATTGT	TGAAGCAACA	240
AGTGGAAACA	CTGGTATTGG	ACTTTCATGG	GTAGGTGCTG	CTAAAGGGTA	TAAAGTCGTC	300
ATCGTTATGC	CTGAAACTAT	GAGTGTAGAA	CGACGTAAAA	TTATCCAAGC	TTATGGTGCT	360
GAACTCGTCC	TAACTCCTGG	TAGCGAGGGA	ATGAAAGGTG	CTATTGCTAA	GGCTCAAGAA	420
ATCGTGCTG	AACGTGATGG	TTTCCTTCCT	CTTCAATTTG	ACAATCCAGC	TAATCCAGAA	480
GTACACGAAA	GAACAACAGG	AGCTGAGATA	CTAGCTGCTT	TCGGTAAAGA	TGGATTAGAT	540
GCCTTTGTTG	CTGGAGTAGG	TACCGGTGGA	ACGATTTCCTG	GTGTTTCTCA	TGCACTCAAA	600
TCAGAAAATT	CTAACATTCA	AGTTTATGCA	GTGGAAGCTG	ATGAATCTGC	TATTCTATCT	660
GGTGAAAAAC	CTGGTCCTCA	CAAAATTCAA	GGTATCTCAG	CTGGATTTAT	TCCTGATACA	720
CTTGATACTA	AAGCCTATGA	TGGTATCGTT	CGTGTAACAT	CAGATGATGC	TCTTGCACTC	780
GGACGTGAAA	TTGGTGGA	AGAAGGCTTC	CTTGTAGGGA	TTTCCTCAGC	TGCAGCTATC	840
TACGGAGCCA	TCGAGGTTGC	CAAAAAATTA	GGTACAGGTA	AAAAAGTCCT	TGCTCTAGCA	900
CCAGATAACG	GTGAACGTTA	TCTCTCTACA	GCACTCTATG	AATTTGAAGT	TTAG	954

(2) INFORMATION FOR SEQ ID NO:1930:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 801 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1930:

GTGGATTTCT	TTATGAAGAG	GTTTGAAGTA	TCTACAGAAA	TTGGTAGTCT	CTCTGTTGCT	60
TATCAAAAGC	AAAAGAAAGT	GCTAGTTTGT	CTAAATGGAG	CAGGTTTGCT	ACCAAGTTAT	120
GAAAATTTTT	CACTTATACT	TGAAAAACCT	CCTCCTACAA	TTGGTTATTT	GACAATTGAT	180
TTTCCGAACA	CAGGTAGGAG	TCCGATTTAT	GACCAAGCTG	GAAAAAATCT	AGATAATCTT	240
GCAGATGTGG	TTTATGAAGC	ACTTGAAGAA	TTAGGGATTT	CTGAATATAT	ACTTTGTGTA	300
CATAGTTGGA	GTGGAATTTT	AGCTTGCAAA	TTACTCGAGA	AACCAATTAA	GTGTCAGACT	360
TTAGTAGTAA	TTGAACCGAC	AACTAAAAAA	GTCATGTTTG	CTGATTTTTT	AGAAAATCCT	420
TATCCAGAAA	TGGAAGAGCA	GATGAGGCTG	ATTGACGAGT	GTGGTCCTGA	ACTTTATTTT	480
AAGAACTTAA	CTCAAGCAAC	ATTTAGTCCT	GAAACGAATA	AAAAAATCTG	GGAATTAATG	540
CAAGAAAAAG	GCTTAGAGTT	GGAAAATCAA	GATCCAGAAT	TTCAGATATC	TGGAGAGATT	600
ACTGAGGAAG	ATTTTGAGAA	TTTGTGCGATA	GAATCTCATG	TCCCTGTATT	TATTTTTTGT	660
CAGACTTATA	GAGAAAAAGA	GTACAGAGAA	TCAGAAATATT	GGACTTCCAA	TACTAAACTC	720
ATTTTAGGAG	GGAATCACCA	TTATTTACAA	TGGTCAGAAT	CGGAAAAAAT	TGCGGCTATT	780
ATTTCGAGAAT	TGTCAGAATA	A				801

(2) INFORMATION FOR SEQ ID NO:1931:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1968 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1931:

AATGGTCTTA	TGAATAAAAG	AATGAATGAG	TTAGTCGCTT	TGCTCAATCG	CTATGCGACT	60
GAGTACTATA	CCAGCGATAA	TCCCTCGGTT	TCAGACAGTG	AGTATGACCG	CCTTTACCGT	120
GAGTTGGTCG	AGTTAGAAAC	TGCTTATCCA	GAGCAAGTGC	TAGCAGACAG	TCCGACTCAT	180
CGTGTGGTG	GCAAGGTTTT	AGATGGTTTT	GAAAAATACA	GTCATCAGTA	TCCTCTTTAT	240
AGTTTGACAG	ATGCTTTTTT	ACGTGAGGAG	CTAGATGCTT	TTGATGCGCG	TGTTTCGTAAG	300
GAAGTGGCTC	ATCCGACCTA	TATTTGTGAG	CTGAAAATCG	ATGGCTTATC	TATCTCGCTG	360
ACTTATGAAA	AGGGGATTTT	GGTTGCTGGG	GTAACACGTG	GAGATGGTTC	AATTGGTGAA	420
AATATCACAG	AAAACCTCAA	GCGTGTTAAG	GACATCCCTT	TGACTTTGCC	AGAAGAACTA	480
GATATCACAG	TTCGTGGGGA	ATGTTACATG	CCACGCGCTT	CCTTTGACCA	AGTTAACCAA	540
GTGCGCCAAG	AAAATGGAGA	GCCTGAATTT	GCTAATCCTC	GTAATGCGGC	AGCAGGAACT	600
CTGCGTCAGT	TGGATACAGC	AGTAGTTGCC	AAGCGTAATC	TTGCAACGTT	TCTCTATCAA	660
GAAGCCAGCC	CTTCAACTCG	TGATAGCCAA	GAAAAGGGTT	TGAAGTACCT	AGAACAACTA	720
GGTTTTGTGG	TCAATCCTAA	GCGAATCTTG	GCTGAAAACA	TAGATGAAAT	CTGGAATTTT	780
ATCCAAGAAG	TAGGACAGGA	ACGGGAAAAT	CTGCCTTACG	ATATTGATGG	AGTGGTAATC	840
AAGGTCAACG	ACCTAGCAAG	TCAAGAAGAA	CTTGGTTTTA	CAGTTAAGGC	TCCAAAGTGG	900

GCAGTAGCCT	ACAAGTTCCC	TGCCGAAGAA	AAAGAAGCTC	AACTCTTATC	AGTTGACTGG	960
ACAGTTGGCC	GTACCGGTGT	TGTAACCTCCA	ACTGCTAATC	TAACACCAGT	ACAACTTGCC	1020
GGTACGACTG	TTAGCCGTGC	GACCCGTCAC	AATGTAGATT	ATATTGCTGA	AAAAGATATC	1080
CGAAAAGACG	ATACGGTCAT	TGTATATAAG	GCTGGTGACA	TCATCCCTGC	CGTTTTACGT	1140
GTGGTAGAGT	CCAAACGGGT	TTCTGAAGAA	AAACTAGATA	TCCCTACAAA	CTGTCCAAGT	1200
TGTAACCTCTG	AACTGTTGCA	CTTTGAAGAT	GAAGTGGCCC	TACGTTGTAT	CAATCCGCGT	1260
TGCCCTGCTC	AAATCATGGA	AGGCTTGATT	CACTTTGCTT	CTCGTGATGC	TATGAATATT	1320
ACAGGCCTTG	GTCCATCTAT	TGTTGAGAAG	CTTTTTGCTG	CTAATTTAGT	CAAGGATGTG	1380
GCGGATATTT	ATCGTTTGCA	AGAAGAGGAT	TTCCTCCTTT	TAGAGGGGGT	TAAGGAAAAG	1440
TCCGCTGCTA	AACTGTATCA	GGCTATCCAA	GCATCAAAGG	AAAATTCTGC	CGAGAAGCTC	1500
TTATTTGGTT	TGGGAATTCG	TCATGTCGGA	AGCAAGGCTA	GTCAGCTTTT	ACTTCAATAT	1560
TTCCATTCAA	TTGAAAATCT	GTATCAGGCA	GATTCAGAGG	AAGTGGCTAG	TATTGAAAGT	1620
CTAGGTGGCG	TGATTGCCAA	AAGTCTTCAG	ACTTATTTTG	CGACAGAAGG	CTCTGAAATT	1680
CTGCTCAGAG	AATTGAAAGA	AACTGGGGTC	AATCTGGACT	ATAAAGGACA	GACGGTAGTA	1740
GCGGATGCGG	CCTTGTCAAG	TTTGACCGTG	GTATTGACAG	GAAAATTGGA	ACGACTCAAG	1800
CGCTCAGAA	CTAAAAGTAA	ACTCGAAAGT	CTGGGTGCCA	AAGTGACAGG	TAGTGTTCCT	1860
AAAAAGACCG	ACCTCGTCGT	GGTAGGTGCA	GACGCTGGAA	GTAAACTGCA	AAAAGCACAA	1920
GAACCTTGTA	TCCAGGTCAG	AGATGAGGCA	TGGCTAGAAA	GTTTGTA		1968

(2) INFORMATION FOR SEQ ID NO:1932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1932:

GGATTCCTTA	TGATTTTCATT	CCTTCCTTCTA	TTGGTCTTGG	TTTGGGGATT	TTATATCGGC	60
TATCGGAGAG	GCCTGCTCTT	ACAGGTTTAT	TACCTGATTT	CAGCCATGGC	ATCGGCTTTT	120
ATGGCTGGCC	AGTTTTATAA	GGGGCTTGGA	GAGCAATTCC	ATTTATTGCT	CCCTTATGCA	180
AATTCGCAGG	AAGGTCAGGG	GACTTTCCTT	TTCCCATCGG	ATCAACTCTT	TCAGCTGGAT	240
AAGGTCTTTT	ATGCAGGTAT	CGGCTACTTG	CTTGATTTTG	GGATTGTCTA	TAGCATTGGT	300
CGTTTGCTTG	GTCTTCTCTT	ACACTTGATT	CCTAGCAAAA	AACTGGGTGG	TAAGTTGTTC	360
CAAGTTTCAG	CAGGTATCTT	GTCCATGTTG	GTGACCTTAT	TTGTCTTGCA	AATGGCCTTG	420
ACAATCTTGG	CGACCATCCC	CATGGCAGTT	ATACAAAATC	CTCTTGAAAA	GAGTATCGTC	480
GCAAAACACA	TCATCCAGAG	CATACCGATA	ACAACCAGTT	GGCTCAAACA	AATCTGGGTG	540
ACAAATTTAA	TCGATAA					558

(2) INFORMATION FOR SEQ ID NO:1933:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2406 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1933:

ATTATGCTTA	TATCTTATAA	ATGGTTAAAA	GAATTGGTGG	ACATTGATGT	GCCATCACAA	60
GAGTTGGCTG	AAAAAATGTC	AACTACAGGA	ATCGAGGTAG	AGGGTGTCGA	ATCACCAGCT	120
GCTGGTCTCT	CAAAAAATTGT	CGTCGGTGAG	GTCTTGTCCT	GCGAAGATGT	GCCAGAGACT	180
CACCTCCATG	TTTGTTCAGGT	TAACGTTGGC	GAAGAAGAGC	GTCAGATCGT	TTGTGGTGCC	240
CCAAATGTGC	GTGCTGGGAT	CAAGGTCATG	GTGGCTCTTC	CAGGAGCTCG	TATCGCTGAT	300
AACTACAAAA	TCAAAAAAAGG	AAAAATCCGT	GGTTTGGAGT	CACTTGGAAT	GATCTGTTCA	360
CTTGGTGAAT	TGGGAATTTT	TGACTCAGTT	GTGCCTAAGG	AATTCGCAGA	TGGCATCCAA	420
ATCTTGCCTG	AAGATGCCGT	GCCAGGTGAG	GAAGTCTTTT	CTTACCCTAGA	CTTGGATGAT	480
GAAATCATCG	AACTTTCCAT	CACACCAAAC	CGTGCAGATG	CCCTTTCTAT	GTGTGGAGTG	540
GCTCACGAAG	TGGCAGCCAT	CTATGACAAG	GCAGTCAACT	TTAAAGAATT	TACTCTAACA	600
GAAACTAATG	AAGCTGCGGC	AGATGCCCTT	TCTGTCTAGC	TTGAGACAGA	CAAGGCGCCT	660
TACTATGCAG	CTCGTATCTT	GGACAATGTG	ACCATCGCAC	CAAGTCCACA	ATGGTTGCAA	720
AACCTTCTCA	TGAACGAAGG	AATCCGTCCC	ATCAATAACG	TAGTGGACGT	GACCAACTAC	780
ATCCTGCTCT	ATTTTGGTCA	ACCAATGCAT	GCCTTTGACT	TGGATAACTT	TGAAGGGACT	840
GACATCCGTG	TGCGTGAAGC	GCGTGCTGGT	GAAAAATTGG	TGACCTTGGA	CGGTGAAGAA	900
CGTGACTTGG	ACGTGAATGA	CCTAGTCATC	ACTGTCCGAG	ACAAGCCAGT	AGCCCTTGCA	960
GGTGTCATGG	GTGGTCAAGC	AACAGAAATC	TCTGAAAAAT	CTAGTCGTGT	TGTCCTTGAA	1020
GCTGCTGTTT	TCAATGGCAA	ATCTATCCGT	AAGACAAGTG	GTCGCCCTGAA	CTTCGTTCT	1080
GAGTCATCTT	CTCGCTTTGA	AAAAGGAATT	AATGTGGCAA	CAGTTAATGA	AGCCCTTGAT	1140
GCGGCAGCTA	GCCTGATTGC	GGAACCTTGCA	GGTGCAGACG	TGCGTAAGGG	CATCGTTTCA	1200
GCGGGTGAGC	TTGATACTTC	AGATGTAGAA	GTTTCTTCAA	CCCTTGCTGA	TGTTAACCCT	1260
GTCTTCGGAA	CTGAGCTGTC	TTATGCTGAT	GTAGAAGACG	TCTTCCGTCG	TCTTGGCTTT	1320
GGTCTTTCTG	GAAATGCAGA	CAGCTTTTACA	GTCAGAGTCC	CACGTCTGTC	TTGGGATATC	1380
ACAATCGAAG	CTGACCTCTT	TGAAGAAATT	GCTCGTATCT	ATGGTTATGA	CCGCTTGCCA	1440
ACTAGTCTAC	CAAAAGACGA	TGGTACAGCA	GGTGAATTGA	CAGCCACACA	AAAACCTCCG	1500
CGTCAAGTTC	GTAATATTGC	TGAAGGAGCA	GGTTTGACAG	AAATCATCAC	CTATACTCTA	1560
ACAACCTCCT	AAAAAGCAGT	TGAGTTTACG	GCTCAACCAA	GTAACCTTAC	GGAACCTCAT	1620
TGGCCAATGA	CTGTGGATCG	TTCACTCCTC	CGTCAAAATA	TGATTTTCAG	TATCCTTGAT	1680
ACCGTTGCCT	ACAACGTGGC	TCGTAAAGAA	AAAAACTTGG	CCCTTTTACG	GATTGGAAAA	1740
GTCTTTGAAC	AAACAGGTAA	TCCAAAAGAA	GAACCTTCAA	ATGAAATCAA	CAGTTTGTGC	1800
TTTGCCTTGA	CAGGCTTGGT	TGCTGAAAAA	GATTTCCAAA	CAGCAGCAGT	TCCAGTTGAT	1860
TTCTTCTATG	CTAAGGGAAT	CCTTGAAGCC	CTATTTACTC	GTTTGGGACT	CCAAGTAACC	1920
TATACAGCAA	CATCTGAAAT	CGCTAGCCTT	CATCCAGGTC	GTACAGCCGT	GATTTCACTC	1980
GGTGACCAAG	TTCTTGGTTT	CCTTGGCCAA	GTGCATCCAG	TCACTGCCAA	GGCTTACGAT	2040
ATTCCAGAAA	CGTATGTGGC	TGAGCTTAAC	CTTTCAGCTA	TCGAAGCTGC	GCTTCAGCCA	2100
GCGACTCCAT	TTGTAGAAAT	CACCAAATTC	CCGGCAGTCA	GCCGTGACGT	TGCCCTTCTC	2160
CTCAAGGCAG	AAGTGACTCA	TCAAGAGGTT	GTAGATGCTA	TCCAAGCTGC	CGGCGTGAAA	2220
CGTTTGACAG	ATATCAAAC	CTTTGACGTC	TTCTCAGGTG	AGAAATTGGG	ACTTGGTATG	2280

AAGTCAATGG CTTATAGCTT GACCTTCCAA AATCCAGAAG ATAGCTTAAC GGACGAAGAA	2340
GTCGCACGCT ATATGGAAAA AATCCAAGCA TCGCTCGAAG AAAAAGTCAA TGCAGAAGTG	2400
CGTTAA	2406

(2) INFORMATION FOR SEQ ID NO:1934:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 243 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...243
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1934:

TTCCAGCTTA TCCTCAGTGA TATTTTGGGA ACCAAGGAAT TGGCCGCTCT GCATGGTTAT	60
ATTTTAAACAG CTTGGACAAT GGCTGGTTTA GCGNGACCTA TTTTATTAGC AGAGACTTAT	120
AAAATGGCTC ATTTCGTACAC ACAAACGTTG TTCGTATTTT TCATTTTATA CAGTATCGCC	180
TTGGCTTTGT CTTATTATCT AGGTCGTTCA ATCAAAAAAG AAAGTCAAAA ACCGCTTACA	240
TGA	243

(2) INFORMATION FOR SEQ ID NO:1935:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...303
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1935:

AAACAGCTTA TCAAAAAAGT CGGACAAGCT GGTAATCT TGGCTGACAG TGGTTATCAA	60
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GGGCTCATGA	AGATATATCC	TCAAGCACAA	ACTCCACGTA	AATCCAGCAA	ACTCAAGCCG	120
CTAACAGTTG	AAGATAAAAC	CTATAACCAT	GCGCTATCTA	AGGAGAGAAG	CAAGGTTGAG	180
AACATCTTTG	CCAAAGTAGA	AACGTTTAAA	ATGTTTTCAA	CAACCTGTCG	AAATCATCGT	240
AAACGCTTCG	GATTACGAAT	GAATTTGAGT	GCTGGTATTA	TCAATCATGA	ACTAGGATTC	300
TAG						303

(2) INFORMATION FOR SEQ ID NO:1936:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1936:

GAGGAGCTTA	TGATAAAAGA	TGAACGTGTA	CTTGAATTGA	TTGAAATTAT	TATAAAGAAA	60
AAAAGAATTG	CCGTAAAAGA	GCTGGCAGAA	ATCACTTTCT	CCAGCACAAAG	TACCTTACGT	120
CGTGATTTAA	TTTTCTTAGA	AAATCAAGGT	CTTATCAAAA	GAAAGCACGG	ATACGTGACC	180
CTGTCCTCTA	TGAACACAAT	TGAACTTTCT	CATCAAATAC	GGGAAGGAGA	AAGTACTAGG	240
CAAAAAGAC	TAATCGCTAG	TCTCGCTAAA	GACTTTATTC	GGTCTGGTAT	GTGTATCTAT	300
CTGGATTCCA	GTACGACTGT	CTACGAACTC	TGTCCTATC	TTTCTGAACT	TGATAATTTG	360
ATTATTTTTA	CAAAATGGTTT	ACATACTGCA	CAAAACCCTAT	CTGAAACTGT	TAAAGATAGC	420
TCCAAAATCT	TTATCACATC	TGGCGAGGTC	AAACATCAAT	CCTGTTCCGT	GGTCAACTAT	480
GATAAGGAAA	ATTCTTTATT	AGATCATTTT	AATATCGATT	TAGCATTTTG	TTCAGCAAGA	540
GGTATTGATG	ACCAATATGT	TTATGAAGCT	TCTCTCAGCC	AAGCTATTTT	AAAAAAGAAT	600
ATTATTGACA	AAGCCCATGA	AACCATCTTA	CTGATTGATA	GTTCTAAATT	TTACAAGACT	660
GGATTTTFTA	AAATTAATCC	CCTATCCAAA	TACACAACCT	TTATTTCTGA	CACCTTGCCA	720
GACCAAAAAT	TATTAGATGC	AGTAGAATTA	TTTGATGGAG	AATGGGTTTC	TGATATTCAA	780
TGA						783

(2) INFORMATION FOR SEQ ID NO:1937:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1965 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1937:

CAATTTATTA	TCCATTCTTC	AAAATTGCAG	ATAAACGCAA	TCTTGAAAAA	GAAAAAGCTA	60
CTGTTGGAGG	GAAATAAGAT	GGTTATCAGA	GTATTTGATC	AACAGAAAAA	TACTTATTCT	120
AGCTTTGCCCT	TAGAGGAATT	AAGTTACTAT	ATGAATCGGG	TCTTTAAGAC	TAACATAGAG	180
CTTGTCGAGG	AGAAGGAAGC	GGATATTTTT	GTAGGATTAG	TCAATAAAGA	GGACAGAAAA	240
GACCATGTTT	TTATCTCATT	AGACAAGGGT	AAGGGGAGAA	TTGAGTCTAA	TACAATTGTA	300
GGTTTACTTA	TTGGAATTTA	CCGAATGTTT	CATGAATTTG	GGGTTGTGTA	CACTAGACCA	360
GGGCGCAGAC	ATGACTTTGT	TCCAGAGTTA	CGATTTGAAG	ATTTTTTTAGA	TAAAGAGCTA	420
TCTATAGATG	AAACAGCCAG	TTACTATCAT	AGGGGAGTAT	GTATAGAGGG	AGCGGATTCA	480
TTTGAAAATA	TACTAGATTT	CATTGATTGG	CTACCTAAGA	TTGGGATGAA	CAGTTTTTTT	540
ATCCAGTTTG	AAAATCCTTA	CTCTTTTTTT	AAACGTTGGT	ATGAACATGA	GTTTAATCCA	600
TACCTAAATA	AAGAAAAATT	CTCAAATGAA	TTAGTACAAG	AATTGAGTGA	TAGGTTGGAT	660
AAAGAATTGC	AAAAAAGAGG	TCTTATTTCAT	CATCGTGTG	GTCATGGATG	GACAGGTGAG	720
GTTTTAGGTT	ACTCTTCAAA	ATTTGGCTGG	GAATCAGGTC	TTAGTATTTT	AGAGGAGAAG	780
AAACCGTATG	TCGCTGAAAT	AAACGGGAAA	CGAGAATTAT	TTAATACGGC	TCCGATTTTA	840
ACCAGTCTGG	ATTTTTTCAAA	TCCAGATGTG	GCGGATAAGA	TGGTAGAAAT	TATCAAGGAT	900
TATGCCAAGA	AAAGACCTGA	TGTTAACCTAC	TTACATGTAT	GGTTGTCGGA	TGCTCGTAAT	960
AATATTTGTG	AATGCGAAAA	CTGTAGACAA	GAATTGGTTT	CGGATCAGTA	TATTCGTATT	1020
CTCAATCAAT	TGGATAGGGC	TTTAACGAGT	GAGGGATTAG	ATACAAAGAT	TTGT'TTCTG	1080
CTTTACCATG	AGTTGCTATG	GGCGCCTCAG	AAAGAAAAAT	TAGATAATCC	TGAACGCTTT	1140
ACCATGATGT	TTGCACCGAT	TACAAGAACA	TTTGAAATGA	GTTATGCAGA	TGTAGATTTT	1200
GACAATTCCA	TACCTACGCC	TAAACCTTAT	CTGCGTAATA	AAATTATACT	TCCGAATTCT	1260
CTTGAGGAAA	ATTTATCTTA	TCTTTTTTGAG	TGGCAAAAAA	CATTTAAAGG	AGATAGTTTC	1320
GTATATGACT	ATCCTTTAGG	GCGTGCTCAT	TATGGCGATT	TAGGCTATAT	GAAAATTAGT	1380
CAAACCATTT	ACAGAGATGT	ATCTTATCTT	TCTAACCTAC	ATTTGAACGG	TTACATTTTCG	1440
TGTCAAGAAT	TACGTGCCCG	ATTCCCTCAT	AATTTTCCTA	ATTATGTTAT	GGGGGAAATG	1500
CTCTGGAAGA	AGACAAGAAG	TTATGAAGAA	TTGATTGAAG	AATACTTTTC	TGCTTTGTAT	1560
GGGGAAAAT	GGCAGTCTGT	TGTTGAATAT	TTAGAAAAAT	TATCCAGTTA	TTCTCATGT	1620
GATTATTTTA	ATGCAATTGG	CAGTCGTCAA	AATGATGTTT	TAGCGAATCA	TTATTATATA	1680
GCTTACAATC	TAGCTGATAA	TTTTTTGCCA	ATTATTGAGG	AAAATATTTT	TAAGTTATTA	1740
AATAGTCAAA	AGGATGAATG	GAAACAGCTC	AGTTATCATC	GTGAATATGT	TGTTAAGATG	1800
GCGAAGGCTT	TATATCTTCA	AGCAACCGGA	AAAACAAGGC	AAGCTCAAGA	TGAATGGAGA	1860
AATGTGTTGA	ATTATATCCG	TGGGCACGAA	CTGCTATTCC	AATCTAATTT	GGATGTTTAT	1920
CGTGTAATTG	AAGTAGCAAA	AAATTACGCT	GGTTTCCACT	TATAA		1965

(2) INFORMATION FOR SEQ ID NO:1938:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 807 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1938:

GAGTTTATTA	TGGTTTCTTC	AGAATTTTATC	TCAAAGATTG	AATTTGCTTG	CAATAAGAAA	60
GAAAGTCTTT	ATAGTCAAAG	CAAATTTAAG	TATGCGATTG	GTTGATGTT	CGCAGGTGCA	120
TTTTTAACCT	TCAGTACTGC	TGCAGGTGCA	GTTGGGGCTG	ACTTGATTAA	TAAAATTGCA	180
CCAGGTAGTG	GACGCTTCCT	CTTTCCATTC	GTTTTTGCTT	GGGGCTTGGC	CTACATTGTT	240
TTTTTGAATG	CCGAGTTGGT	CACITCAAAC	ATGATGTTCT	TGACTGCTGG	TAGTTTCTTA	300
AAAAAAATCT	CTTGAGAGAA	AACAGCTGAG	ATTTTACTAT	ACTGTACCTT	GTTCAACCTT	360
ATCGGAGCCT	TGATAGCAGG	GTGGGGCTTT	GCTCATTCGG	CAGCCTATGC	GAATCTGACA	420
CACGATAGTT	TCATCTCAGG	TGTTGTTGAG	ATGAAGTTAG	GCCGCTCAAA	TGAATTGGTC	480
TTGCTTGAGG	CGATTTTGGC	AAATATTTTC	GTAAATATTG	CGATTCTGTC	ATTTATTTTG	540
GTCAAAGATG	GTGGTGCCAA	ACTTTGGCTT	GTGTTGTCAG	CTATTTACAT	GTTTGTATTC	600
TTAACAAACG	AGCACATTGC	GGCGAACCTT	GCTTCTTTTCG	CGATTGTGAA	ATTCAGTGTT	660
GCTGCGGATT	CAATTGCCAA	CTTCGGTGTT	GGAAATATGC	TTCGCCACTG	GGGTGTGACT	720
TTCATCGGAA	ACTTTATCGG	AGGAGGCCTC	TTGATGGGTC	TTCCATATGC	CTTCCTCAAT	780
AAAAACGAAG	ATACTTATGT	AGATTAA				807

(2) INFORMATION FOR SEQ ID NO:1939:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1320 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1939:

AGGATTATTA	TGAAATCAAG	AGTAAAGGAA	ACGAGTATGG	ATAAAATTGT	GGTTCAAGGT	60
GGCGATAATC	GTCTGGTAGG	ATACGTGACG	ATCGAGGGAG	CAAAAAATGC	AGTCTTACCC	120
TTGTTGGCAG	CGACTATTCT	AGCAAGTGAA	GGAAAGACCG	TCTTGCAGAA	TGTTCCGATT	180
TTGTCGGATG	TCTTTATTAT	GAATCAGGTA	GTTGGTGGTT	TGAATGCCAA	GGTTGACTTT	240
GATGAGGAAG	CTCATCTTGT	CAAGGTGGAT	GCTACTGGCG	ACATCACTGA	GGTAGCCCCCT	300
TACAAGTATG	TCAGCAAGAT	GCGCGCCTCC	ATCGTTGTAT	TAGGGCCAAT	CCTTGCCCCGT	360
GTGGGTCATG	CTAAGGTATC	CATGCCAGGT	GGTTGTACGA	TTGGTAGCCG	TCCTATTGAT	420
CTTCATTTGA	AAGGTCTGGA	AGCTATGGGG	GTTAAGATTA	GTCAGACAGC	TGGTTACATC	480
GAAGCCAAGG	CAGAACGCTT	GCATGGTGCT	CATATCTATA	TGGACTTTCC	AAGTGTTGGT	540

GCAACGCAGA	ACTTGATGAT	GGCAGCGACT	CTGGCTGATG	GGGTGACAGT	GATTGAGAAT	600
GCTGCGCGTG	AGCCTGAGAT	TGTTGACTTA	GCCATTCTCC	TTAATGAAAT	GGGAGCCAAG	660
GTCAAAGGTG	CTGGTACAGA	GACTATAACC	ATTACTGGTG	TTGAGAACT	TCATGGTACG	720
ACTCACAATG	TAGTCCAAGA	CCGTATCGAA	GCAGGAACCT	TTATGGTAGC	TGCTGCCATG	780
ACTGGTGGTG	ATGTCTTGAT	TCGAGACGCT	GTCTGGGAGC	ACAACCGTCC	CTTGATTGCC	840
AAGTTACTTG	AAATGTGTGT	TGAAGTAATT	GAAGAAGACG	AAGGAATTCC	TGTTTCGTTCT	900
CAACTAGAAA	ATCTAAAAGC	TGTTTCATGTG	AAAACCTTGC	CCCACCCAGG	ATTTCCAACA	960
GATATGCAGG	CTCAATTTAC	AGCCTTGATG	ACAGTTGCAA	AAGGCGAATC	AACCATGGTG	1020
GAGACAGTTT	TCGAAAATCG	TTTCCAACAC	CTAGAAGAGA	TGCGCCGCAT	GGGCTTG CAT	1080
TCTGAGATTA	TCCGTGATAC	AGCTCGTATT	GTTGGTGGAC	AGCCTTTGCA	GGGAGCAGAA	1140
GTTCTTTCAA	CTGACCTTCG	TGCCAGTGCA	GCCTTGATTT	TGACAGGTTT	GGTAGCACAG	1200
GGAGAACTG	TGGTCGGTAA	ATTGGTTCAC	TTGGATAGAG	GTTACTACGG	TTTCCATGAG	1260
AAGTTGGCGC	AGCTAGGTGC	TAAGATT CAG	CGGATTGAGG	CAAGCGATGA	AGATGAATAA	1320

(2) INFORMATION FOR SEQ ID NO:1940:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2820 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1940:

TTTGTATTATTA	TTTATAAAGG	AGATAACCATG	AAACTCAAAG	ACACCCTTAA	TCTTGGGAAA	60
ACTGAATTCC	CAATGCGTGC	AGGCCTTCCT	ACCAAAGAGC	CAGTTTGGCA	AAAGGAATGG	120
GAAGATGCAA	AACTTTATCA	ACGTCGTCAA	GAATTGAACC	AAGGAAAACC	TCATTTTACC	180
TTGCATGATG	GCCCTCCATA	CGCTAACGGA	AATATCCACG	TTGGACATGC	TATGAACAAG	240
ATTTCAAAAAG	ATATCATTTG	TCGTTCTAAG	TCTATGTCAG	GATTTTACGC	ACCATTATAT	300
CCTGGTTGGG	ATACTCATGG	TCTGCCAATC	GAGCAAAGTAT	TGTCAAAAACA	AGGTGTCAAA	360
CGTAAAGAAA	TGGACTTGGT	TGAGTACTTG	AAACTTTTGCC	GTGAGTACGC	TCTTTCTCAA	420
GTAGATAAAC	AACGTGAAGA	TTTTTAAACGT	TTGGGTGTTT	CTGGTGACTG	GGAAAATCCA	480
TATGTGACCT	TGACTCCTGA	CTATGAAGCA	GCTCAAATTC	GTGTATTTGG	TGAGATGGCT	540
AATAAGGGTT	ATATCTACCG	TGGTGCCAAG	CCAGTTTACT	GGTCATGGTC	ATCTGAGTCA	600
GCCCTTGCTG	AAGCAGAGAT	TGAATACCAT	GACTTGGTTT	CAACTTCCCT	TTACTATGCC	660
AACAAGGTAA	AAGATGGCAA	AGGAGTTCTA	GATACAGATA	CTTATATCGT	TGTCTGGACA	720
ACGACTCCAT	TTACCATCAC	AGCTTCTCGT	GGTTTGACGG	TTGGTGCAGA	TATTGATTAC	780
GTTTTTGTTT	AACCTGCTGG	TGAAGCTCGT	AAGTTTGTCT	TTGCTGCTGA	ATTATTGACT	840
AGCTTGTCTG	AGAAATTTGG	CTGGGCTGAT	GTTCAAGTTT	TGGAAACTTA	CCGTGGCCAA	900
GAACTCAACC	ACATCGTAAC	AGAACACCCA	TGGGATACAG	CTGTAGAAGA	GTTGGTAATT	960
CTTGGTGACC	ACGTTACGAC	TGACTCTGGT	ACAGGTATTG	TCCATACAGC	CCCTGGTTTT	1020
GGTGAGGACG	ATTACAATGT	TGGTATTGCT	AATAATCTTG	AAGTCGCAGT	GACTGTTGAT	1080
GAACGTGGTA	TCATGATGAA	GAATGCTGGT	CCTGAATTTG	AAGGTCAATT	CTATGAAAAG	1140
GTAGTTCCAA	CTGTTATTGA	AAAACCTGGT	AACCTCCTTC	TTGCCCAAGA	AGAAATCTCT	1200

CACTCATATC	CATTTGACTG	GCGTACTAAG	AAACCAATCA	TCTGGCGTGC	AGTTCCACAA	1260
TGGTTTGCCCT	CAGTTTCTAA	ATTCCGTCAA	GAAATCTTGG	ACGAAATTGA	AAAAGTGAAA	1320
TTCCACTCAG	AATGGGGTAA	AGTCCGTCTT	TACAATATGA	TCCGTGACCG	TGGTGACTGG	1380
GTTATCTCTC	GTCAACGTGC	TTGGGGTGTT	CCACTTCCTA	TCTTCTACGC	TGAAGATGGT	1440
ACAGCTATCA	TGGTAGCTGA	AACTATTGAA	CACGTAGCTC	AACTTTTTGA	AGAACATGGT	1500
TCAAGCATTT	GGTGGGAACG	TGATGCCAAA	GACCTCTTGC	CAGAAGGATT	TACTCATCCA	1560
GGTTCACCAA	ACGGCGAGTT	CAAAAAAGAA	ACTGATATCA	TGGACGTTTG	GTTTGACTCA	1620
GGTTCATCAT	GGAATGGAGT	GGTGGTAAAC	CGTCCTGAAT	TGACTTACCC	AGCCGACCTT	1680
TACCTAGAAG	GTTCTGACCA	ATACCGTGGT	TGGTTTAACT	CATCACTTAT	CACATCTGTT	1740
GCCAACCATG	GCGTAGCACC	TTACAAACAA	ATCTTGTCAC	AAGGTTTTGC	CCTTGATGGT	1800
AAAGGTGAGA	AGATGTCTAA	ATCTCTTGGA	AATACCATTG	CTCCAAGCGA	TGTTGAAAAA	1860
CAATTCGGTG	CTGAAATCTT	GCGTCTCTGG	GTAACAAGTG	TTGACTCAAG	CAATGACGTG	1920
CGTATCTCTA	TGGATATTTT	GAGCCAAGTT	TCTGAAACTT	ACCGTAAGAT	TCGTAACACT	1980
CTTCGTTTCT	TGATTGCCAA	TACATCTGAC	TTTAACCCAG	CTCAAGATAC	AGTCGCTTAC	2040
GATGAGCTTC	GTTCACTTGA	TAAGTACATG	ACGATTCGCT	TTAACCAGCT	TGTCAGAGACC	2100
ATTCGTGATG	CCTATGCAGA	CTTTGAATTC	TTGACGATCT	ACAAGGCCTT	GGTGAACTTT	2160
ATCAACGTTG	ACTTGTACGC	CTTCTACCTT	GATTTTGCCA	AAGATGTTGT	TTACATTGAA	2220
GGTGCCAAAT	CACTGGAACG	CCGTCAAATG	CAGACTGTCT	TCTATGACAT	TCTTGTCAAA	2280
ATCACCAAAC	TCTTGACACC	AATCCTTCCT	CACACTGCGG	AAGAAATTTG	GTCATATCTT	2340
GAGTTTGAAA	CAGAAGACTT	CGTCCAATTG	TCAGAATTAC	CAGAGGCTCA	AACTTTTGCT	2400
AACCAAGAAG	AAATCTTGGA	TACATGGGCA	GCCTTCATGG	ACTTCCGTGG	ACAAGCACAA	2460
AAAGCCTTGG	AAGAAGCTCG	TAATGCAAAA	GTTATCGGTA	AATCACTTGA	AGCACACTTG	2520
ACAGTTTATC	CAAATGAAGT	GGTGAAAAC	CTACTCGAAG	CAGTAAACAG	CAATGTAGCT	2580
CAACTTTTGA	TCGTGTCAGA	CTTGACCATC	GCAGAAGGAC	CAGCTCCGGA	AGCTGCCCTT	2640
AGCTTCGAAG	ATGTAGCCTT	CACAGTTGAA	CGTGCTGCTG	GTGAAGTATG	TGACCGTTGC	2700
CGTCGTATCG	ACCAACAAC	AGCAGAACGC	AGCTACCAGG	CAGTCATCTG	TGATCATTTG	2760
GCAAGCATCG	TAGAAGAAAA	CTTTGCGGAC	GCTGTGCGAG	AAGGATTTGA	AGAGAAATAA	2820

(2) INFORMATION FOR SEQ ID NO:1941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1941:

TTTAGTATTA	TCGTAGAAAA	TGGACTCGGT	GCTATGGATA	CACCGGATGA	GAATGGTTAT	60
GTAGCAGATA	ACTATCGGAT	TACTTACTTA	GAGGCCACA	TCAAGGCCAT	GCGAGATGCC	120
ATTTACCAAG	ACGGGGTTGA	CTTGCTTGGT	TATACGACTT	GGAGCTGTAT	CGATCCGGTT	180
TCAGCTGGCA	CAGGGGAAAT	GAATAAGCGC	TATGGCTTTA	TCTATGTAGA	TCGAGATAAT	240
GTAGGAAACG	GAGCTCTCAA	ACGTAGCAAG	AAGAAGTCCT	TCTATTGGTA	CAAGGATGTC	300
ATTGATAGCA	ATGGTGCAAG	CATCGGGTAG				330

(2) INFORMATION FOR SEQ ID NO:1942:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...297
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1942:

GTATTAATTA	TTTTTAAGGC	TAAAGCTTGG	CTGGATATGA	GGGAACGCTC	TGCTACAGGT	60
GCTCAAGGTT	TAAGTAAAGTC	CATTAAAAAG	CATTTGAATG	ACATTACCCG	TTTGACAGCT	120
TCCTTGCTAG	GAGATGAAAA	GTTATCGGCT	ATAACATCAA	GTAGTGCGGT	AAAAGCAGAC	180
ATGCACCGCT	TTGTGATAGA	ATTAGAGCTT	GTGAAGTCAA	CTATTCTTCA	AAATGATGAC	240
ATTTTCATTAG	ATCAAAATGA	AATTTTTTGAA	ATTCTGAAAA	ATTTTTTCGA	TGGTTAA	297

(2) INFORMATION FOR SEQ ID NO:1943:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...360
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1943:

ATGTCAATTA	TTTTAACAAC	GATCGTTGCT	TTGGAGCATT	TTTACATTTT	TTATTTGGAA	60
AGTATTGCCA	CGCAATCAGA	TGCGACTAGT	CGTGTATTTA	ATATGGAAAA	GGAAGAATTG	120
GCTCATCCGT	CAGTAAGTTC	ATTGTTCAAA	AATCAAGGAA	TTTATAAGGC	TCTGCTAGGA	180
GTCTTTCTCT	TGTATGTCAT	TTATTTCTCA	CAGAATTTAG	AAATTGTGAC	TATTTTGTGC	240

TTATTTGTGA TTGGTGCTGC GACTTACGGC TCTTTAACAG CGGATAAAAAA AATTATTTTG	300
AAACAAGGTG GATCAGCTAT TTTGGCCTTG ATTAGTATTT TACTCTTTAA ATACACTTGA	360

(2) INFORMATION FOR SEQ ID NO:1944:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 804 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...804
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1944:

TGCCAAATTA TAGAGTGGAG GTCATTTAAA ATGATTGATA AAGTAATTGA ACAATATAAA	60
AGTCATGATA ATCTTGATAT TCGAGTAGAA TTGCATAAGA AGTATTCAAA AAATAAATTG	120
GGATTTAATA ATTGGATATT TTCTAACTAC CAAATCACTG ATGAAGTAAA GGTTC TAGAA	180
TTGGGATGTG GTACAGGAGA ATTGTGGAAA AGTAATAGTG ATTCTATAGA TAAAATGAAG	240
CAGTTGATTG TTACAGATTT TTCTAAAGAT ATGGTAAAAAT CAACGAAGTC AGTGATTGGA	300
AATAGAAACA ATGTCAATTA TGAGATAATG GATATTCAAA AGATTTCTTT TGAGAATGAA	360
ACTTTTGATA TTGTTATTGC TAATATGCTT CTACATCATG TGAATGATAT TCCTAAAGCT	420
CTCTCTGAGG TGAATAGGGT CTTAAAAACC GGAGGCATTT TTTACTGTGC TACATTTGGT	480
GAAAAATGGAG TTGTAAATTA TTTGGCAAGT TTATTTAAAG ATGAGGTTAA TCAAGATTTA	540
GAAAAATAGAA CGTTTACTTT ACAAATGGT AAAAGGTACC TGAGTAGGTA TTTTAACTCT	600
GTCGATACAT TACTCTATGA TGATGAGTTA CAGGTAAC TAATAGATGA CCTAGTTAAA	660
TACATCCAAT CGTTTAAAGG AATTTTCAGAA ATAGGTTTAC TAGAAGAGGA AATAATACGT	720
AAAAGATTGG AAAGTGAGTT TAATAATGGT ATGTTGATCA TTCCTAAAGA ATATGGTATG	780
TTTATCGCTC GAAAAGAAAAG TTAA	804

(2) INFORMATION FOR SEQ ID NO:1945:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 816 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1945:

TCACAAATTA	TGAAAAATAA	CGAATATAAG	TATGGAGGTG	TTCTTATGAC	AAAACCATAC	60
TACAATAAAA	ATAAGATGAT	TCTTGTTTCAT	TCAGATACGT	TCAAGTTCTT	ATCAAAAAATG	120
AAACCAGAAA	GTATGGATAT	GATTTTTGCT	GATCCACCTT	ATTTTTTAAG	TAATGGTGGA	180
ATATCTAATT	CTGGGGGACA	AGTTGTTTCT	GTTGATAAAG	GAGATTGGGA	TAAAATTTCT	240
TCATTCTAAG	AAAAACATGA	GTTTAATCGT	AAATGGATTG	GCCTAGCAAA	AGAAGTTCTG	300
AAGCCTAATG	GGACGGTATG	GATTTTCAGG	AGTTTGCACA	ACATATACTC	AGTTGGAATG	360
GCATTAGAAC	AAGAAGGTTT	TAAAATTCTG	AATAATATTA	CTTGGCAGAA	AACAAACCCT	420
GCCCCCAATT	TATCTTGTCG	TTATTTTACC	CATTCTACTG	AAACCATTTT	ATGGGCCAGA	480
AAAAATGATA	AAAAAGCTCG	TCATTACTAC	AATTATGATT	TAATGAAAGA	ATTGAATGAT	540
GGAAAACAAA	TGAAAGATGT	CTGGACCGGT	TCTTTAACAA	AGAAAGTTGA	AAAATGGGCT	600
GGGAAACATC	CAACTCAAAA	ACCAGAGTAT	TTGTTAGAAC	GCATTATTTT	AGCCTCTACT	660
AAAGAGGGTG	ACTATATTCT	AGACCCATTT	GTTGGTAGTG	GCACTACGGG	TGTTGTTGCG	720
AAGCGGTTAG	GTAGAAGATT	TATAGGTATC	GATGCTGAAA	AAGAATATTT	AAAAATTGCA	780
AGGAAGAGGT	TGGAGGCAGA	AAATGAAACA	AACTAG			816

(2) INFORMATION FOR SEQ ID NO:1946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1946:

CCTAAAATTA	TAAAAGGTAG	TAGTGTAGAT	ATAGAAGATA	ATGTAGCTGC	TCCAAGGCTA	60
CCTATTTGCC	AAAACTAAA	TTTGTCTAAG	ACGTTATTAT	TCGGTAAAAT	TAAAAAAGCTT	120
ACAAAAGTGC	TTAAAGCCAT	ACTAACACAA	GTTCTTGATA	AGGCTAGTTT	TATAGGGGTA	180
AGGCCTGCTT	TTCCGCTTAC	AGCAATCGCG	TATACAAAAA	TTACACTTAC	TAAGCCACCA	240
ATGATTGCAA	AACTTATATG	GCTTATGCTT	GATGAAATTC	CTAAAAAAGA	AAGACCAATT	300
ACTACACTAA	GACTTGCTCC	TGTGTTTATA	CCGAGTATAC	CTGGATCAGC	TATTGGGTTT	360
CTAGTAACTG	ATTGCATCAA	TACACCGCTT	ATGGCAAGAC	TAGAACCTGC	TAAAATTGCA	420
AAAAATAGTTC	TAGGTATTCT	TTTATATATA	ATTGATTTAA	TAAAAATCATC	ATTTGTATTG	480
CCCATTCCAA	AAGCTGCTAA	AAAATCTCTG	ATATTAATTT	CTTTTGTTCC	AAGCTTTAAT	540
GACAAAAATA	TTGTAATAAG	AAGACCTAGG	CAGATTACAA	AAATTATGCC	TAGGTGTATT	600
TGTGTTTTAT	TTCGCATTTT	TGCATGCATT	TCCTAA			636

(2) INFORMATION FOR SEQ ID NO:1947:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 909 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...909
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1947:

GAGGAAATTA	TGACTTTTAA	ATCAGGCTTT	G TAGCCATTT	TAGGACGGCC	CCATGTTGGG	60
AAGTCAACCT	TTTTAAATCA	CGTTATGGGG	GCAAAGATTG	CCATCATGAG	TGACAAGGCG	120
CAGACAACGC	GCAATAAAAT	CATGGGAATT	TACACCACCG	ATAAGGAGCA	AATTGTCTTT	180
ATCGACACAC	CAGGGATTCA	CAAACCTAAA	ACAGCTCTCG	GAGATTTTCAT	GGTTGAGTCT	240
GCCTACAGTA	CCCTTCGCGA	AGTGGACACC	GTTCTTTTCA	TGGTGCCTGC	TGATGAAGCG	300
CGTGGTAAGG	GGGACGATAT	GATTATCGAG	CGTCTCAAGG	CTGCCAAGGT	TCCTGTGATT	360
TTGGTGGTGA	ATAAAATCGA	TAAGGTCCAT	CCAGACCAGC	TCTTGTCTCA	GATTGATGAC	420
TTCCGTAATC	AAATGGACTT	TAAGGAAATT	GTTCCAATCT	CAGCCCTTCA	GGGAAATAAC	480
GTGTCTCGTC	TAGTGGATAT	TTTGAGTGAA	AATCTGGATG	AAGGTTTCCA	ATATTTCCCG	540
TCTGATCAAA	TCACAGACCA	TCCAGAACGT	TTCTTAGTTT	CAGAAATGGT	TCGCGAGAAA	600
GTCTTGACAC	TAACTCGTGA	AGAGATTCCG	CATTCTGTAG	CAGTAGTTGT	TGACTCTATG	660
AAACGAGACG	AAGAGACAGA	CAAGGTTTCA	ATCCGTGCAA	CCATCATGGT	CGAGCGCGAT	720
AGCCAAAAAG	GGATTATCAT	CGGTAAAGGT	GGCGCTATGC	TTAAGAAAAAT	CGGTAGCATG	780
GCCCGTCGTG	ATATCGAACT	CATGCTAGGA	GACAAGGTCT	TCCTAGAAAC	CTGGGTCAAG	840
GTCAAGAAAA	ACTGGCGCGA	TAAAAAGCTA	GATTTGGCTG	ACTTTGGCTA	TAATGAAAAA	900
GAATACTAA						909

(2) INFORMATION FOR SEQ ID NO:1948:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1329 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1948:

```
AGGTTGATTA TGGGAGATAA GAAATACACA GTAGAAAAAG CCAATCGTTT TATAGCAGAA      60
AATAAACATC TCGTTAATAC TCAATATAAG CCTGAAGAAC ATTTTTCAGC TGAGATTGGT      120
TGGATCAATG ATCCAAATGG ATTTGTCTAT TTTCGTGGAG AATACCATCT CTTTATCAA      180
TTCTATCCAT ATGATAGTGT TTGGGGACCT ATGCACTGGG GACATGCTAA AAGTAAGGAC      240
TTGGTGACTT GGGAGCACTT GCCAGTGGCA CTTGCTCCTG ACCAAGATTA TGACCGAAAT      300
GGTTGTTTCT CAGGCTCTGC CATTGTCAAG GATGATCGCC TCTGGCTCAT GTACACTGGG      360
CATATCGAAG AAAAAACCGG TGTCCGCCAA GTGCAAAATA TGGCATTTTC AGATGACGGG      420
ATTCACTTTG AAAAGATTTT CCAAAATCCA GTTGTAAC TGACAGACTT GCCAGATGAG      480
TTGATTGCTG CTGATTTCCG TGATCCAAAA CTCTTTGAAA AAGATGGACG CTATTACTCC      540
GTAGTAGCTG TCAAACACAT GGATAATGTG GGCTGTATCG TTCTACTAGG GTCCGATAAC      600
CTAGTAGAAT GGCAGTTCGA ATCCATCTTT TAAAAGGGG GAGAACACCA AGGCTTTATG      660
TGGGAATGCC CAGATTACTT CGAGTTAGAT GGGAAAGATT GCCTTATTAT GTCACCCATG      720
CGTTATCAGC GTGAGGGAGA CTCATATCAT AACATCAACT CATCGCTTTT GTTCACGGGT      780
AAGGTAGATT GGAGAGAAAA ACGTTTTATC CCAGAATCAG TTCAAGAAAT TGATCATGGC      840
CAAGACTTCT ATGCGCCTCA AACATTGTTG GACGATCAAA ATCGTCGTAT CCTGATTGCT      900
TGGATGCAGA CATGGGGGCG TACCCTTCCA ACCCATGACC AAGAACACAA ATGGGCATGT      960
GCCATGACTT TACCTAGAAT TCTAAGATTG GAAGATGGCA AACTAAGACA ATTCCCTGTT     1020
AAAAAAGGCC AATATCAAAAT CCAAATAGAT AAAGATTGTC ATTACCACTT AGGAAATGAT     1080
ATAGATTATC TTGAATTTGG TTATGACAGT AATGCGCAGC AAGTTTACAT TGATCGTAGC     1140
CATCTTATTC AAAAAATTCT AGGTGAAGAA GAACAGGACA CTAGTCGACG GTATGTAGAT     1200
ATTGAAGCTA AAGAATTGGA AGTTGTTCTA GATAAAAATT CCATCGAGAT TTTTGTCAAT     1260
CAAGGTGAAG CAAGCTTGAC TGCAACTTAT TACTTAACGG TGCCAGCTGA GCTATCACGA     1320
ATTGATTAA                                     1329
```

(2) INFORMATION FOR SEQ ID NO:1949:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 513 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1949:

```
ATAATGATTA TAAAAGTAGA AATGGCAGAT GTTGAGGTGT TGGCTAAAAT TGCCAAACAA      60
ACCTTTCGTG AAACCTTTGC GTATGATAAT ACGGAAGAGC AGTTACAGGA ATACTTTGAA      120
GAGGCTTATA GTCTGAAAAC TTTGTCAACT GAGTTGGGAA ATCCTGACTC TGAAACCTAT      180
```

TTCATTATGC	ATGAGGAGGA	GATAGCTGGT	TTTCTCAAAG	TCAACTGGGG	AAGTGCTCAA	240
ACTGAGAGAG	AATTAGAGGA	CGCTTTTGAA	ATTCAACGCC	TCTATGTGCT	ACAAAAATTC	300
CAAGGATTTG	GACTAGGTAA	GCAACTGTTT	GAATTCGCAC	TTGAACTTGC	TACAAAAAAT	360
AGTTTTTCTT	GGGCTTGGCT	AGGTGTTTGG	GAGCATAATA	CAAAAGCTCA	AGCCTTTTAT	420
AATCGATATG	GTTTTGAAAA	ATTTAGCCAA	CATCATTTTA	TGGTTGGTCA	AAAAGTAGAT	480
ACGGATTGGT	TACTGAGAAA	GAAATTAAGG	TAA			513

(2) INFORMATION FOR SEQ ID NO:1950:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1950:

TCAGTGATTA	TATTAAAGGA	GTTTAAGCCT	ATGTCATTAC	TAGCATTTGA	AAATGTATCC	60
AAATCATATG	GAGCAACACC	AGCCCTTGAA	AATGTTTTCTC	TTGACATTCC	AGCTGGAAAA	120
ATTGTCGGCC	TTCTTGGGCC	AAACGGCTCA	GGAAAAACAA	CCCTGATTAA	ACTAATTAAT	180
GGCCTCTTAC	AACCAGATCA	AGGACGTGTC	CTCATCAACG	ACATGGACCC	AAGCCCAGCA	240
ACCAAGGCCG	TTGTAGCTTA	TTTGCCTGAT	ACGACCTATC	TCAATGAGCA	AATGAAGGTC	300
AAAGAAGCCC	TAACCTACTT	CAAGACCTTC	TATAAAGATT	TCAATCTTGA	ACGCGCCCAT	360
CATCTACTTG	CAGACCTGGG	CATTGATGAA	AATAGTCGTC	TCAAGAAACT	ATCAAAAGGA	420
AACAAAGAAA	AGGTTCAACT	GATTTTGGTT	ATGAGCCGTG	ATGCTCGTCT	CTATGTTTTG	480
GATGAACCCA	TTGGTGGGGT	GGATCCAGCA	GCCCGTGCTT	ATATCCTCAA	TACCATTATC	540
AACAACACT	CACCAACTTC	TACCGTTTTG	ATTTCTACCC	ACTTGATTTT	TGATATCGAG	600
CCAATCTTGG	ATGAAATTGT	CTTCCTAAAA	GACGAAAAAG	TCGTCCGTCA	AGGAAATGTA	660
GATGATATTC	GCTACGAGTC	AGGTGAATCC	ATTGACCAAC	TCTTCCGTCA	GGAATTTAAG	720
GCCTAA						726

(2) INFORMATION FOR SEQ ID NO:1951:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1951:

GAAAAGATTA TTGACTCATA CAGACTTTTCG CAGATGATAT CCAACCACGT GTCTTTATTG	60
TTATCCAAAG ATGCCAAGGC CTTTGAGTTC TGGGAATATG CGCCTGAGTT GTTTGTAGAA	120
GAACAACAAG CAGTAGAACA GGAACGACAG AAACAAGCAC TTTTGTGCA TAAGGAACGG	180
ATGCGTGAAT TTGCAGAGAG ACATAATCGA AAAAGGAAGG AGGAAGTAAA TGGCAACTCT	240
TGA	243

(2) INFORMATION FOR SEQ ID NO:1952:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 627 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1952:

AACGAGATTA TCGAGTGGCG ACGTAATCGC TGGAGGACAA TTATGTCAGA AGAAATCAAT	60
GCAACTGTAT CTACTGAATC AACTGAGACT GTCGACACTC AAGGAAATGT TGATTCAGTG	120
CAGGAAGAAA AGCACGAACG AACTTTCACT CGTGCTGAAA TCGGTAAGAT GCTATCTGCC	180
GAACGCTCTA AATGGGAAGC TGAGCAAGAA GCCAAGGAAA ACGAAGCTAA GAAACTTGCC	240
AAGATGAACG CTGACGAGAA ACAAAAATAT CAGTTGGATC AGCGTGAGCA AGAACTAGCT	300
GACCGTGAGA AGGCTATTGC TCGCAAGGAA TTGACCGCAG AAGCTAAAGC AATGCTAAGT	360
GAACGTGACT TACCTGTTGA GTTAGTAAAT GTAGTTGATT TGACAAGCGC AGAGACGGTA	420
TCGCAGTCTG TCGCTGTATT GCAGAAATCA TGGGAGCAAG CCGTGCAAAA AGGCGTTCAA	480
GAAAACTAA AAGGCGGAGC TCCAATGAAA CAAGCGCCAG TCGATAGTGA CGGTATCACA	540
AAAGAAGAAT TTGCTCGTAT GGGTTATCAG AGTCGAAATG AGCTCTATCA AAAGAACCCA	600
GAGCTTTATA AGAAATTGAA AGGATAA	627

(2) INFORMATION FOR SEQ ID NO:1953:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1098 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1098
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1953:

AGGGAGATTA	TCATGATGGA	CAGTCCAAAA	AAATTAGGCT	ATCACATGCC	AGCAGAGTAC	60
GAACCCCATC	ATGGTACCCT	CATGATATGG	CCGACTCGAC	CAGGATCATG	GCCTTTTCAA	120
GGAAAGGCTG	CTAAAAGAGC	ATTTACTCAG	ATCATCGAGA	CCATAGCAGA	AGGGGAAAAGA	180
GTCTATCTTT	TGGTGGAGCA	GGCCTATCTA	TCTGAAGCCC	AATCCTATCT	TGGAGACAAG	240
GTTGTTTATT	TAGACATTCC	CACCAATGAT	GCCTGGGCGC	GTGATACTGG	CCCAACCATT	300
CTCGTCAATG	ATAAAGGTAA	GAAATTAGCC	GTGGATTGGG	CCTTCAATGC	TTGGGGAGGC	360
ACCTATGATG	GTCTTTATCA	AGATTATGAA	GAGGATGACC	AAGTAGCCAG	TCGTTTTGCT	420
GAGGCCTTGG	GAAGGCCTGT	CTATGATGCT	AAACCTTTTG	TACTGGAAGG	AGGCGCAATC	480
CATAGCGATG	GTCAAGGAAC	TATTCTCGTA	ACTGAAAGTT	GCTTGCTTAG	TCCTGGTCGC	540
AATCCTAACC	TGACTAAAAG	GGAGATTGAA	AACACATTAT	TAGAAAGTCT	TGGTGCTGAA	600
AAAGTTATTT	GGCTTCCTTA	TGGTATTTAT	CAGGATGAAA	CCAATGAACA	CGTCGATAAT	660
GTTGCTGCCT	TTGTTGGTCC	TGCTGAGCTT	GTTTTGGCTT	GGACAGATGA	CGAAAAATGAT	720
CCCCAGTATG	CCATGTCAAA	AGCAGATCTC	GAACCTTTAG	AACAGGAAAC	AGATGCAAAA	780
GGTTGTCACT	TCACCATTCA	TAAATTGCCT	ATCCCTGCAG	TTCGACAAGT	TGTGACAGAA	840
GAAGATTTGC	CAGGCTACAT	CTATGAAGAA	GGAGAAGAAA	AGCGATACGC	AGGTGAACGA	900
CTAGCAGCTT	CCTACGTAAA	CTTTTATATC	GCCAACAAGG	CTGTCTTGGT	TCCACAGTTT	960
GAGGATGTAA	ACGACCAAGT	GGCCTTAGAT	ATCCTCAGCA	AGTGTTTCCC	AGACCGTAAA	1020
GTTGTCGGAA	TACCAGCCAG	AGATATTCTC	TTAGGTGGTG	GCAATATCCA	CTGTATCACC	1080
CAACAAATTC	CAGAATAG					1098

(2) INFORMATION FOR SEQ ID NO:1954:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 435 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1954:

AGCCACTTCT	TGAGGGTATT	TATAGGCCAG	AAGGAGTGA	ATAAGATTTT	CGAAAATCAT	60
CAGATAAAAG	AGGACGATAA	AGACTTGGTT	CCCAATACTA	TCGGCCTCAC	GCCGTTTGTA	120
TTCGTCAAGG	GGACCAGAAA	TACCGTATGT	GCGTTTGATC	AGTTTTTCAG	TGAAGGTTTC	180
TTTTTTCATG	AGTTTGCTCC	TTTTTTAAAA	ATCTTCCTTC	CAAAAGAGAC	TGTTGAGGTC	240
AGTTTGGAGG	CTGCGGGCGA	GATTGAGACA	GAGTTCCAGA	GTTGGATTGT	ACTTGTCGTT	300
TTCAATCATA	TTGATGGTCT	GTCTCGAGAC	ACCGATATCC	TTGGCGAGCT	CGAGCTGGGA	360
AATGCCCAGT	TCCTTGCGAA	ATTCTTTCAC	ACGATTCATC	TGGTCTCCTT	TCTGATTTGT	420
GTCGTATATA	TTTGA					435

(2) INFORMATION FOR SEQ ID NO:1955:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1955:

GAGTTTGTTA	TGGATTTATT	AGAGAAAGAA	TGTTTAAAT	GTGATAAAAA	TTTCCAACAG	60
GGTGATATTT	GGAATTACTA	TTATTTATCA	GATAAGGTGC	CTGCACAAGG	GTGGAAAATA	120
CACATAAGCT	CCCAAATAAA	AGACGCTGTA	AATATTTTTA	AGATTGTGTA	TAAACTATCC	180
CAACTAAATA	ATTGTAGCTT	TAAAGTCGTT	AAAAATTTAG	AGGAATTAAA	AAAAATTAAT	240
TCCCTAGGG	AAATGAGCCC	TACTGCTAAC	AAATTTATAA	CTCTATATCC	TAAGTCAGAA	300
TCTGAAGCTA	AGAGTATGAT	TTGTAATCTT	ACGAATAGAC	TGTCAGAATT	TAAGGCTCCA	360
AAAATACTAT	CTGACTATCA	ATGTGGAATG	CATTCTCTAG	TTCATTATAG	ATATGGGGCT	420
TTTTAA						426

(2) INFORMATION FOR SEQ ID NO:1956:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 693 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1956:

```
GAATGTGTTA TGAAAGTATT AGCTTTTGAT ACGTCCAGCA AGGCTCTTTC TCTGGCTATT      60
TTAGAGGACA AGCAGGTTCT TGCTGAGACG ACGATTAAATA TCAAGAAAAA TCACAGTATT      120
ACCCTCATGC CAGCCATTGA TTTTTTGATG GAGAGTTTGG ACTGGACGCC CAAGGATTTG      180
GACCGAATCG TGGTGGCGGA AGGGCCAGGT AGCTACACAG GCTTGCGAAT CGCGGTAGCC      240
ACTGCCAAGA CCTTGACTCA TACTCTGAAC ATTGAGTTAG TTGGTATGTC TAGCCTCTTG      300
GCTCTGGTGC CATATCAACA AGAAGGCTTG TTCGTTTCCTT TGATGGATGC GCGTCGCAAC      360
AATGTTTATG CAGGATTTTA TGAAAATGCT AAACCTGTCA TGCCAGAAGC GCACCTATCT      420
TTTGAAGAGG TGCTAGAAAA AGTCAAGGGT GCTAGTCAGG TAACCTTTGT CGGAGAAGTT      480
GCCCCCTTTG TGGAGCAGAT TCAAGAACAC TTGCCAAGGA CTAATTATAA AGAAACCTTG      540
CCTAATGCAG CCAATCTTGC TCTTTTAGCT TGGGACAAGG AAGCAGACTC CTTGCATGAT      600
TTTGTGCCGA ACTACCTCAA GCGTGTCGAA GCTGAGGAAA ATTGGCTCAA GAATCACACC      660
GAGTCTGGTG AGTCCTACAT TAAACGCCTA TGA                                     693
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(2) INFORMATION FOR SEQ ID NO:1957:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1407 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1957:

```
TCGCGCGTTA TAAGGTCAGG GAAGTGCTCTG AGGCTATTAA TAACTTACAC TGAGCTAGGA      60
GAGTTTATGA ATGTTGCTTG GATATTGTTG TATACACTTG TTAATCACGG ATTAATAAAT      120
GTCATATTCT TTAAGGTAGA TGGAATTAGT CTCACTTTTG AGAGGATTTT TAAGGCCTTT      180
CTTTTAAAGA TACTGTTGGC CGTTGTTTTT GGAATGCTTG GCTATATGGT AGGAAATGTT      240
TACCTATCTT ATTTTATGGA ACCCTGTGAC GGCATAGGCT TATCTTCTTT ATTGTTAAGA      300
GAACTTCCTA AAAAATCCTT TCTCTTTTAT GGTCTCTTTC CAATGATATT AGTGAATCTC      360
TTTTATAGAG GTGTTTCCTA TTTTGTGCTT CCATTTTGGG GACAAGGGCA AGTATATGAT      420
GACTACTCAT TTATTTGGTT ATGTATAATA ATTTTCAATT TCTTCATTTT TCTAGCTTTT      480
TTGAAATGGT TGGACTATGA TTTCACTAGC TTGAGAAAAG GGATTCTCGA TAAAGATTTT      540
CAAAAGTCCC TGACTCAGAT TAACTGGATA ATGGGGGCTT ACTATTTGGT GATACAAAAT      600
```

CTGTCTTACT	TTGAATATGA	ACAGGGGATT	CAATCAACGA	CTGTTGCGCA	TCTCATCCTA	660
GTCTTTTACC	TGCTCTTTTT	TATGGGGATT	ATCAAGAAAT	TGGATACCTA	TTTGAAGGAC	720
AAACTCCATG	AGAGACTGAA	CCAAGAGCAG	GACTTGCCT	ACAGAGAGAT	GGAGCGGTAT	780
AGTCGGCATA	TAGAGGAGCT	TTATAAGGAA	GTACGGAGTT	TTCGCCATGA	CTACACCAAC	840
CTCTTGACTA	GCTTACGCT	GGGCATTGAA	GAGGAGGATA	TGGAGCAGAT	AAAAGAGATC	900
TACGACTCGG	TCTTAAAGGA	TTCTAGTGAA	AAATTGCAGG	ACAATAAATA	TGACCTTGGC	960
CGATTGGTGA	ATGTTCTGGGA	TCGTGCCCTC	AAAAGTCTCC	TAGCTGGAAA	ATTTATAAAA	1020
GCTAGAGATA	AGAACATTGT	CTTTAATGTC	GAAGTTCCAG	AGGAGATTCA	GGTAGAGGGG	1080
GTGAGTCTAC	TTGATTTTCT	AACCGTTGTG	TCTATCCTTT	GTGACAACGC	TATTGAAGCT	1140
AGTGTAGAAG	CCTGTCAACC	TCATGTTTCA	ATTGCCTTTT	TTAAAAATGG	AGCACAGGAG	1200
ACCTTTATCA	TTGAAAATTC	CATCAAAGAA	GAGGGAATCG	ATATTTCTGA	AATCTTCTCC	1260
TTTGGAGCAA	GTTCTAAAGG	GGAGGAGAGA	GGAGTTGGTC	TCTATACCGT	TATGAAAATT	1320
GTGGAAAGTC	ATCCCAATAC	CAGTCTCAAT	ACCACCTGCC	AAGATCACGT	TTTTTCGTCAG	1380
GTACTTACTG	TAATACATAT	AGAATGA				1407

(2) INFORMATION FOR SEQ ID NO:1958:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...513
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1958:

TTGACAGTTA	TTCTAAGTTA	CCAGGTATCG	GGATTAAGAC	GGCTACGCGT	CTGGCCTTTT	60
ATACGATTGG	GATGTCTGCT	GATGATGTCA	ATGAATTTGC	AAAAAATCTC	CTTTTCTGCT	120
AAGAGAGAAAT	TGACATATTG	TTCTATTTGT	GGACGTTTGA	CAGACGACGA	TCCTTGTTCT	180
ATCTGTACTG	ATCCGACTCG	TGACCAGACA	ACAATTTTAG	TTCTTGAGGA	TAGTAGAGAT	240
GTGGCAGCCA	TGGAATAATAT	CCAAGAATAC	CATGGACTCT	ATCATGTCCT	TCATGGCCTC	300
ATTTCTCCTA	TGAATGGTAT	CAGTCCGGAC	GATATCAATC	TCAAGAGCCT	TATGACTCGT	360
CTTATGGATA	GTGAAGTTTC	AGAAGTGATT	GTGGCGACTA	ATGCTACAGC	GGATGGTGAA	420
GCGACTTCCA	TGTATCTTTC	ACGTTTGCTC	AAGCCGGCTG	GTATCAAGGT	TACGCGTCTA	480
GACACGAGGT	CTCGCTGTGG	GAGCGGACAT	TGA			513

(2) INFORMATION FOR SEQ ID NO:1959:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1959:

ACTAGAGTTA	TGACACGCAA	AGTATATGAT	ACTGATTTAA	ACGATCAAGA	ATGGGCTAAG	60
ATTGAACCCCT	ATTTCTCCAA	ACACCGCACC	TATAAATGGC	CGAAACGAGT	ACTTGTTAAT	120
GAGACTTTGT	ACGTCACTAA	AACAGGTTGT	CAATGGCGCA	TGCTCCCTCA	CGACTTTCCT	180
CTTACTTAA	TGGTATGGAG	TTTCTTTCGT	CGTTCTATGA	CGACAGGTTG	GTTCCAGGTC	240
AATGGCAGAT	GGTACTACGC	TTATAGCTCA	GGTGCCTTGG	CAGTGAATAC	GACCGTAGAT	300
GGCTATTCTG	TCAACTATAA	TGGTGAAATG	GTTCGGTAA			339

(2) INFORMATION FOR SEQ ID NO:1960:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1791 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1960:

AGGAGAGTTA	TCATTATGAC	TCAAGGGAAA	ATTACTGCAT	CTGCAGCAAT	GCTTAACGTA	60
TTGAAAACAT	GGGGCGTAGA	TACAATCTAC	GGTATCCCAT	CAGGAACACT	CAGCTCATTG	120
ATGGACGCTT	TGGCTGAAGA	CAAAGATATC	CGCTTCTTAC	AAGTTCGCCA	CGAAGAGACA	180
GGTGCTCTTG	CAGCGGTTAT	GCAAGCTAAA	TTCGGCGGCT	CAATCGGGGT	TGCAGTTGGT	240
TCAGGTGGTC	CAGGTGCGAC	TCACTTGATT	AACGGTGTTT	ACGATGCAGC	TATGGATAAC	300
ACTCCATTCC	TAGCGATCCT	TGGATCACGT	CCAGTTAACG	AATTGAACAT	GGATGCTTTC	360
CAAGAGCTTA	ACCAAAACCC	AATGTACAAC	GGTATCGCTG	TTTACAACAA	ACGTGTAGCT	420
TACGCTGAGC	AATTGCCAAA	AGTAATTGAC	GAAGCCTGCC	GTGCTGCAAT	TTCTAAAAAA	480
GGTCCAGCTG	TTGTTGAAAT	TCCAGTAAAC	TTCGGTTTTC	AAGAAATCGA	TGAAAACCTCA	540
TACTACGGTT	CAGGTTTCATA	CGAACGCTCA	TTCATCGCTC	CTGCTTTGAA	CGAAGTTGAA	600
ATCGACAAAAG	CTGTTGAAAT	CTTGAACAAT	GCTGAACGCC	CAGTTATCTA	TGCTGGATTT	660
GGTGGTGTTA	AAGCTGGTGA	AGTGATTACT	GAATTGTCAC	GTAAAATCAA	AGCACCAATC	720
ATCACAACTG	GTAAAAACTT	TGAAGCTTTC	GAATGGAAC	ATGAAGGTTT	GACAGGTTCT	780

GCTTACCGTG	TTGGTTGGAA	ACCAGCCAAC	GAAGTGGTCT	TTGAAGCAGA	CACAGTTCTT	840
TTCCTTGGTT	CAAACTTCCC	ATTTGCTGAA	GTTTACGAAG	CATTCAAGAA	CACTGAAAAA	900
TTCATCCAAG	TCGATATCGA	CCCTTACAAA	CTTGGTAAAC	GTCATGCCCT	TGACGCTTCA	960
ATCCTTGGTG	ATGCTGGTCA	AGCAGCTAAA	GCTATCCTTG	ACAAAGTAAA	CCCAGTTGAA	1020
TCAACTCCAT	GGTGGCGTGC	AAACGTTAAG	AACAACCAAA	ACTGGCGTGA	TTACATGAAC	1080
AAACTCGAAG	GTAAACTGA	GGGTGAATTG	CAATTGTATC	AAGTTTACAA	TGCAATCAAC	1140
AAACATGCTG	ATCAAGACGC	TATCTACTCA	ATCGACGTAG	GTAACACTAC	TCAAACATCT	1200
ACTCGTCACC	TTCACATGAC	ACCTAAGAAC	ATGTGGCGTA	CATCTCCACT	CTTTGCGACA	1260
ATGGGTATTG	CCCTTCCTGG	TGGTATCGCT	GCTAAGAAAAG	ACAATCCAGA	TCGCCAAGTA	1320
TGGAACATCA	TGGGTGACGG	AGCATTCAAC	ATGTGCTACC	CAGACGTTAT	CACAAACGTT	1380
CAATACGACC	TTCCAGTTAT	CAACCTTGTC	TTCTCAAATG	CTGAGTACGG	CTTCATCAAG	1440
AACAAATACG	AAGATACAAA	CAAACACTTG	TTTGGTGTAG	ACTTCACAAA	CGCTGACTAC	1500
GCTAAAATTG	CGGAAGCTCA	AGGAGCTGTT	GGATTACACAG	TTGACCGTAT	CGAAGACATC	1560
GATGCAGTTG	TTGCAGAAGC	TGTTAAATTG	AACAAAGAAG	GTAAACTGT	TGTCATCGAT	1620
GCTCGCATCA	CTCAACACCG	TCCACTTCCA	GTAGAAGTAC	TTGAATTGGA	TCCAAAACCTT	1680
CACTCAGAAG	AAGCTATCAA	AGCCTTCAAG	GAAAAATACG	AAGCAGAAGA	ACTCGTACCA	1740
TTCCGTCTCT	TCTTGAAGA	AGAAGGATTG	CAATCACGCG	CAATTAAATA	A	1791

(2) INFORMATION FOR SEQ ID NO:1961:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1961:

ATGACGGTTA	TTATCAAATC	AATGGAACT	CCTGAAGAGA	TAGAAGGTAA	ATCCCTTGTT	60
CACTGGCAAA	CGTGGAGAGA	GGCTTATGAT	GACCTTTTGC	CTGCAGAATT	TCAGGAGACA	120
ATGACATTAG	AAAGATGTCG	ATTCTTTAGT	CAAAAGTATC	CAGAAAATAC	ATTGATTGCG	180
ATAGGTGATC	TGAAGGTAGT	TGGTTTTATC	AGTTATGGTA	ACTTTCGTGA	TGAGACTATT	240
CAAGCTGGTG	AAATTATTGC	TTTATATGTT	TTAAAAGACT	ATTACGGAAA	AGGCATAGCA	300
CAAAAGTTAA	TGAAAGCAGC	TTTGA CTGCT	CTGAATCATT	TTTCTGAAAT	TTTCTTATGG	360
GTATTGAAAAG	ATAACAAGCG	AGCCATTGCT	TTCTATCAAA	AAATGGGTTT	TACTTTTGAT	420
GGACAAGAAA	AGATACTTGA	ACTTGAAAAG	CCTATAAAGG	AAAAACGAAT	GGTATTCTAT	480
TCTAAAATAA	TTTTAAAAAG	TAGAAGCTAA				510

(2) INFORMATION FOR SEQ ID NO:1962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 744 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1962:

AGGAAGGTTA	TAATCATGAA	ATTAAATAAA	TTGAATTTTC	TTAAGGAAAA	TATAAGAAAT	60
TTATATTTCAT	CAGGCGTAAT	ATATCTCAGT	TTGCTTATCT	CGTTTATACC	GCCGATATTG	120
CTTACATTCT	TTATTCTAAA	GACTCAAGGG	ACATCGCTTG	GTATTAAGCA	TATTTCAAAC	180
TTTTATGCTA	TGCTCGGTAT	GTTAATGGCT	GTTATACATG	CTAATCGAGT	TATTAGTAGA	240
GATTTTCCC	ACAATACGGT	AAGTTTGTTT	TATAATCAAC	AGAAGAATCG	GATGATTTAC	300
GTCTTGCTA	ATTTTCTATA	TGCCATCTCA	GTTTCCATTA	TTTATGCTTT	GAATGGCATT	360
GTGTTACTAG	TCATAGTAAG	TAAATTGGGT	ATTCCAGGTG	ATTTAGGATT	AGATTTTATA	420
GTAGCTATTG	TAGTCAATAC	AATTTTGTTA	GTCCTGTTTT	ATTTTCTATT	ATCTTACATT	480
TTCTATTTAT	ACAAATTGAA	AAGTGGCTTG	GTATTTGGTA	TTTTAGTAGC	TTTACTACTC	540
TTTATCCCTA	ATATATTAAA	TACGATGATG	ATGAATACTA	GTAATGATTT	GTTTATCAAA	600
GCAATTGAAC	TTCTTCCTTT	TTATTCTTTA	CCTGTATTTG	TGGCTTCAAA	TACGATGTCT	660
ATTAGTCAGT	ATCTTGTGCT	AATCACTACA	ATCATTTTAT	TGTACTTTTT	CACTCTCAAG	720
AAAAGCAAGA	AGTATTCATT	TTAG				744

(2) INFORMATION FOR SEQ ID NO:1963:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 954 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1963:

GAGAGGGTTA	TGCCGATTCG	AATTGATAAA	AAATTGCCAG	CTGTTGAGAT	TTTACGGACA	60
GAGAATATCT	TTGTCATGGA	TGATCAACGT	GCTGCCCCACC	AAGATATCCG	TCCTTTGAAG	120
ATTTTAATTT	TAAATCTCAT	GCCACAGAAA	ATGGTCACAG	AGACCCAGTT	GTTGCGCCAC	180

TTGGCTAATA	CACCCCTACA	ACTGGATATT	GATTTTCTCT	ATATGGAGAG	CCACCGTTCT	240
AAAACAACTC	GTTCAAGGCA	CATGGAGACC	TTCTATAAAA	CTTTTCCTGA	AGTCAAGGAT	300
GAGTATTTTG	ATGGGATGAT	CATCACGGGT	GCTCCAGTTG	AGCATTTACC	ATTTGAGGAA	360
GTGGACTATT	GGGAGGAATT	TAGACAGATG	CTTGAGTGGT	CTAAGACTCA	TGTCTATTCT	420
ACCCTTCATA	TCTGTTGGGG	GGCTCAGGCT	GGGCTTTATC	TGCGCTATGG	TGTAGAAAAA	480
TACCAGATGG	ACAGTAAGCT	ATCAGGTATT	TATCCTCAGG	ACACCCATAA	AGAAGGTCAC	540
CTTCTATTTA	GAGGCTTTGA	TGATAGCTAT	GTATCCCTC	ATTACACGGCA	CACGGAGATT	600

TCTAAGGAAG	AGGTCTTAAA	CAAGACCAAT	CTCGAGATTT	TATCAGAAGG	ACCTCAGGTT	660
GGGGTTTCTA	TTTTGGCCAG	TCGTGATTTA	CGAGAAATTT	ATAGTTTTGG	TCATTTGGAG	720
TATGACCGTG	ATACCTTGGC	AAAAGAGTAT	TTTCGAGATC	GTGATGCAGG	TTTCGACCCA	780
CATATTCAG	AAAATTACTT	TAAAGATGAT	GATGTTAATC	AGGTACTTGT	TCTTTGTTGG	840
TCTTCATCTG	CAGCCCTCTT	TTTCAGTAAT	TGGGTAAACC	ATGCGGTCTA	TCAGGAGACG	900
CCTTTTGATT	GGAGAAAGAT	AGAAGATGAT	GCATCTGCAT	ATGGGTATTT	ATAA	954

(2) INFORMATION FOR SEQ ID NO:1964:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1964:

ACGCATTCTA	TTGAGTGTGA	TAAAGGAGAA	TTTATGGCAA	ATCGTAAAAT	TGTAGTAGCT	60
TTGGGAGGAA	ATGCGATTCT	TTCTTCTGAC	CCATCAGCAA	AGGCTCAACA	AGAAGCTTTA	120
GTGAAACAG	CTAAGCATCT	TGTAAAATG	ATTAAAAATG	GAGATGATTT	GATTATCACT	180
CACGGTAATG	GACCTCAAGT	TGGGAATCTC	TTGCTCCAAC	ATTTGGCATC	AGACTCTGAA	240
AAGAACCCTG	CCTTCCCACT	CGACTCACTT	GTCGCTATGA	CAGAAGGTAG	CATCGGTTTC	300
TGGTTGAAAA	ATGCTTTGCA	AAATGCTCTC	TTGGATGAAG	GCATCGAAAA	AAATGTTGCC	360
TCTGTTGTAA	CGCAAGTTAT	CGTAGATAAA	AATGATCCAG	CTTTTGTTAA	CTTGAGTAAA	420
CCAATCGGTC	CTTTCTATTC	AGAAGAAGAA	GCAAAAGCAG	AAGCCGAAAA	GAGCGGAGCG	480
ACTTTCAAGG	AAGATGCTGG	CCGTGGCTGG	CGTAAGGTCG	TTGCCTCACC	AAAACCTGTT	540
GACATCAAAG	AAATTGAAAC	CATCCGTACT	CTTTTAAATA	ATGGTCAAGT	CGTCGTAGCT	600
GCAGGTGGTG	GCGGTATTCC	CGTCGTCAAA	GAAAACAATG	GACATTTGAC	TGGTGTGCGAA	660
GCGGTTATTG	ATAAAGACTT	CGCTTCCCAA	CGTTTGGCAG	AATTGGTTGA	TGCAGACCTC	720
TTTCATCGTTT	TGACAGGTGT	AGATTATGTA	TTTGTTAACT	ACAACAAGCC	AAACCAGGAA	780
AAATTGGAAC	ATGTGAATGT	TGCCCAGCTG	GAAGAATATA	TCAACAAGA	TCAGTTTGCA	840
CCAGGTAGCA	TGCTTCCAAA	AGTAGAAGCA	GCTATCGCTT	TTGTCAATGG	TCGTCCAGAA	900
GGAAAAGCAG	TTATTACTTC	CCTTGAAAAAT	CTAGGCGCCT	TGATTGAATC	TGAAAGCGGA	960
ACAATTATTG	AAAAAGGATA	A				981

(2) INFORMATION FOR SEQ ID NO:1965:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...216
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1965:

TGCTTCTCTA TTATCCATAT ACTCCCTTTC TCCTGTAAGC GTTTTCTATG TTTTATTAT	60
ACTACCTTTT TAGAGAAGAT TCAAGTAAAT TACTATACTT CTTTAATTAT TTTGAAAATC	120
TACAACAAGT TCACTTACTC GTTCAATTGT AAATCAATAT TTTTCAAAA AATTGCGAAA	180
ACACCTTTCT TTTTCTACTA TAGTGAAATG AAATAA	216

(2) INFORMATION FOR SEQ ID NO:1966:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...225
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1966:

TTTCAATCTA TTATATCTAT TATGCACACC ACTATAGGAT CTAATAAAAA TCACAACAAG	60
TTCAATTCATA GATGGTTACC TCAGGGAAC TAAAGAAACGA CTACAAAGGA AGTCGCATTC	120
ATCGAAAAGT GGATTAACAA CTATCCTAAA AAATGCTTGA ACTACAAGTC CCCCAGAGAA	180
GACTTCTGGA TGACTAACTT GAACTTGAAA TTTAGCAATA ATTAA	225

(2) INFORMATION FOR SEQ ID NO:1967:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 714 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...714
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1967:

ATTATGTCTA	TCCATATTGC	TGCTCAGCAG	GGTGAAATTG	CTGATAAAAT	TCTTCTTCCT	60
GGGGATCCTC	TTCGTGCTAA	GTTTATTGCG	GAGAATTTCC	TTGGTGATGC	TGTTTGTTTT	120
AACGAAGTGC	GTAACATGTT	TGGTTACACT	GGTACTTACA	AGGGTCACCG	TGTATCTGTC	180
ATGGGAAGTG	GGATGGGAAT	GCCATCTATT	TCGATTTATG	CGCGTGAGTT	AATCGTAGAC	240
TACGGTGTGA	AGAAATTGAT	TCGTGTGGGA	ACTGCAGGTT	CTTTGAATGA	AGAGGTTCAT	300
GTTTCGTGAAT	TAGTTTTTGGC	GCAGGCGGCT	GCAACCAACT	CAAACATCGT	TCGTAATGAC	360
TGGCCACAGT	ACGATTTTCC	ACAAATTGCT	AGCTTTGATT	TGCTTGATAA	AGCCTACCAT	420
ATCGCCAAAG	AAC TTGGTAT	GACTACTCAC	GTTGGGAACG	TTTTGTGCATC	TGATGTCTTT	480
TACTCAAATT	ACTTTGAAAA	GAATATCGAG	CTTGGTAAAT	GGGGAGTCAA	GGCTGTGGAA	540
ATGGAAGCAG	CAGCTCTTTA	CTATCTTGCT	GCCCAATACC	ATGTTGATGC	GCTAGCTATC	600
ATGACCATCT	CTGATAGCTT	GGTCAATCCA	GACGAAGACA	CAACTGCAGA	AGAACGTCAA	660
AATACCTTCA	CTGATATGAT	GAAGGTTGGT	TTGGAAACCT	TGATTGCAGA	ATAA	714

(2) INFORMATION FOR SEQ ID NO:1968:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1494 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1494

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1968:

TTATGGTCTA	TAGAGAGGAA	AGACATGTAC	CAATATTTAA	CCTATCCACG	GGATGGATAT	60
GATGAGGGTT	CTTTGAAGAA	AGACCTGATT	TACAAATTGA	TAACGATACA	TAACACTGAA	120
AGCTCACGCT	TGAAGAATTT	AAAAAGCTAC	TACATGGGTG	ATCATGCTAT	TTTAAATCAC	180
AAGAGACGCA	ACGTGAACGC	ACCCAATTAC	AAGACGGTAG	CTAATCATGC	CAAGGATATC	240
GCAGACACGG	CTACGGGCTA	TTTTATGGGC	AATCCTATCA	AGTATAACAA	TACTGCTGAC	300
GGTGATATTG	ATGAACTACT	TACAGCCTTT	GATGGTGCTG	AGATTGACCA	AGTGGATGCG	360
CAGAACGCAC	TAAATATGGC	TATCTACGGC	CGTGCTTACG	AGTACATCTA	TGCTAAAGAG	420
GGTATGACTG	AGTTGGATTCT	AAC TAGTATT	GATCCGGAGA	ATACTTTCAT	GGTCTACGAT	480
GATAGTATTG	AGCGGAAGCC	TTTGTTTGCG	GTCTATTACT	ATGAAGTAAA	AGACGATACG	540
AAAGACACTA	CCAAGCACCA	GGCTGAGGTC	TTTACCGAAA	ATCTGCACTA	TCACATGGTG	600
CTGAGAAAGTA	CAGATTCAGG	AACAACCTCAG	AGCGAGGAGG	CAACACCTCA	CAACCTTGGT	660
CAAATCCCAA	TTATCGAGTA	TCGCAATAAT	CAC TTTGCGA	TTGGCGACTA	CGAGCAACAA	720
ATTAGCTTGA	TAGACGCTTA	TAATTCCTTG	ATGGGGAATC	GTGTCAATGA	TAAGGAACAG	780
GCTGTAGAGT	CTATCCTTGT	CTTGTATGGC	ACGCAGTTAG	CAGACACTCC	AGAAGACGCT	840
AAGGTAGCAA	TGAAGATTCT	TTCTGAAGAA	GGTCTTTTGG	AATTGCCGGG	CGATAGTGCA	900
AGGGCTGAGT	TCTTGAAGAA	TACGCTGGAC	GAAAGTGCTA	CTGAAATCTT	GCGTACAGCT	960
CTTAAAGAGG	ACATCTACAC	ATTTAGCCAT	GTGCCTAATT	TGACTGATGA	GAATTTTCGCA	1020
GGGAATACAT	CAGGCGTAGC	CATGGAATTT	AAGCTGATGG	GCCTTGAGAT	GATTACTAAG	1080
ACCAAGGAAG	CGAACTATAA	GCGAGGATTG	CGTCAGCGTA	TTGCGATTTT	TGCTCATTAC	1140
TTAGGCATGA	AGCAGATTGC	TTTAGAGTCT	CATTCAATCG	TTCCACAATT	CAGTCGTGGT	1200
TTGCCTAAGA	ACTTATTAGA	AATCTCTCAG	ATTGTGAACA	ATTTGGAAGG	CAAAGTGACC	1260
AATAGACAGC	TTATTTCTCT	CTTGCCGTTT	GTGGAAGACC	CTGACGCTGA	GCTGGAAGCC	1320
TTGGAAGAAG	AGAAAAAGAA	GAACATGGAA	GACATGCCGA	TGTTCAACAA	AGACAACACG	1380
AAACCCGAAG	ACGAGGTAGA	GGATGAAGAA	TCAGGAGTAT	TGGGCGAAGA	GGAAAGCCAA	1440
TCTGATTTAC	CAGCAGATGG	ACAAGGCCGA	AAAGCAGGCA	GACCAGTTTCG	ATAA	1494

(2) INFORMATION FOR SEQ ID NO:1969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1969:

GGAGTTCCTA	TGGCAAAAAC	AATCTATATC	GCAGGTCTTG	GGTTGATTGG	AGCCTCTATG	60
GCACTTGGTA	TCAAACGCGA	TCATCCAGAT	TATGAAATTT	TAGGTTATAA	TCGTAGTCAA	120
GCTTCGAGAG	ATATCGCCTT	GAAAGAAGGC	ATGATTGACC	GTGCAACGGA	TGATTTTGCT	180
AGTTTTGCTC	CTTTGGCAGA	TGTCATTATA	CTCAGCTTGC	CAATCAAACA	AACTATTGCT	240
TTCATTAAGG	AGTTGGCCAA	TTTGGATTTG	CGAGAAGGCG	TTATTATTTT	AGATGCTGGT	300
TCGACCAAGT	CAACCATTGT	GGATGCGGCG	GAGCAGTATT	TGGCTGGCAA	GTCTGTTCGC	360

TTTGTCTGGGG	CCCATCCCAT	GGCTGGTAGT	CACAAGACAG	GGGCTGCTTC	GGCAGATGTC	420
AATCTTTTTT	AAAAATGCCA	TTATATCTTT	ACACCTTCAA	GCCTGACAAG	TCAGGACACG	480
CTTAAGGAAA	TGAAGGATCT	GCTTTTCAGG	CTTCATGCTC	GTTTTATCGA	GATTGATGCC	540
AAGGAGCATG	ATCGTGTAC	TTCTCAGATT	AGCCATTTTC	CTCATAATTT	GGCTTCTAGT	600
CTCATGGAGC	AGACTGCGGT	CTATGCTCAA	GAGCATGAGA	TGGCAAGGCG	CTTTGCGGCA	660
GGTGGTTTTT	GAGATATGAC	CCGAATTGCG	GAAAGCGAGC	CAGGAATGTG	GACCTCCATT	720
TCTTGTCCA	ATAGCGAGAC	CATTCTGGAT	AGAATTGAGG	ATTTCAAGGA	ACGTTTGGAA	780
GCGATTGGTC	AGGCCATTAG	TAAGGGAGAT	GAAAGCAAAA	TTTGGAACCT	TTTTAACCBA	840
GCGCGTGAAC	AACGCCAGAC	CATGGAAATC	CATAAGCGTG	GTGGTGTGGA	TAGCTCTTAC	900
GACCTCTATG	TTGACGTTCC	TGATGAAGAA	GATGTCATCC	TGCGGATTTT	GGAACTGCTA	960
CGTGGAACTT	CCTTGGTTAA	CATCCACATC	AACGAGGAAA	ATCGTGAGGA	TATTCACGGA	1020
ATCCTACAAA	TTTCATTTAA	AAATGCTCAA	GACTTGGAAG	GAGCTGAGCA	TCTCATAACA	1080
GAAAATACCG	ACTATACAGT	CGTCATCAAA	TAA			1113

(2) INFORMATION FOR SEQ ID NO:1970:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 612 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...612
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1970:

CAGGTTCCTA	TGTCTTTAAG	GGAGAAAGTCA	ATGAGCGAGT	ACAAACTCTC	AGAAAAACAAC	60
TGGACTAGGG	TTGCAGTTTT	TGCAGGCGGA	AACCGCGGTC	ATTATCGGAC	AGATTTTGAT	120
GCTTTTGTTG	GGGTGGATCG	AGGCTCGCTC	TGGGTCTTGG	AAGAAGACTT	ACCTCTTGCT	180
CTAGCAGTCG	GAGATTTTGA	TTCTGTGACG	GAAGAAGAGC	GACAGGTGAT	TCAAAAACGT	240
GCCCAGTATT	TTGTCCAAGC	CCGACCAGAA	AAAGATGATA	CCGATTTGGA	ATTGGCTCTC	300
TTAACCATCT	TTGAGAAAAA	TCCTCAGGCT	CAGGTTACTA	TTTTCGGTGC	CTTGGGTGGC	360
CGTATTGACC	ATATGTTGGC	CAATGTCTTT	CTGCCTAGCA	ATCCTAAGTT	NNNNNNNNNN	420
NNNNNNNNNN	NNNNNNNNNN	NNNNNCAAAA	AAANNNNNNN	NNNNNGNNNN	NNNNNNNNGN	480
GGGNNNNNGG	GGNGNGGGGN	GNNGGGGGGG	GGGGGGGGGG	GGGGGNGGGG	GGGGGGGGGG	540
GGGGGGGGGG	GGNGGGGNNG	GGGGGGGGGG	GGGGNGGGGG	GGGGGGGNGG	GGNGGGNGGG	600
GGGGGGGGGG	GG					612

(2) INFORMATION FOR SEQ ID NO:1971:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...288
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1971:

AAATATCCTA	TGTACAATGA	TGTAATCGAA	AGGATATCTT	TATATGAGTT	TATCGGTGAT	60
ATTTTCTATT	CTAAAAATAAT	AAGTTGTTGC	ATCGTAGCTA	GCGATTTATC	TAAAAATACT	120
ATGAAATTGG	ACGTCATATT	TTTGTAGGAT	AAAAATAAAA	GATCCGCAGT	TTTAGGTTTA	180
CGAAGAGACA	AAAGCGGAGT	ATTTAAACCA	GTTACTCTAC	ATTTTACAAG	CGCTAAGAAA	240
TATGCTAAAG	TTCGTAAAAAC	AGATGTGAAA	GAAATGAAAT	GGCTATAA		288

(2) INFORMATION FOR SEQ ID NO:1972:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...258
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1972:

AACGTGTTCT	TCAACGTTAC	CATGAATTGC	AAGATATCAT	TGCTATCCTT	GGTATGGATG	60
AGCTTTCTGA	TGAAGAAAAG	ACCTTG GTTG	CTCGCGCCCG	TCGTATCCAG	TTCTTCTTGT	120
CACAAAACCT	CAACGTTGCG	GAACAATTTA	CTGGTCAGCC	AGGTTCTTAT	GTTCCAGTTG	180
CTGAAACTGT	ACGTGGCTTT	AAGGAAATCC	TTGATGGTAA	ATACGACCAC	TTGCCAGAAG	240
ATGCCTTCCG	TGGTGTAG					258

(2) INFORMATION FOR SEQ ID NO:1973:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1973:

ATTGAGCCTA	TTTTATCACA	AAATATAAGA	GAAAGCTATG	TGGGATTTC	GAAGAATACT	60
TTTAATACTC	TTCGAAAATC	TCTTCAAACC	ACGTCAGTTT	TATCTGCAAC	CTCAAAGCTG	120
TGCTTTGAGC	AACCTGCAGC	TAGCTTCCTA	GTTTGCTCTT	TGATTTTCAT	TGAGTATAAC	180
TCAAAAAAGT	AA					192

(2) INFORMATION FOR SEQ ID NO:1974:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 669 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1974:

GAGGTACTA	TGGAATCTAT	TTTAGAAATT	TTAACCCAG	ATAACCTAGT	CTTTATCTTT	60
AAAGGATTTG	GCTTGACCCCT	CTATATTTCT	CTGATTGCCA	TCATCCTCTC	TACTATCATC	120
GGTACCGTGC	TTGCCGTCAT	GCGAAATGGA	AAAAATCCTA	TCTTACGCAT	TATTTCCAGT	180
ATTTATATCG	AGTTTGTGCG	CAACGTTCCC	AACCTTCTCT	GGATTTTAC	TATCTTTTGT	240
GTGTTCAAAA	TGAAATCCAC	ACCAGCAGGT	ATTACAGCCT	TTACTCTCTT	TACATCAGCA	300
GCCTTGGCTG	AGATTATTCG	AGGCGGTCTC	AATGCCGTAA	ACNAGGGACA	ATACGAAGCA	360
GGAATGTCAC	AAGGCTTCAC	CTCAGCCCAA	ATCCTCTACT	ACATCATTTCT	CCCACAAGCC	420
ATCCGCAAAA	TGCTACCAGC	CATCATTTCT	CAGTTTGTTA	CCGTGATTAA	GGATACCAGT	480
CTCCTCTACT	CTGTTATCGC	CCTACAAGAA	CTCTTTGGAG	CCAGCCAAAT	TCTCATGGGC	540
CGTTATTTTCG	AACCAGAGCA	GGTCTTCAGT	CTTTACATCC	TGATTGCCCT	CATCTACTTC	600
AGCTTTAACC	TAGCAATTTT	TAACCTGTCT	CATATGCTAG	CAAAACGTTG	GCAACAAGCT	660
GCAGAATAA						669

(2) INFORMATION FOR SEQ ID NO:1975:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 186 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...186
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1975:

CACTATACTA	TACCGGCGGC	CGGGGTCGAA	CCGGCACGTC	CTTGCGGACA	CTGGATTTTG	60
AGTCCAGCGC	GTCTGCCAAT	TCCGCCACGC	CGGCAAATAG	TAACTGGGGT	AGCTGGATTC	120
GAACCAACGC	ATGAGGGAGT	CAAAGTCCCT	TGCCTTACCG	CTTGGCTATA	CCCCAATATA	180
AAATAG						186

(2) INFORMATION FOR SEQ ID NO:1976:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1692 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1692
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1976:

TATAATACTA	TGGAATACAA	TCACAAGGAG	AGAACGATGT	CATTTGACGG	ATTTTTTTTA	60
CACCACATAG	TTGAGGAATT	GCGAAGCGAA	TTAGTGAATG	GTCGCATCCA	GAAAATCAAT	120
CAGCCTTTTG	AACAAGAGTT	GGTCTTGCAA	ATCCGCAGCA	ATCGCCAAAAG	CCATCGCCTG	180
CTCCTTTCTG	CCCATCCAGT	TTTTGGACGC	ATTGAGCTGA	CCCAAACGAC	TTTTGAAAAT	240
CCAGCCCAAC	CTTCTACCTT	TATCATGGTT	TTGAGAAAAGT	ATTTGCAGGG	GGCCCTGATT	300
GAGTCGATTG	AGCAAGTGGA	AAATGACCGT	ATTGTGGAAA	TTACAGTTTC	CAATAAAAAC	360

GAGATTGGAG	ACCATATCCA	GGCTACCTTG	ATTATCGAAA	TTATGGGGAA	ACACAGTAAT	420
ATTCTACTGG	TCGATAAAAG	CAGTCATAAA	ATCCTCGAAG	TTATCAAACA	CGTCGGTTTT	480
TCACAAAATA	GCTACCGCAC	CTTACTTCCA	GGATCGACCT	ATATCGCTCC	GCCAAGTACA	540
GAATCTCTCA	ATCCTTTTAC	TATCAAGGAT	GAAAAGCTCT	TTGAAATCCT	GCAAACCCAA	600
GAACTAACAG	CAAAAAATCT	TCAAAGCCTT	TTTCAAGGTC	TGGGACGCGA	TACGGCAAAT	660
GAATTGGAAA	GGATACTGGT	TAGTGAAAAA	CTTTCCGCTT	TCCGAAATTT	TTTCAATCAG	720
GAAACCAAGC	CATGCTTGAC	TGAGACTTCC	TTCAGTCCAG	TTCTTTTTCG	AAATCAGGTG	780
GGAGAGCCTT	TTGCAAATCT	TTCTGATTTG	TTGGACACCT	ACTATAAGGA	TAAGGCTGAG	840
CGCGACCGCG	TCAAACAGCA	GGCCAGTGAA	CTGATTTCGT	GTGTTGAAAA	TGAAC TTCAG	900
AAAAACCGAC	ACAAACTCAA	AAAACAGGAA	AAAGAGTTAC	TGGCGACAGA	CAACGCTGAA	960
GAATTTTCGT	AAAAAGGAGA	ATTGCTGACA	ACCTTCCTCC	ACCAAGTGCC	TAACGACCAA	1020
GACCAGGTTA	TCCTAGACAA	CTACTATACC	AACCAACCTA	TCATGATTGC	GCTTGATAAG	1080
GCTCTGACTC	CCAACCAGAA	TGCCCAACGC	TATTTTAAAC	GGTATCAGAA	ACTCAAAGAA	1140
GCTGTCAAAT	ACTTGACTGA	TTTGATTGAA	GAAACCAAAG	CCACTATTCT	CTATCTGGAA	1200
AGTGTAGAAA	CCGTCCCTCA	CCAAGCTGGA	CTGGAAGAAA	TCGCTGAAAT	CCGTGAAGAA	1260
TTGATTCAAAA	CAGGTTTTAT	CCGCAGAAGA	CAACGGGAGA	AAATCCAGAA	ACGCAAAAAA	1320
CTAGAACAAT	ATCTAGCAAG	CGATGGCAAA	ACCATCATCT	ATGTCGGACG	AAACAATCTT	1380
CAAAATGAGG	AATTGACCTT	TAAAATGGCC	CGCAAGGAGG	AAC TTTGGTT	CCATGCTAAG	1440
GACATTCCTG	GAAGCCATGT	TGTCATCTCA	GGAAATCTTG	ACCCATCTGA	TGCAGTCAAG	1500
ACAGACGCAG	CAGAGTTAGC	TGCCTACTTC	TCTCAAGGGC	GCCTGTCGAA	TCTGGTGCAG	1560
GTAGATATGA	TTGAAGTCAA	AAAAC TCAAT	AAACCAACTG	GTGGAAAACC	CGGCTTTGTC	1620
ACTTACACAG	GACAAAAGAC	CCTCCGCGTC	ACACCAGACT	CAAAAAAAT	TGCATCCATG	1680
AAAAAATCCT	GA					1692

(2) INFORMATION FOR SEQ ID NO:1977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1977:

AGGTGTACTA	TTCTAGTTTC	AATATACTAT	AAAATCGGTT	TAAGTTCATC	TGGTGTCTAT	60
AAAGCAGTCG	CTGATGGAGA	AATGACTGTT	GGTCTCTCTT	ATGAAGATCC	AGCAGTTAAA	120
CTCTTAAATG	ACGGAGCTAA	CATTAAGGTA	GTCTATCCAA	AAGAAGGAAC	CGTCTTCCCTA	180
CCTGCTAGTG	CTGCTATCGT	TAAAAAATCT	AAAAATATGG	AAAATGCCAA	GAAATTTTATC	240
GATTTTATTA	TCTCTCAAGA	AGTACAAGAT	ACACTTGGTA	CAACCACTAC	TAACCGTCCCT	300
GTTTCGTAAAA	ATGCTAAAAC	AAGCGAAAAC	ATGAAAACCA	TTGACAAAAT	CAAAACACTC	360
ACTGAAGATT	ATGATTATGT	CATCAAGAAT	AAATCAGATA	TCGTTAAGAA	ATACAACGAA	420
GTCTTTACAG	ATATCCAATC	TAAACAGTAA				450

(2) INFORMATION FOR SEQ ID NO:1978:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...240
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1978:

AGGTGTACTA TTCTAGTTTC AATCTACTAT ATTATGGACA ATGCAAGATT CCATAGAATG	60
GGTAAGCTAG AACTTTTATG TGAAGAGTTT GGGCATAAAC TTTTACCTCT TCTTCCCTAC	120
TCACCTGAGT ACAATCCTAT TGAGAAAACA TGGGCTCATA TCAAAAAGAA CCTCAAAAAG	180
GTATTACCAC GTTGCCATAC CTTTACGAG GCTCTTTTGT CCTGCTCTTG TTTCAATTGA	240

(2) INFORMATION FOR SEQ ID NO:1979:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 183 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...183
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1979:

AGGTGTACTA TTCTAGTTTC AATCTACTAT ATTATGGATA ATGCAAGATT CCATAGAATG	60
GGTAAGCTAG AACTCTTGTG TGAAGAGTTT GGGCATAAAC TTTTACCTCT TCCTCCCTAC	120
TCATCTGAGT ACATCCTATT GAGAAAACAT GGGCTCATAT CAAAAAGCAC CTCAAAAAGG	180
TGA	183

(2) INFORMATION FOR SEQ ID NO:1980:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 246 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...246
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1980:

AACACCACTA	TAATCTCTAT	CAGCTCTTGC	TTTCCACCC	TGTTTAAAAC	CTTCCTCAAA	60
GATAAAGAGA	AAATCGTCAA	CGCCCTTCAA	TTACCTTATT	CCAACGCCAA	ACTGGAAGCC	120
ACCAATAATC	TCATCAAAC	TATCAAGCAC	AATGCCTTTG	GTTTTAGGAA	CTTTGAAAAC	180
TTCAAAAAAG	AAAGGACGAA	ATTTGTCCTT	TCTAGATCTT	CGCTTTCTTC	AACCCACTAC	240
AGTTGA						246

(2) INFORMATION FOR SEQ ID NO:1981:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...297
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1981:

TTTGAAACTA	TATATCTGTT	TCGGACAAAA	GAAAAAGACT	TGAAGCAAAC	GTCTCAAATC	60
CTTGTATAG	CTTGTTTTAT	AGCTTTATTT	CAGTTAGACG	GTTCAAACGC	GTTATTAGTA	120
ATTCTTATAA	GTGACTATGG	CTTGTTATTA	GAAAAAGACTA	TAACTGATTC	TAGTCAACTT	180
TTTCCCTGTT	CAAGTGGAAC	GACTGCTAGT	GTCFTTCCCTA	GACTAGCTAG	GACTTTTAAG	240
ACTGTGTCCA	ACTGTGGACT	AGTCTTACCT	GTCCTCCATCC	TAGCTATAAC	AGGCTGA	297

(2) INFORMATION FOR SEQ ID NO:1982:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1644 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1644
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1982:

GTGGAGACTA	TGACAGAAAT	TGTGAAAGCA	AGCTTAGAAA	ATGGCATTCA	AAAAATCCGT	60
ATCCGAGCTG	AAAAAGGCTA	TCATCCAGCC	CATATCCAGC	TTCAAAAGGG	AATTCAGCT	120
GAGATTACCT	TTCATCGTGC	TACTCCTTCA	AACTGTTATA	AGGAAATTCT	GTTTGAAGAA	180
GAAGGTATCT	TGGAACCAAT	CGGCGTAGAT	GAGGAGAAAG	TCATTTCGTTT	TACACCTCAA	240
GAATTAGGGC	GACATGAATT	TTCTTGTTGGC	ATGAAGATGC	AAAAGGGAAG	CTATATAGTC	300
GTTGAGAAGA	CTCGAAAATC	TCTATCTCTC	CTGCAACGTT	TTTGGATTAC	TAGTATCTTT	360
ACTGTGCCCTC	TTGTGATTCT	CATGATTGGG	ATGTTGACAG	GTAGCATTAG	TCATCAAGTC	420
ATGCATTGGG	GAACCTTTCT	AGCAACAACG	CCTATTATGT	TAGTTGCAGG	TAAGCCATAT	480
ATCCAGAGTG	CTTGGGCCAG	TTTAAAAAAG	CACAATGCCA	ACATGGATAC	CTTGGTTGCG	540
CTGGGAACTC	TAGTGGCTTA	TTTCTATAGC	CTAGTTGCTC	TCTTTGCTGG	TCTCCCTGTT	600
TACTTCGAAA	GTGCTGGATT	TATCCTCTTT	TTCGTTCTTT	TGGGAGCAGT	TTTTGAGGAA	660
AAAATGAGAA	AAAATACGTC	CCAAGCTGTG	GAGAAATTAC	TGGACTTGCA	AGCTAAAACC	720
GCAGAAGTCT	TGAGTGATGA	TAGTTATGTC	CAAGTTCCTT	TGGAACAAGT	CAAGGTAGGC	780
GACCTGATTC	GAGTGCGTCC	CGGTGAAAAG	ATTGCTGTTG	ATGGTGTCGT	AGTAGAAGGT	840
GTCTCTAGTA	TTGACGAATC	CATGGTGACA	GGTGAGAGTC	TGCCGTGTTG	CAAGACAGTT	900
GGAGATACTG	TCATTGGCTC	AACCATCAAT	CATAGTGGA	CGCTTGCTCT	TAGAGCAGAA	960
AAAGTTGGCT	CAGAGACTGT	TTTGGCTCAG	ATTGTGGATT	TTGTGAAGAA	AGCTCAGACA	1020
AGTCGTGCGC	CGATTACAGG	CTTGACGGAT	AAGATTTTCT	GGATTTTTGT	CCCAGTAGTT	1080
GTCATTTTAG	GAATCATGAC	CTTTTGGGTT	TGGTTCGTCT	TGCTCAGGGA	TAGTGTGGTC	1140
GTGCTTGGAG	CTAGCTTTGT	GTCCTCTCTT	CTCTACGGAG	TGGCGGTTTT	GATTATCGCC	1200
TGTCCTTGTG	CCTTGGGACT	TGCAACACCG	ACAGCCCTTA	TGGTGGGGAC	AGGACGTAGT	1260
GCCAAGATGG	GGGTTCCTCT	CAAAAATGGA	ACTGTCCTTAC	AGGAAATCCA	GAAAGTTCAA	1320
ACTCTTGTCT	TTGATAAGAC	CGGGACTTTG	ACGGAAGGGA	AACCTGTGGT	AACAGATATC	1380
ATCGGCGACG	AAGTAGAAGT	GTTTGGATTG	GCAGCCTCCT	TGGAAGATGC	TTCTCAACAC	1440
CCACTGGCTG	AGGCTATCGT	TAAGCGAGCG	AGTGAAGCTG	GACTTGAGTT	TAAAACGTGT	1500
GAAAAATTTT	AGGCCTTGCA	CGGGAAAAGG	GTTTCAGGGC	GAATCAATGG	AAAACAAGTT	1560
TTACTTTGGAA	ATGCTAAAAT	GCTGGATGGC	ATGGATATTT	CTAATACTTA	TCGAGATAAA	1620
CTAGAAGAAC	TAGAAAAAGG	CTAA				1644

(2) INFORMATION FOR SEQ ID NO:1983:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 297 base pairs
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...297
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1983:

GGAGTTGCTA	TGAAATTATC	CAACCTACTG	CTATTTGCAG	GAGCTGCAGC	CGGAAGTTAT	60
CTGGTTACAA	AAAAATCGCCA	AACCATCACA	GATGAAGTCT	TGAATACCAC	TGACCGCGTT	120
CAAGCTATCA	AAGACGATGT	GGATATTATC	CAAAATAGCC	TGCAAATCAT	CGACCAGCAA	180
AAAGAACTTA	TCAAGGAATA	CCAAGAAGAC	TTGACTTACA	AGTTTAAGGT	CTTGAAAAAG	240
GATATCCAGA	CTAGACTAGC	TGTGATAAAA	GAAATGCAGG	GAAGTGAAGA	TAAGTAA	297

(2) INFORMATION FOR SEQ ID NO:1984:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 585 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...585
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1984:

AAAAATGCTA	TAATGAAGGG	TATGAAATAT	CACGATTACA	TCTGGGATTT	AGGTGGAAC	60
TTACTGGATA	ATTATGAAAC	TTCAACAGCT	GCATTTGTTG	AAACATTGGC	ACTGTATGGT	120
ATCACACAAG	ACCATGACAG	TGTCTATCAA	GCTTTAAAGG	TTTCTACTCC	TTTTGCGATT	180
GAGACATTCG	CTCCCAATTT	AGAGAATTTT	TTAGAAAAGT	ACAAGGAAAA	TGAAGCCAGA	240
GAGCTTGAAC	ACCCGATTTT	ATTTGAAGGA	GTTTCTGACC	TATTGGAAGT	CATTTCAAAT	300
CAAGGTGGCC	GTCATTTTTT	GGTCTCTCAT	CGAAATGATC	AGGTTTTTGA	AATTTTAGAA	360
AAAACCTCTA	TAGCAGCTTA	TTTTACAGAA	GTGGTGACTT	CTAGCTCAGG	CTTTAAGAGA	420
AAGCCAAATC	CCGAATCCAT	GCTTTATTTA	AGAGAAAAGT	ATCAGATTAG	CTCTGGTCTT	480
GTCATTGGTG	ATCGGCCGAT	TGATATCGAA	GCAGGTCAAG	CTGCAGGACT	TGATACCCAC	540
TTGTTTACCA	GTATCGTGAA	TTTAAGACAA	GTATTAGACA	TATAA		585

(2) INFORMATION FOR SEQ ID NO:1985:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1068 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1068
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1985:

AAAAATGCTA	TAATTGAAAAG	GACTATATCG	AAGGAGAACA	AAATGACTAA	ACCCATTATT	60
TTAACAGGAG	ACCGTCCAAC	AGGAAAATTG	CATATTGGAC	ATTATGTTGG	AAGTCTCAAA	120
AATCGAGTAT	TATTACAGGA	AGAGGATAAG	TATGATATGT	TTGTGTTCTT	GGCTGACCAA	180
CAAGCCTTGA	CAGATCATGC	CAAAGATCCT	CAAACCATTG	TAGAGTCTAT	CGGAAATGTG	240
GCTTTGGATT	ATCTTGCAGT	TGGATTGGAT	CCAAATAAGT	CAACTATTTT	TATTCAAAGC	300
CAGATTCCAG	AGTTGGCTGA	GTTGTCTATG	TATTATATGA	ATCTAGTTTC	GTTAGCACGT	360
TTGGAGCGAA	ATCCAACAGT	CAAGACAGAG	ATTTCTCAGA	AAGGATTTGG	AGAAAGCATT	420
CCGACAGGAT	TCTTGGTCTA	TCCAATCGCT	CAAGCAGCTG	ATATCACAGC	TTTCAAGGCT	480
AATTATGTTT	CTGTTGGGAC	AGATCAGAAA	CCAATGATTG	AGCAAACCTG	TGAAATTGTT	540
CGTTCCTTTT	ACAATGCATA	TAAGTGTGAT	GTCTTGGTAG	AGCCGGAAGG	TATTTATCCA	600
GACAAATGAG	GAGCAGGGCG	TTTGCCTGGT	TTAGATGGAA	ATGCTAAAAT	GTCTAAATCA	660
CTAAATAATG	GTATTTATTT	AGCTGATGAT	GCGGATACCT	TGCGTAAAAA	AGTAATGAGT	720
ATGTATACAG	ATCCAGATCA	TATCCGCGTT	GAGGATCCAG	GTAAGATTGA	GGGAAATATG	780
GTTTTCCATT	ATCTAGATGT	TTTTGGTCGT	CCAGAAGATG	CTCAAGAAAT	TGCTGATATG	840
AAAGAACGTT	ATCAACGAGG	TGGTCTTGGT	GATGTGAAGA	CCAAGCGTTA	TCTACTTGAA	900
ATATTAGAAC	GTGAAGTGGG	TCCTATTTCG	GAGCGCCGTA	TTGAATTTGC	TAAGGATATG	960
GGAGAAGTTT	ATAATATGAT	TCAAAAAGGT	AGTGAAAGAG	CGCGTGAAGT	TGCGGGTCAA	1020
ACCCTATCTG	AGGTAAAAGG	GGCAATGGGA	CTTCATTACT	TTAACTAA		1068

(2) INFORMATION FOR SEQ ID NO:1986:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 441 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1986:

AAATGTGCTA	TAATAGAAGG	AGGAAAAGGA	GGATTCTCAG	ACATCCGGGT	ATCAGCCCAA	60
CTAATGATTT	GTCAATTTAT	CCGCGATATG	CTGGACTTGC	CAGCAAAAAA	TGTGACGATT	120
TTGGAGGGAA	GTAACATTCA	CGTCTTGCCT	TCCATGCCCT	ACTCAGCGCA	GGATTTCTAT	180
ACTAGTATAG	ACGTCTTGGC	GGAGTTAGAT	AATGGAATCC	AAGTTATCAT	CGAAATTCAG	240
GTTTCATCATC	AGAATTTTTT	CATCAATCGC	CTATGGGCTT	ATCTGTGCAG	TCAGGTTAAT	300
CAAAACCTAG	AAAAAATTCG	CCAACGTGAA	GGTGATACCC	ACCAGAGCTA	CAAACAAATC	360
GCACCAGTAT	ACGCTATCGC	AATTGTCTGAT	AGTAATTACT	TCTCAGATGA	CCTAGCTTTT	420
CATAGTTTTA	TAGTAAAAATG	A				441

(2) INFORMATION FOR SEQ ID NO:1987:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 492 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1987:

TACAACGCTA	TCCAAGTTGG	TTTCGATGAC	AAACGCGAAG	TATTGAGCAA	CAAACCTGCT	60
AAAGGACATG	TAGCGAAAAGC	TAACACGGCT	CCTAAGCGCT	TCATTTCGTGA	ATTCAAAAAC	120
GTTGAAGGCT	TGGAAGTTGG	TGCTGAAATT	ACAGTTGAAA	CATTTCGCAGC	TGGAGACGTT	180
GTTGACGTAA	CTGGTACTTC	TAAAGGTAAA	GGTTTCCAAG	GTGTTATCAA	ACGCCACGGA	240
CAATCACGTG	GACCAATGGC	TCACGGTTCT	CGTTACCACC	GTCGTCCAGG	TTCTATGGGA	300
CCTGTTGCAC	CTAACC GCGT	ATTCAAAGGT	AAAAACCTTG	CAGGACGTAT	GGGTGGTGAC	360
CGCGTAACAA	TTCAAAATCT	TGAAGTTGTA	CAAGTTGTTT	CAGAAAAGAA	CGTTATCCTT	420
ATCAAAGGTA	ACGTACCAGG	TGCTAAGAAA	TCTCTTATCA	CTATCAAATC	AGCAGTTAAA	480
GCTGGTAAAT	AA					492

(2) INFORMATION FOR SEQ ID NO:1988:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 186 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1988:

AATTTGATTT	TATACTCTTC	GAAAATCTCT	TCAAGCCACG	TCAGCATCGC	CTTACCGTAT	60
GTATGGTTAC	TGACTTCGTC	AGTTTCATCT	ACAACCTCAA	AACAGTGTTT	TGAGCAACCT	120
GCGGCTAGCT	TCCTAGTTTG	TTCTTTGATT	TTGAGTATTA	GATTTACTCA	AAATCAAGGA	180
TTTGA						186

(2) INFORMATION FOR SEQ ID NO:1989:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1704 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1989:

AAAAATTATA	TTGAGGTTAA	TACTATGTCA	AAAGAAAAAA	TAAAAGTATA	CCTCTATACA	60
CGAGTATCTA	CGTCAATACA	GATAGAGGGG	TATTCGTTAG	AGGCACAAAA	ATCACGAATG	120
AAAGCTTTTG	CTATTTACAA	CGATTATGAA	ATTGTTGGAG	AGTATGAAGA	TGCCGGGAAG	180
TCTGGCAAGT	CTATTGAAGG	TAGAATACAG	TTCAATCGAA	TGATGGAAGA	TATAAAATCT	240
GGAAAAGATG	GAGTATCTTT	TGTTCTTGTTG	TTTAAGTTAT	CAAGATTTGC	AAGAAATGCC	300
GCTGATGTTT	TTTCTACACT	TCAGATAATG	CAGGATTATG	GAGTTAATCT	TATCTGCGTT	360
GAAGATGGCA	TTGATTCATC	TAAAGATGCT	GGGAAACTAA	TGATTTCTGT	TTTATCAGCT	420
GTGGCTGAAA	TAGAAAAGAGA	AAACATCCGT	ATTCAAACAA	TGGAAGGTCG	CATTCAAAAA	480
GCAAGGGAAG	GAAAATGGAA	TGGTGGCTTT	GCTCCGTATG	GATATAAACT	TGAAGACGGC	540
AAGCTGTTTA	TAAATGAGGA	AGAGGCAGTT	GCAATAAGAA	CGATTTTCGA	CCAGTATGTA	600

AATACTACGA	TAGGAGCCAA	TGGGATATCT	AAATACTTAG	AGAATCATGG	AATTAGAAAA	660
ATCCCAAGAC	AGAATGGTAA	GAATCCTTTG	TTTGATGCAG	GTCTTATAAG	AAAGATATTA	720
AAGAATCCTG	TATATAATGG	AAAAATAGCA	TTTGGAAGAA	GAACTTTAGA	AAAAGTTCAT	780
GGTACAAGAA	ATGAATATAA	GCAGGTTGAA	CAAGATGAAT	ATCTAATATC	TGAAGGGATA	840
CATGAAGCTA	TAGTTTCCGA	TGAAGTTTGG	CAAGCTGCTC	AGGTTAAGCT	AAAATCTCAA	900
GCAAAGAAAT	ATGAGCATGT	GAATAAAGGA	AAAGATACAC	GCACACACTT	GCTTTCTGGA	960
ATTGTAAAAT	GCCCGATATG	TGGAGTGGGA	ATGTTTGGGA	ACAAGTGTAT	CAAGAAAAAG	1020
AAAGATGGCA	CAAAGTATAA	AGATTTTTTAT	TACTATGGTT	GTAAACATAG	GCAGATGATA	1080
AGAGGTCATA	AGTGACATT	CAGTAAGCAA	ATTAGAGAAG	AATTGTTAGA	TGATGCTGTT	1140
GCAGAGGTGA	TTGTCAAGAT	AGTAAGTAAT	CCGAAATTTG	CTTCTATGAT	GCAAGAAAAA	1200
ATCAACATGA	AGGTGGATAC	CTCTGAAATA	GAAAAAGAAA	TAGATAATTA	CCAAAAGGAA	1260
TTGAGAAAGA	GTCATTCTAC	AAAGTTTAAG	CTAATTGAGG	AAATAGATAA	TTTAGATGTT	1320
GAAGATAAGC	ATTATAAGAG	AAGGAAACAG	GATTTAGATG	ATAGACTATA	TCGTATGTAT	1380
GACAAAATAG	ATGAATTAGA	ATCATCACTA	ATTGATGCGA	AAGCAAAGAA	ACAGACTATT	1440
GAAGCTGAAA	AGCTTACAGG	AGATAACATA	TATAAGGTTC	TAATCTATTT	TGATAAGCTC	1500
TATAAAGTCA	TGAATGATGT	AGAGCGTAGG	CAGTTAATTT	CAGCTTTGAT	TTCTGAAATT	1560
CAAGTTTATG	AAGAAAAACA	ATCTAACGGA	CAATGGCTAA	AATCCATTAC	TTTTAAGCTA	1620
CCAATTATAG	AAGAAAATCT	CAACATAGGT	TTGGACAATG	ATGAACAAGT	TGAATGTGTA	1680
AGTTTATTAG	AGAAACGTAG	TTAA				1704

(2) INFORMATION FOR SEQ ID NO:1990:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 189 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...189
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1990:

CCAGTTCTCT	TCATTATACC	ACAAAATAAC	AAGCATAAAG	CGGATTCAAA	GATAAAGATT	60
AAGGTTCATA	TACTAATTTT	CTTTATTGAC	TTTTTGTCTT	CTGTATTAGG	GAGTTTATCA	120
TTTTCCAAAA	ACTTTATCTT	CAATTTGTTA	TCTAAAATTT	CTACAATAAA	AAAGCCTACC	180
TTTCAGTAG						189

(2) INFORMATION FOR SEQ ID NO:1991:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 456 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1991:

TGTAGCTATA	TTATATCAAA	ATTCAGTACA	GTAGAGGTAG	ATTTTATGTC	AGATTGCATT	60
TTTTGTAAAA	TCATCGCAGG	GGAAATTGCT	GCTTCAGAAG	TATATGAAGA	TGAGCAGGTC	120
CTTGCCTTTC	TTGATATCTC	TCAAGTAACA	CTAGGACACA	CCTTGGTCGT	GCCAAAAGAA	180
CACTATCGCA	ATCTTTTGGA	GATGAATGCT	ACGAGCGCCA	GCCAACTCTT	TGCCCAAGTA	240
CCAAAAGTAG	CTCAAAAAGT	CATGAAAAGT	ACTAAGGCTG	CTGGTATGAA	TATCATTTCC	300
AACTGTGAAG	AAGTCGCTGG	TCAAACAGTT	TTTCATACTC	ACG TTCACCT	TGTGCCTCGC	360
TACAGTGCTG	ACGATGACCT	CAAGATTGAT	TTTATCGCCC	ACGAACCAGA	CTTTGACAAA	420
CTTGCTCAAG	TCGCTGAAAC	CATCAAAAAC	GCTTAA			456

(2) INFORMATION FOR SEQ ID NO:1992:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1980 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1980

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1992:

GAGGAATATA	TGTCACTACA	ATCAGTTAAC	GCCATTCGTT	TTCTTGCGCT	AGATGCTATT	60
AACAAATCTA	ATTCTGGTCA	CCCGGAATC	GTCAATGGGTG	CTGCGCCAAT	GGCTTATAGC	120
CTATTTACAA	AGCACCTTAG	AATTACACCT	GAGCAGCCAA	ACTGGATTAA	CCGAGATCGC	180
TTTATCTTGT	CTGCGGGTCA	TGGATCAATG	CTACTGTATG	CTCTCTTGCA	TTTAACAGGG	240
TATAAGGATG	TATCCATGGA	CGAGATTAAA	AATTTCCGGC	AATGGGGATC	TAAGACACCT	300
GGTCATCCTG	AAGTGACGCA	TACGTCTGGT	GTGGATGCGA	CATCTGGTCC	GCTTGGTCAG	360
GGGATTTCTA	CTGCCGTTGG	TTTCGCCCCA	GCAGAGCGTT	TTTTAGCTGC	TAAGTACAAC	420
AAAGATGGTT	TTCCTATTTT	TGACCATTAT	ACTTATGTTA	TCGCTGGAGA	CGGTGACTTC	480
ATGGAAGGAG	TGTCTGCGGA	GGCGGCTTCT	TATGCAGGTC	ATCAAGCTTT	AGATAAGCTT	540
ATCGTCTCTT	ACGACTCCAA	CGATATCTGC	TTGGATGGTG	AGACCAAAGA	TACTTTCTCT	600

GAAAATGTTT	GCGCCCGTTA	CGATGCTTAT	GGTTGGCATA	CAGTTCTGGT	AGAAGATGGA	660
ACAGATTTAG	CAGCAATTTT	TACAGCAATT	GAGACGGCCA	AGTTTTCTGG	TAAGCCGAGT	720
TTGATTGAAG	TGAAAACGGT	AATTGGTTAC	GGCTCACCCA	ATAAAAGTGG	TACAAAATGCT	780
GTTTCATGGT	CACCACTAGG	AGCAGAAGAA	ACAGGAGCAA	CTCGTAAGTT	TTTGGGATGG	840
GATTACGATC	CAATTTGAAGT	ACCAGAGGAA	GTATATTTCTG	ATTTCAAGAC	AAATGTAGCG	900
GATCGTGGTC	AGGAGGCATA	CGATGCTTGG	GCTAGTTTGG	TGTCTGATTA	CAAGGTTGCT	960
TATCCCGAAG	TTGCTAGTGA	GATTGACGCT	ATTGTAGCTG	GAAAAATCCCC	TGTAACCATT	1020
ACTGAAAAAG	ACTTCCCTGT	CTATGAGAAT	GGCTTCTCTC	AAGCAACTCG	TAATTCGTCC	1080
CAAGATGCTA	TTAATACAGC	AGCAGCAGTT	TTACCAACCT	TCTTAGGTGG	ATCGGCAGAC	1140
TTAGCTCACT	CCAACATGAC	CTACATCAAG	GCAGATGGCT	TACAAGATAA	ATATAATCCA	1200
TTAAACCGCA	ATATTCAGTT	TGGGGTACGT	GAATTTGCCA	TGGGAACAAT	CCTCAATGGA	1260
ATGGCTCTTC	ATGGTGGTTT	ACGAGTTTAT	GGCGGAACCT	TCTTTGTTTT	CTCTGACTAC	1320
GTCAAAGCTG	CTATTCGGCT	ATCAGCCATT	CAGGAGTTGC	CTGTAACCTA	TGTCCTTTACC	1380
CATGATTCAA	TTGCCGTTGG	TGAAGATGGT	CCAACATCATG	AACCAGTTGA	ACATTTGGCA	1440
GGTTTACGCT	CAATGCCAAA	CTTGACTGTT	ATCCGTCCAG	CGGATGCCCG	TGAAACTCAA	1500
GCGGCTTGGC	ATCATGCCTT	GACCAGTACC	ACCACCTCAA	CTGTCATTGT	CTTAACCCGT	1560
CAAACTTGG	TAGTTGAAGA	AGGGACAGAC	TTTGGTAAGG	TCGCTAAAGG	AGCCTACGTC	1620
GTGTATGATA	CCCCGGGATT	TGATACTATT	ATCATTGCTA	CAGGATCTGA	GGTCAATCTA	1680
GCTATCAAAG	CTGCTAAGGA	ATTGGTTTTA	CAAGGTGGTA	AAGTACGTGT	GGTATCTATG	1740
CCCTCAACCG	AACTATTTGA	TGCTCAAGAT	GCTACCTACA	AGGAAGACAT	TTTACCATCT	1800
AAGACTCGTC	GTCGTGTGGC	CATTGAAATG	GCAGCGACCC	AAAGTTGGTA	CAAGTATGTT	1860
GGTTTGGATG	GCGCGGTCAT	CGGTATTGAC	ATCTTCGGTG	CGTCTGCCCC	AGCTCAGACT	1920
GTGATTGATA	ATTATGGATT	TACGGTAGAG	AATATCGTTG	CTCAAGTTAA	GTCCCTATAG	1980

(2) INFORMATION FOR SEQ ID NO:1993:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1854 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1993:

CAGCTTCATA	TCAATCCAGC	TCAACCAAAC	TGGATTAACC	GCGACCGCTT	TATTCTTTCA	60
GCAGGTCATG	GTTCAATGCT	CCTTTATGCT	CTTCTTCACC	TTTCTGGTTT	TGAAGATGTC	120
AGCATGGATG	AGATTAAGAG	CTTCCGTCAA	TGGGGTTCAA	AAACACCAGG	TCACCCAGAA	180
TTTGGTCATA	CGGCAGGGAT	TGATGCTACG	ACAGGTCCTC	TAGGGCAAGG	GATTTCAACT	240
GCTACTGGTT	TTGCCCAAGC	AGAACGTTTC	TTGGCAGCCA	AATATAACCG	TGAAGGCTAC	300
AATATCTTTG	ACCACTATAC	TTACGTTTATC	TGTGGAGACG	GAGACTTGAT	GGAAGGTGTC	360
TCAAGCGAGG	CAGCTTCATA	TGCAGGCTTG	CAAAAACCTG	ATAAGTTGGT	TGTTCTTTAT	420
GATTCAAATG	ATATCAACTT	GGATGGTGAG	ACAAAGGATT	CCTTTACAGA	AAGTGTTTCGT	480
GACCGTTACA	ATGCCATACG	TTGGCATACT	GCCTTGGTTG	AAAATGGAAC	AGACTTGGA	540
GCCATCCATG	CTGCTATCGA	AACAGCAAAA	GCTTCAGGCA	AGCCATCTTT	GATTGAAGTG	600

AAGACGGTTA	TTGGATACGG	TTCTCCAAAC	AAACAAGGAA	CTAATGCTGT	ACACGGCGCC	660
CCTCTTGGAG	CAGATGAAAC	TGCATCAACT	CGCCAAGCCC	TCGGTTGGGA	CTACGAACCA	720
TTTGAAATTC	CAGAACAAGT	ATATGCTGAT	TTCAAAGAAC	ATGTTGCAGA	CCGTGGCGCA	780
TCAGCTTATC	AAGCTTGGAC	TAAATTAGTT	GCAGATTATA	AAGAAGCTCA	TCCAGAACTG	840
GCTGCAGAAG	TAGAAGCCAT	CATCGACGGA	CGTGATCCAG	TCGAAGTGAC	TCCAGCAGAC	900
TTCCCAGCTT	TAGAAAATGG	TTTTTCTCAA	GCAACTCGTA	ATTCAAGTCA	AGATGCCTTG	960
AATGTTGTGG	CAGCTAAATT	ACCAACCTTC	CTAGGTGGAT	CAGCTGACCT	TGCTCACTCA	1020
AACATGACTT	ATATAAAGAC	GGATGGACTT	CAAGACGATG	CCAATCGCTT	GAATCGTAAC	1080
ATTCAGTTTG	GTGTTTCGTA	ATTTGCAATG	GGAACAATCT	TGAACGGGAT	GGCCCTTCAT	1140
GGTGGACTTC	GTGTATACGG	TGGAACTTTC	TTCGTCTTCT	CTGACTATGT	GAAGGCAGCT	1200
GTCCGCTTGT	CAGCCTTACA	AGGACTTCCT	GTGACTTATG	TCTTTACCCA	TGATTCAATC	1260
GCAGTTGGGG	AAGATGGTCC	GACTCACGAA	CCAGTTGAGC	ATTTAGCAGG	TCTTCGTGCT	1320
ATGCCAAATC	TAAATGTTTT	CCGTCCAGCA	GATGCGCGTG	AAACTCAAGC	AGCTTGGTAC	1380
CTTGCAGTGA	CAAGTGAGAA	AACACCAACT	GCCCTTGTTT	TGACACGTCA	AAACTTGACT	1440
GTTGAAGATG	GAACAGACTT	CGACAAGGTT	GCTAAAGGTG	CTTATGTTGT	ATATGAAAAT	1500
GCAGCCGACT	TTGATACCAT	CTTGATTGCG	ACAGGTTTCAG	AGGTTAATCT	TGCTGTCTCA	1560
GCTGCTAAAG	AATTGGCTAG	TCAAGGCGAA	AAAATCCGCG	TAGTCAGCAT	GCCATCTACA	1620
GATGTCTTTG	ATAAACAAAG	TGCAGCTTAC	AAGGAAGAGA	TTCTTCCAAA	TGCAGTCCGT	1680
CGTCGTGTTG	CAGTCGAAAT	GGGTGCAAGT	CAAACTGGT	ACAAATATGT	TGGTCTCGAT	1740
GGTGCCGTTT	TAGGTATTGA	TACCTTCGGA	GCCTCTGCCC	CAGCACCAAA	AGTATTGGCA	1800
GAATATGGCT	TTACTGTAGA	AAATCTTGTA	AAAATTGTTC	GAAACTTGAA	ATAA	1854

(2) INFORMATION FOR SEQ ID NO:1994:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...324
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1994:

GAGGTTTATA	TGAATCAAGA	GGAAGTGCAG	GTTGCAGCAT	TTGAAATTAT	CCTGCATTTCG	60
GGAAATGCAA	GGTCAGAAAT	ACATGAAGCA	TTTGCAAAAA	TGAGAGAAGG	TAGTTTTTGAT	120
GATGCAGAAA	GTAAATTAAA	TCAATCAAAT	GAGATAATTC	TTGAAGCGCA	TCATGCACAA	180
ACCAAACCTC	TGCAAGAATA	CGCAAGTGGA	GTGGAAATTA	AAATTGAAAT	TATCATGGTA	240
CATGCTCAAG	ATCATTTAAT	GACCACTATG	ACATTATTAG	AAGTAGCAAA	GGAAATGTTA	300
GCTCTTTATA	AGAAAGTTAA	CTAA				324

(2) INFORMATION FOR SEQ ID NO:1995:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...339
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1995:

ACTTGTCATA	TTGAAATCCT	TCCTTTTTCAC	TTTATACGAT	CTACTGATTT	CGATTTTATCT	60
CTATCTTTTCG	TTAAGAAATT	TTTTTCATTT	ACGTTGAATG	ATTTATACTC	AATGAAAATC	120
AAAGAGCAAA	CTAGGAAGCT	AACCGCAGAT	TGCTCAAAAC	ACTGCTTTGA	ACCTGTAGAT	180
AAGACTGACG	AAGTCAGCTC	AAAACACTGT	TTTGAGGTTG	TGGATAGAAC	TGACGAAGTC	240
AGTAACCATA	CCTACGGCAA	GGTGAACTG	ACGTGGTTTG	AAGAGATTTT	CGAAGAGTAT	300
TACCTCATCA	AATTTGTAAA	TATCATGAGC	CTTCTCTAG			339

(2) INFORMATION FOR SEQ ID NO:1996:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1083 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1083
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1996:

AATAGTCATA	TGAAAAGGAT	CCAACTGAAT	ATGAATGAAA	CGAAAAAATA	TCTTGTGATA	60
AAAGCTATAG	CCCAAGGAAA	GAAAACAAAG	AAACGGGCCT	GTGTCGAACT	CAATCTTTCT	120
GAAAGACAAA	TCAATCGTCT	GCTACTAGCC	TATCAACAGA	AAGAAAAAGA	AGCCTTCAGA	180
CACGGAAACA	GAAATCGAAA	ACCAAAACAT	GCAATCCCTG	ATGAAATCAA	AGAACGTATC	240
CTAAAGAAAT	ACCTCTCCTA	TCAAACATAT	AAACCAAATG	TCCGTCATTT	CTGTGAATTG	300
CTAGCTGAAG	AAGAAGGAAT	TCAGCTCTCT	GATACAACTG	TTAGAAAAAT	ACTCTATAAG	360
AAAAATATCC	TGTCGCCTAA	GTCTCACAGA	AAGACAAAGA	AGAGAGTAAG	AAAACAAGCT	420
AAACTGAACC	CCAAGCAACC	CCTAGACAAT	CCAATCTTAC	CGACAGCTGA	AAACTTCCTG	480
GAAGACCCTA	AAAAGGTACA	TCCTAGTAGA	CCCAGAAAAA	AATTTGCTGG	AGAACTCATC	540

CAAATGGATG	CCAGCCCTCA	TGCCTGGTTT	GGAGTAGAAA	CCTCTAACTT	ACACCTAGCC	600
ATTGATGATG	CTTCTGGCAA	TATCCTAGGC	GCTTATTTTG	ACAAACAAGA	GACCTTGAAT	660
GCTTACTATC	ATGTCCTCGA	ACAAATCTTA	GCCAACCACG	GCATTCCTCT	TCAAATTAAA	720
ACAGATAAGA	GAAGTGTGTT	TACCTATCAA	GCCTCCAAC	CTAAGAAAAT	GGAGGACGAC	780
ACCCATACAC	AATTTGGATA	CGCCTGTCAC	CAACTGGGAA	TTCTCCTTGA	GACAACCTCT	840
ATCCCTCAAG	CTAAAGGGAG	AGTCGAAAGA	CTCAATCAGA	CACTACAATC	TCGCCTGCCT	900
ATCGAACTGG	AACGAAACAA	TATTCATACC	TTGGAAGAAG	CCAATACCTT	TCTACCTTCC	960
TATATCCAAA	CCTTTAATGA	ACAGTTTGGA	AACAAGACAA	AACCTCTCTG	CTTTGAGGAG	1020
GCTCCTAAGC	CCTCTGAACG	AAATCTCATT	CTAGCTAGAC	TGGCGGGAGA	GAGTCGTCGA	1080
TAG						1083

(2) INFORMATION FOR SEQ ID NO:1997:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1997:

TTCAAACATA	TGGAGGCAAA	TATGAAACAT	CTAAAAACAT	TTTACAAAAA	ATGGTTTCAA	60
TTATTAGTCG	TTATCGTCAT	TAGCTTTTTT	AGTGGAGCCT	TGGGTAGTTT	TTCAATAACT	120
CAACTAACTC	AAAAAAGTAG	TGTAAACAAC	TCTAACAAAC	ATAGTACTAT	TACACAAACT	180
GCCTATAAGA	ACGAAAATTC	AACAACACAG	GCTGTTAACA	AAGTAAAAGA	TGCTGTTGTT	240
TCTGTTATTA	CTTATTCGGC	AAACAGACAA	AATAGCGTAT	TTGGCAATGA	TGATACTGAC	300
ACAGATTCTC	AGCGAATCTC	TAGTGAAGGA	TCTGGAGTTA	TTTATAAAAA	GAATGATAAA	360
GAAGCTTACA	TCGTACCAAA	CAATCACGTT	ATAAATGGCG	CCAGCAAAGT	AGATATTCGA	420
TTGTCAGATG	GGACTAAAGT	ACCTGGAGAA	ATTGTCGGAG	CTGACACTTT	CTCTGATATT	480
GCTGTCCGTC	AAATCTCTTC	AGAAAAAGTG	ACAACAGTAG	CTGAGTTTGG	TGATTCTAGT	540
AAGTTAACTG	TAGGAGAAAC	TGCTATTGCC	ATCGGTAGCC	CGTTAGGTTC	TGAATATGCA	600
AATACTGTCA	CTCAAGGTAT	CGTATCCAGT	CTCAATAGAA	ATGTATCCTT	AAGATCGGAA	660
GATGGACAAG	CTATTTCTAC	AAAAGCCATC	CAAACTGATA	CTGCTATTAA	CCCAGGTAAC	720
TCTGGCGGCC	CACTGATCAA	TATTCAAGGG	CAGGTTATCG	GAATTACCTC	AAGTAAAATT	780
GCTACAAATG	GAGGAACATC	TGTAGAAGGT	CTTGGTTTTG	CAATTCCTGC	AAATGATGCT	840
ATCAATATTA	TTGAACAGTT	AGAAAAAAAC	GGAAAAGTGA	CGCGTCCAGC	TTTGGGAATC	900
CAGATGGTTA	ATTTATCTAA	TGTGAGTACA	AGCGACATCA	GAAGACTCAA	TATTCCAAGT	960
AATGTTACAT	CTGGTGAGT	TGTTCTGTTG	GTACAAAGTA	ATATGCCTGC	CAATGGTCAC	1020
CTTGAAAAAT	ACGATGTAAT	TACAAAAGTA	GATGACAAAG	AGATTGCTTC	ATCAACAGAC	1080
TTACAAAGTG	CTCTTTACAA	CCATTCTATC	GGAGACACCA	TTAAGATAAC	CTACTATCGT	1140
AACGGGAAAAG	AAGAACTAC	CTCTATCAAA	CTTAACAAGA	GTTTCAGGTGA	TTTAGAATCT	1200
TGA						1203

(2) INFORMATION FOR SEQ ID NO:1998:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 933 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...933
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1998:

CCTATGATTT	TAACAGTCAC	AATGAACCCA	TCCATTGATA	TTTCCTATCC	CTTGATGAG	60
TTGAAGATTG	ATACTGTCAA	TCGTGTGGTG	GATGTAACCA	AAACGGCTGG	TGGTAAGGGA	120
CTTAATGTTA	CCCAGTACT	TTCAGAATTT	GGTGATTCTG	TTCTTGCTAC	TGGTTTAGTG	180
GGTGGCAAAC	TTGGTGAGTT	TTTGGTTGAA	CATATCGATG	ATCAAGTAAA	GAAAGATTTT	240
TTTTCTATT	AGGGAGAAAC	TCGTAAGTGT	ATCGCTATT	TCCACGGTGA	CAACCAAACA	300
GAAGTTCTTG	AAAAAGGTCC	TGAAGTATTG	GAACAGGAAG	GTCAAGACTT	TTTGGAACAT	360
TTCAAAAAAC	TCTTGAGTGC	AGTTGAAGTA	GTAGCCATCT	CAGGTAGTCT	GCCAGCTGGC	420
CTTCCAGTTG	ATTACTATGC	GAGCTTGGTA	GAGCTTGCTA	ATCAAGCTGG	CAAGCTAGTA	480
GTCTTGACT	GCTCTGGTGC	AGCACTTCAG	GCGGTTCTTG	AATCACCCCA	TAAACCGACA	540
GTAATCAAAC	CCAATAATGA	GGAATTGTCT	CAGCTTCTAG	GAAGAGAAGT	TTCTGAGGAT	600
TTGGAGGAAT	TAAAAGAAGT	CCTTCAAGAA	TCTTTGTTTA	CAGGGATTGA	ATGGATTATC	660
GTTTCACCTG	GTGCCAACGG	TACTTTTGCC	AAACATGGTG	ACACTTTCTA	CAAGGTAGAT	720
ATTCCTAGAA	TTCAGGTGGT	AAATCCTGTT	GGATCTGGAG	ACTCTACTGT	GGCAGGAATT	780
TCTTCAGGAC	TTCTTCACAA	AGAATCGGAT	GCAGGATTAC	TCATCAAGGC	AAATGTCCTT	840
GGTATGCTCA	ATGCTCAAGA	AAAAATGACT	GGTCATGTCA	ACATGGCCAA	CTATCAAGCT	900
CTATATGATC	AATTAATAGT	AAAAGAGGTA	TAA			933

(2) INFORMATION FOR SEQ ID NO:1999:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 990 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1999:

GAGACTAATA	TGTTTATTTT	CATCAGTGCT	GGAATTGTGA	CATTTTTTACT	AACTTTAGTA	60
GGAATTCCGG	CCTTTATCCA	ATTTTATAGA	AAGGCGCAA	TTACAGGCCA	GCAGATGCAT	120
GAGGATGTCA	AACAGCATCA	GGCAAAAGCT	GGGACTCCTA	CAATGGGAGG	TTTGGTTTTT	180
TTGATTACTT	CTGTTTTGGT	TGCTTTCCTT	TTCGCCCTAT	TTAGTAGCCA	ATTGAGTAAT	240
AATGTGGGAA	TGATTTTGT	CATCTTGGTC	TTGTATGGCT	TGGTCGGATT	TTTAGATGAC	300
TTTCTCAAGG	TCTTTCGTAA	AATCAATGAG	GGGCTTAATC	CTAAGCAAAA	ATTAGCTCTT	360
CAGCTTCTAG	GTGGAGTTAT	CTTCTATCTT	TTCTATGAGC	GCGGTGGCGA	TATGCTTTCT	420
GTCTTTGGTT	ATCAAGTGCA	TCTAGGGATT	TTCTATATTG	TTTTCGCTCT	TTTCTGGCTA	480
GTCGGTTTTT	CAAACGCAGT	AAACTTGACA	GACGGTGTG	ACGGTTTAGC	TAGTATTTCC	540
GTTGTGATTA	GTTTGTCTGC	CTATGGAGTT	ATTGCCTATG	TGCAAGGTCA	GATGGATATT	600
CTTCTAGTGA	TTCTGGCCAT	GATTGGTGGT	TTGCTCAGTT	TCTTCATCTT	TAACCATAAG	660
CCTGCTAAGA	TCTTTATGGG	TGATGTGGGA	AGTTTGGCTT	TAGGTGGAAT	GCTGGCAGCT	720
ATCTCTATGG	CTCTCCACCA	AGAATGGACT	CTCTTGATTA	TCGGAATTGT	GTATGTTTTT	780
GAAACAACTT	CTGTTATGAT	GCAAGTCAGT	TATTTCAAAC	TGACAGGTGG	TAAACGTATT	840
TTCCGTATGA	CGCCTGTACA	TCACCATTTT	GAGCTTGGGG	GATTGTCTGG	TAAAGGAAAT	900
CCTTGAGAGC	AGTGGAAGGT	TGACTTCTTC	TTTTGGGGAG	TTGGGCTTCT	AGCAAGTCTC	960
CTGACCCTAG	CAATTTTATA	TTTGATGTAA				990

(2) INFORMATION FOR SEQ ID NO:2000:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 990 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2000:

AGAAATAATA	TGATGAAAAG	CCTTGAGGGA	GTGATCGATA	TGTCAAGTAA	AGCCAATCAT	60
GCAAAGACAG	CTATTTGCGG	AATTATCAAT	GTAACCCAG	ATTCCTTTTC	GGATGGTGGT	120
CAATTTTTTT	CTCTTGAGCA	GGCACTCCAG	CAGGCTCGTA	AATTGATAGC	AGAAGGAGCC	180
AGCATGCTAG	ATATCGGTGG	AGAATCAACT	CGGCCGGGAA	GTAGCTATGT	TGAGGTTGAG	240
ATAGAAGAGG	AAATCCAGCG	TGTTGTTCCA	GTGATCAAAG	CTATTCGCAA	GGAAAGTGAT	300
GTCCCTCATTT	CTATTGATAC	TTGGAAAAGT	CAGGTGGCAG	AGGCTGCTTT	GGCTGCTGGT	360
GCTAATCTAG	TTAATGATAT	CACTGGTCTC	ATGGGTGATG	AAAAAATGGC	CCATGTGATA	420
GCTAAAGATG	GAGCGAAAAGT	GGTCATTATG	TTTAATCTTG	TTATGGCTCG	ACCTCAGCAT	480
CCTAGCTCGC	TCATATTCCC	TCATTTTGGA	TTTAATCAAG	CTTTTACAGA	GGAAGAGTTA	540
GCTGACTTTG	AAACATTGCC	AATCGAAGAG	TTGATGGAGA	CTTTCTTTGA	AAGAGCACTA	600
GCGAGAGCAA	ATCAAGCTGG	AATTGCACAA	GAAAATATCC	TGTTGGATCC	AGGAATCGGC	660

TTTGGGCTGA	CTAAGAAAGA	AAATTTGCTT	CTTTTACGAG	ACCTGGATAA	ACTACATCAG	720
AAGGGCTATC	CAATCTTTCT	TGGAGTGTCT	CGCAAGAGGT	TTGTCATCAA	TATCCTAGAA	780
GAAAATGGTT	TTGAAGTCAA	TCCTGAGACA	GAAC TTGGTT	TCCACAATTG	GGACACAGCT	840
TCGGCTCATG	TAAC TAGTAT	CGCTGCGAGA	CAGGGTGTAG	AAGTGGTGCG	CGTGCATGAC	900
GTAGCTAGTC	ACAAGATGGC	GGTTGAAATT	GCCTCCGCTA	TTCGTCTGGC	TGATGAAGCG	960
GAAAATTTAG	ATTTAAAACA	ATATAAATAA				990

(2) INFORMATION FOR SEQ ID NO:2001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2073 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2001:

GTGAATAATA	TGTC TTTTAA	AGTGCTACAT	AAAGGATACC	AACATATCCG	ACTATCATCT	60
TCTTTTTTAC	TTACCTTGGA	TATTCAAAAC	TATCTTCGTT	CCTTGGCGAG	AGATGAAAAG	120
GGGATTGAGT	CTATCCAGTT	TTACATGGAT	CAACAGCACT	TTACTCTACG	CATAAAAGAA	180
GGCTTTTCTG	TATTAGATAA	TGCAGAAGCC	TTTTTAAAAA	GAATTGATAA	AGGGAAAGTT	240
TCTGAGTTGA	TGACTCTTCC	CATTCGTAGA	GAAGAGAGTG	CTTATTCTAT	TGTTTCAGGT	300
GCAGCGGTTA	AGCGTGTACT	TTTTCGTAGT	TTTGTGCCGT	ATCCTATTCG	CTATATATGG	360
ACTAGTTATC	AGGCTTTGGG	TTATATTAGA	GAAGCCTATC	AAACAATAGC	GCGTAAGGAA	420
CTAACGATGG	AAGTCTTGGA	CTGTTCCGGCT	ATTTTATTGT	CTTTGTTTAT	GAACCAATCA	480
AAGACAGCTA	GCAATATCAT	GTTTATGCTT	GATTTGGGGA	ATCATTTAGA	TCAGTGGTCC	540
TTGAAAAAAA	CTGCAACAGA	TTTAGAACAG	AGTCTTCTTG	CAAAAGAGAG	CGATGTATTC	600
CTAGTACAGG	GCGATACGGT	TGTTAGTATC	AAGAGTCCG	ATGTTCAAAT	AGGAGATGTC	660
TTGATCTTAT	CTCAAGGAAA	TGAAATTC TG	TTTGATGGAC	AAGTAGTTTC	AGGTTTAGGT	720
ATGGTCAACG	AAAGTTCCCT	GACAGGAGAG	AGTTTTCCAG	TTGAAAAAAG	AGAGTCTGAT	780
TTGGTTTGTG	CAAATACAGT	ATTAGAAACT	GGAGAGTTAC	GCATTCTGTG	AACAGATAAT	840
CAGATGAACA	GCCGTATTTT	ACAGCTGATT	GAGTTGATGA	AGAAATCTGA	AGAAAACAAG	900
AAAACGAAAC	AACGCTATTT	CATCAAGATG	GCGGATAAAG	TCGTCAAATA	TAATTTCTTG	960
GGGGCTGGGC	TGACTTACCT	ATTGACAGGT	TCTTTTCTA	AGGCTATTTT	TTTCCTATTG	1020
GTCGATTTCT	CCTGCGCTTT	GAAAATCTCT	ACTCCTGTAG	CTTATTTGAC	AGTTATCAAG	1080
GAAGGGTTGA	ACCGTGAAAT	GGTGATTAAG	GATGGAGATG	TTCTGGAGAA	ATATCTGGAA	1140
GTTGATACTT	TCTTGTTTGA	TAAGACAGGA	ACAATCACAA	CTAGTTATCC	TATAGTTGAA	1200
AAGGTGTTAC	CTTTTGAGAG	CTATAGTGAG	GAAGATATTC	TCAGAATCAG	TGCCTGTCTT	1260
GAGGAACACA	TTTATCATCC	TATTGCTAAT	GCCATCGTCA	AGCAAGCTGA	GATAGAGGGA	1320
ATTGAACATG	AGGAAAATGCA	TGGGAAACTC	CAATATATCG	CAAGCAAGGG	GATCAAATCT	1380
CATATAGATG	GCCAACCACT	TCTTATTGGG	AATTATGTCT	TGATGCAGGA	TGAGCAGATT	1440
CATATCAGTT	CAGAACAAAA	TGCTTTAATT	GAAGAGTACA	AGAGTCACTA	CAATCTCTTA	1500
TTCTTGCGCT	ATCAAAATGA	ATTGATTGGA	ATGTTCTGCA	TTCATACTCC	TTTGAGAAAA	1560
GAAGCAAAAA	CAGCCTTGGA	TAACTTTAAG	GCACAGGGGA	AAAAATTGAT	TCTGGCAACA	1620

GGAGACACCT	TGATTAGGAC	AGAGGAGTTA	GTCAAAGATT	TGCCCTTTGA	TCAGGTCTAT	1680
ACAGACTTGA	AACCTGATGG	GAAATTTGAG	TTAGTAGAGA	AACTGCAGAA	AGCAGGTCAC	1740
ACTATTTTGA	TGGTTGGAGA	TGGATTGAAT	GACTCAGCGG	CTTTAACTCT	ATCAGATATC	1800
GGTGTGGTGA	TGAATGAGAG	TGCAGATATT	TCTAAGCAGA	TGAGTGATAT	CTTATTGTTA	1860
GATAATCGTT	TGGATTTCTT	CCAAGAGTTG	GATTCGTTAT	CATCATCTTT	GCAAACACTC	1920
ATCAAGAAAA	ATATTCAGGA	TACCGTTGTC	GTAAATAGTA	GTTTGATTGG	CTTTGGCTTA	1980
TTTAATTGGT	TCAGTCCTTC	AAATCTCTCT	ATCTTACATA	ATCTAACAAC	CTTGCGCATT	2040
GTCTTGCCTA	GCCTGTCTAT	TAAAAATAGA	TAG			2073

(2) INFORMATION FOR SEQ ID NO:2002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1068 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2002:

AAGAATAATA	TGAAAAAAT	TGTCTTTACA	GGTGGGGGGA	CGGTTGGACA	CGTTACCCTC	60
AATCTTTTGT	TAATGCCTAA	GTTTCATCGAA	GATGGTTGGG	AAGTCCACTA	TATCGGGGAC	120
AAGCGTGGTA	TCGAACACCA	AGAAATCCTT	AAGTCAGGTT	TGGATGTCAC	CTTCCACTCC	180
ATTGCGACTG	GGAAATTGCG	TCGCTATTTT	TCTTGGCAAA	ATATGCTGGA	CGTCTTCAAA	240
GTTGGCTGGG	GAATCGTCCA	ATCGCTCTTT	ATCATGTTGC	GACTTCGTCC	ACAGACCCCT	300
TTTTCAAAGG	GGGGCTTTGT	CTCAGTACCG	CCTGTTATCG	CTGCGCGTGT	GTCAGGAGTG	360
CCTGTCTTTA	TTCACGAATC	TGACCTGTCT	ATGGGCTTGG	CCAATAAAAT	CGCCTATAAA	420
TTTGCGACTA	AGATGTATTC	AACCTTTGAG	CAAGCTTCGA	GTTTGTCTAA	GGTTGAGCAT	480
GTGGGAGCAG	TGACCAAGGT	TTTCAGATCAA	AAAAATCCAG	AACCAGATGA	ATTGGTGGAT	540
ATTCAAAGCC	ACTTTAATCA	TAAATTGCCG	ACTGTATTGT	TTGTTGGCGG	TTCTGCAGGT	600
GCTCGTGTCT	TTAACCAATT	GGTGACAGAC	CATAAGAAAG	AACTAACAGA	GCGCTACAAT	660
ATTATCAATC	TAACTGGAGA	TTCTAGCCTG	AATGAGTTGA	GCCAAAATCT	TTTTCGTGTT	720
GACTATGTGA	CCGATCTCTA	TCAACCCCTG	ATGGAATTGG	CTGATATTGT	TGTGACACGT	780
GGTGGTGCCA	ATACGATTTT	TGAGCTCTTG	GCGATAGCAA	AATTGCATGT	CATTGTGCCA	840
CTTGGTCGTG	AAGCTAGTCG	TGGTGACCAG	ATTGAAAATG	CAGCTTACTT	TGTTAAGAAA	900
GGCTATGCAG	AAGACCTTCA	AGAAAGCGAT	TTGACCTTGG	ATAGTTTGGA	AGAGAAGCTT	960
TCTCACTTAC	TAAGTCACAA	GGAAGATTAC	CAAGCTAAGA	TGAAAGCTTC	TAAGGAATTG	1020
AAATCTCTAG	CAGATTTTTA	TCAATTGTTG	AAAAAAGATT	TATCATAA		1068

(2) INFORMATION FOR SEQ ID NO:2003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2003:

GGAGATAATA TGTTAGGAAG TATGTTTCGTT GGTCTCCTAG TGGGATTTTT AGCAGGTGCT	60
ATGACCAATC GTGGAGAGCG AATGGGATGT TTTGGAAAAA TGTTTCTCGG TTGGATCGGA	120
GCCTTTCTAG GTCACCTGCT CTTTGGAAC TGGGGGCCAG TTTTATCAGG AACAGCTATT	180
ATCCAGCTG TTTTAGGTGC CATGATTGTC TTAGCTATTT TTTGGAGACG AGGAAGTTAA	240

(2) INFORMATION FOR SEQ ID NO:2004:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 861 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2004:

GGGATGATTT TAAGTAAAAA TAGAGAAGAT GGGTTAAGAA AATTTGCGAC TAACATCCGA	60
TTAAATACTC TTAGAACATT GAATCATCTT GGATTCCGAC ATTACGGAGG AAGTCTGTCT	120
ATCGTAGAAG TTTTAGCAGT GCTTTATGGT GAAATAATGC CAATGACTCC AGAAATATTT	180
GCAGCACGAG ATAGAGATTA TTTCATATTA TCAAAAGGTC ATGGAGGACC AGCTCTATAC	240
AGTACACTCT ATTTGAATGG TTTCTTTGAC AAAGAATTCT TATATTCTTT AAATACAAAT	300
GGAACCAAAT TACCGTCTCA TCCTGATAGA AATCTAACGC CAGGCATAGA TATGACAACG	360
GGCTCTTTAG GACAAGGAAT TAGTGTTGCA ACTGGACTTG CATATGGTCA GAGAATAAGA	420
AAGAGTCCCT TTTATACTTA TGCTATTGTT GGAGATGGTG AGTTAAATGA GGGACAATGT	480
TGGGAGGCTA TACAGTTTGC TTCTCATCAA CAGTTATCCA ACTTAATTGT ATTTGTTGAT	540
GATAACAAAA AACAAATTAGA TGGTTTTTACA AAGGATATTT GTAATCCAGG TGATTTTCGT	600

GAAAAATTTT	CAGCATTTGG	ATTTGAATCC	ATTAGGGTCA	AGGGTTCAGA	TATTAGAGAA	660
ATTTATGAAG	GGATTGTCCA	ATTAAAACAG	TCACATAATT	CATCACCTAA	GTGCATTGTA	720
TTAGATACTA	TTAAAGGTCA	AGGGGTTCAG	GAGCTGGAAG	AAATGAAATC	CAACCATCAT	780
CTTCGCCCTA	CTGTAGAGGA	GAGACAAATG	TTAACTTCAG	TTGTAGAAAAG	ATTAAGTCAG	840
GAATTGGAGG	AAACAGAATG	A				861

(2) INFORMATION FOR SEQ ID NO:2005:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...261
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2005:

TTAGTAAATA	TGGAGGTAAG	AACATTGGCA	AACATTAAAT	CAGCTATCAA	ACGCGCTGAA	60
TTGAACGTTA	AACAAAACGA	AAAGAACTCA	GCTCAAAAAT	CAGCTATGCG	TACTGCTATA	120
AAAGCTTTTCG	AAGCAAACCC	ATCTGAAGAA	CTTTTCCGTG	CTGCTAGCTC	AGCTATCGAT	180
AAAGCAGAAA	CTAAAGGTTT	GATTACAAA	AACAAAGCAA	GCCGCGATAA	AGCTCGTCTT	240
TCAGCTAAAC	TTGCTAAATA	A				261

(2) INFORMATION FOR SEQ ID NO:2006:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1419 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1419
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2006:

GTGGTAAATA	TGAAATTAAA	TAAAAAAATA	TATTTCTTTG	ATAAAGGAAT	TTTTAATCCT	60
TATCGAATGA	GTAATGTAAA	ATTAAAAAGTT	AATCAGGCAG	TAAAGGATAA	AGAAATTTTC	120
TTCAC TGAGG	AAAAACCATG	GGAAATTCGT	TTTGATAACA	GTTATCCAAA	TGTTTTCTTT	180
GATGATTTAG	CAGGTGTTTA	TCGTTGCTAC	TATTTCTACAT	TTACTGATGA	TGAGGAGTCT	240
GAAAAA TACT	CTTTAGAGGA	GCGTAAGGAA	CGTCAATATC	TACCTCGTGC	GAAGCGTATT	300
GTTTCAC TTT	GTTATGCTGA	AAGTAAAGAT	GGTGTTAACT	GGGTGAAACC	AAATCTAGGT	360
ATTACAG AAT	TTTCGAGGATC	AACTGAAAAAT	AATATTATCG	GACATTTTTTT	ACATGGTACA	420
TCTGTTTTTC	TAGATAAAACA	TGACGCAGAT	GAAAATCGTC	GTTATAAAAT	GTTTACAAAG	480
ATTGATTACG	GTAACGGTGT	TCATTTTCATT	GCTGTAGCAT	TTTCAAAAAGA	TGGTCTACAC	540
TTTGATGAAT	ACATTAAAAGT	ACCAAAC TTC	AATCCACGTG	CAGACACTCA	TAACCATATC	600
ATATATGATG	AAGCATTTAAA	TCGCTATGTG	CTAATTACTC	GTACTTGGAG	AGATTTCATTG	660
CGCTTGCCGT	GTGTATCTAC	GAGTGCTGAT	TTCATTTAACT	GGACTCCAAT	TCAAGAAATT	720
TTGAATGTCT	GTGATTATGA	AAATCAAATT	TATTTCTATGC	CTATTTTTTAA	ACGTGGCGAT	780
TATATACTAG	GTTTAGCTTC	AGTTTTTCCAT	GAAGGAGATC	AACTGAACAA	GAATTACGAT	840
ACAGTGGACC	TTCAATTGAC	TTATAGTTAT	CGTCATGTTG	GTTGGCATT A	TCTAAACACT	900
GATACTCCAC	TTATTCCTCG	TGGTAAAGGT	CAATATGGTG	ATGGAGAATT	TGACTGTGGA	960
TGTATCTATT	CTTCTGCACC	AGTTACTATC	GGTGACCGTA	CTTATTTCTA	CTACATGGGA	1020
GGAAATGGAC	AACATACAAA	CTTCCGTGAA	ACAAGCTTGT	CTCGTGCTTA	TATTGAGAAA	1080
GATCACTTTG	CATATTGGGA	TACTAAACGT	CCAGAATATC	CAGGTGTTTT	GTATACCAAT	1140
GGATTTATTT	TCCTCAATGA	TCAAGTTTAC	CTTGATGCAG	ATATTGCAGC	TGGAGGCTTT	1200
GTAACAATTG	AATTGTTTCGA	GAATAATCAC	ACTCCAATGG	AAATTACAGC	TTCCCTTGAA	1260
AAAATAGAAG	ATGGTCGCTA	TCAAGTGTTA	TTCAGCGAAC	CTTTACCTCG	AACTCAAAC T	1320
CGACTGAAAA	TTAGCTTTTAA	AAATGCTAAA	ATCTACGCAA	TCGAAGGAAA	TTTAGATATT	1380
TTCAGAA TTG	AATCAGACAA	TGCTCTATTG	AGGGGGTAA			1419

(2) INFORMATION FOR SEQ ID NO:2007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2007:

AAAGCAAATA	TGATACAATT	TTATTTGAAA	AAAAATAAAA	AAGGAGATTT	TATTATGACA	60
TTAAAAACAC	TTGCTTTAAT	TAGTGGTATC	GTCGGTCTTG	TGGGAGGAAT	TTTACTTCCTT	120
ATTGGTCCTT	TTGTCTTGTT	GGGAACAACG	GTAAACACAG	CTGCTACAAC	TCTTAATGGA	180
GGAGCTACTG	CAGGGGCTTT	TTCAGGTGTT	GCCTGTACTC	TTGAATGCCT	TGAAGATTGA	240

(2) INFORMATION FOR SEQ ID NO:2008:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 585 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2008:

AGGAAAAATA	TGGA	CTTAAA	ATTTGAAGGG	GTTGATT	TTAG	AATACAAAAA	AGCTAAAAAC	60
AATCTTCCAG	AGTCTTTCTG	GGAAACCTAC	TCAGCATTTG	CAAATACAAA	TGGCGGGAAA		120	
ATAATTCTCG	GGATAGATGA	AAAAAACATT	GACACCTACC	AAAGAGTCAA	TAGACTCCCT		180	
GCGAAACAAA	ATTATGAAGC	AAGTAAACAA	CTAACTGATG	CACGATTTAA	GCGTCTTGTT		240	
GGTGTTTCAGC	GTACCACTTT	TGAAGAGATG	TTAGCTGTAT	TAAAAACAGC	TTATCAACTT		300	
AAACACGCAA	AAGGTGGACG	AAAACCTAAA	TTAAGCCTAG	AAGACCTTCT	TATGGCCACT		360	
CTTCAATATG	TGCGAGAATA	TCGCACTTAT	GAAGAAATTG	CGGCTGATTT	TGGTATCCAC		420	
GAAAGCAACT	TAATCCGTCG	GAGCCAATGG	GTTGAAGTAA	CTCTTGTTCA	AAGTGGTGTT		480	
ACGATTTCAA	GAACTCTTCT	CAGTTCTGAG	GACACGGTAA	TGATTGATGC	GACGGAAGTA		540	
AAAATCAATC	GCCCTAAAAA	AACAATTAGC	GAATCATTTCT	GGTAA			585	

(2) INFORMATION FOR SEQ ID NO:2009:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2364 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2009:

AAAGAAAAATA	TGAAAGATAG	AATAAAAAGAA	TATTTACAAG	ACAAGGGAAA	GGTGACTGTT	60
AATGATTTGG	CTCAGGCTTT	GGGAAAAGAC	AGTTCCAAGG	ATTTTCGTGA	GTTGATTAAA	120
ACCTTGTCCT	TAATGGAAAAG	AAAGCACCAA	ATTTCGTTTTG	AAGAAGATGG	TAGTCTGACA	180

TTAGAAATTA	AGAAAAACA	TGAGATTACC	CTCAAGGGGA	TTTTTCATGC	CCATAAAAC	240
GGCTTTGGCT	TTGTTAGTCT	GGAAGGCGAG	GAGGACGACC	TTTTTGTAGG	GAAAAATGAT	300
GTCAACTATG	CTATTGATGG	TGATACCGTC	GAGGTAGTGA	TTAAGAAAGT	CGCTGACCGC	360
AATAAGGGAA	CAGCAGCAGA	AGCCAAAATT	ATTGATATCC	TAGAACACAG	TTTGACAACA	420
GTTGTCTGGG	AAATCGTTCT	GGATCAGGAA	AAGCCTAAGT	ATGCTGGCTA	TATTCGTTCA	480
AAAAATCAGA	AAATCAGTCA	ACCGATTTAT	GTTAAGAAAC	CAGCCCTAAA	GTTAGAAGGA	540
ACAGAAGTTC	TCAAGGTCTT	TATCGATAAA	TACCCAAGCA	AGAAACATGA	TTTCTTTGTC	600
GCGAGTGTTC	TCGATGTGGT	GGGACACTCA	ACGGATGTCT	GAATTGATGT	TCTTGAGGTC	660
TTGGAATCAA	TGGACATTGT	ATCCGAGTTT	CCAGAAGCTG	TTGTTAAGGA	AGCAGAAAGT	720
GTGCCGTGAT	CTCCGTCTCA	AAAGGATATG	GAAGGCCGTC	TGGATCTAAG	AGATGAAATT	780
ACCTTTACCA	TTGACGGTGC	GGATGCCAAG	GACTTGGACG	ATGCAGTGCA	TATCAAGGCT	840
CTGAAAAATG	GCAATCTGGA	GCTTGGGGTT	CACATCGCAG	ATGTTTCTTA	TTATGTGACC	900
GAGGGGTCTG	CCCTTGACAA	GGAAGCCCTT	AACCGTGCAG	CTTCTGTTTA	CGTGACAGAC	960
CGAGTGGTGC	CAATGCTTCC	AGAACGACTA	TCAAATGGCA	TCTGCTCTCT	CAATCCCCAA	1020
GTTGACCGCC	TGACCCAGTC	TGCTATTATG	GAGATTGATA	AACATGGTCG	TGTGGTCAAC	1080
TATACCATTA	CACAAACAGT	TATCAAGACC	AGTTTTCGTA	TGACCTATAG	CGATGTCAAT	1140
GATATCCTAG	CTGGCGATGA	AGAAAAGAGA	AAAGAATATC	ATAAAATTGT	ATCAAGTATC	1200
GAACTCATGG	CCAAGCTTCA	TGAAACTTTA	GAAAACATGC	GTGTGAAACG	TGGAGCTCTC	1260
AATTTTGATA	CCATGAAGC	GAAGATTTTA	GTGGATAAAC	AAGGTAAGCC	TGTTGATATC	1320
GTTCTTCGGC	AGCGTGGCAT	TGCCGAGCGG	ATGATTGAGT	CTTTTATGTT	GATGGCTAAT	1380
GAAACAGTTG	CCGAACATTT	CAGCAAGTTG	GATTTGCCCT	TTATCTATCG	AATTCACGAG	1440
GAGCCTAAGG	CTGAAAAGGT	TCAGAAGTTT	ATTGATTATG	CTTCGAGTTT	TGGCTTGCGT	1500
ATTTATGGGA	CTGCCAGTGA	GATTAGTCTC	GAGGCAC TTC	AAGACATCAT	GCGTGCTGTT	1560
GAGGGAGAAC	CTTATGCAGA	TGTATTGTCC	GATTGCTTTC	TTTCGCTCTAT	GCAGCAGGCT	1620
TGTTATTTCG	AGCACAAATCA	CGGCCACTAT	GGACTAGCTG	CTGACTATTA	TACTCACTTT	1680
ACCAGTCCAA	TTCGTCGTTA	TCCAGACCTT	CTTGTTTCACC	GTATGATTCT	GGATTACGGC	1740
CGTTCCTAAG	AAATAGCAGA	GCATTTTGAA	CAAGTGATTC	CAGAGATTGC	GACCCAGTCT	1800
TCCAACCGTG	AACGTCGTGC	CATAGAAGCT	GAGCGTGAAG	TCGAAGCCAT	GAAAAAGGCT	1860
GAGTATATGG	AAGAATACGT	GGGTGAAGAG	TATGATGCAG	TTGTATCAAG	TATTGTCAAA	1920
TTCGGTCTCT	TTGTGCAATT	GCCAAACACA	GTTGAAGGCT	TGATTACACAT	CACTAATCTA	1980
CCTGAATTTT	ATCATTTCAA	TGAGCGTGAT	TTGACTCTTC	GTGGAGAAAA	ATCAGGTATC	2040
ACTTTCCGAG	TGGGTCAGCA	GATCCGTATC	CGTGTTGAAA	GAGCGGATAA	AATGACTGGA	2100
GAGATTGATT	TTTCATTTCGT	ACCTAGTGAG	TTTGATGTGA	TTGAAAAAGG	CTTGAAACAG	2160
TCTAGTCGTA	GTGGCAGAGG	GCGTGGTTCA	AATCGTCGTT	CGGATAAGAA	GGAAGACAAG	2220
AGAAAATCAG	GACGCTCAAA	TGATAAGCGT	AAGCATTCAC	AAAAAGACAA	GAAGAAAAAA	2280
GGAAAGAAAT	CTTTTACAA	GGAAGTAGCT	AAGAAAGGAG	CCAAGCATGG	CAAAGGGCGA	2340
GGGAAAGGTC	GTCGCACAAA	ATAA				2364

(2) INFORMATION FOR SEQ ID NO:2010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2010:

GGAGAAAATA	TGCCTCAGTT	AGCGACGATT	TGCTACATTG	ATAATGGGAA	AGAACTGCTC	60
ATGCTCCATC	GTAATAAGAA	ACCCAATGAT	GTCCATGAAG	GGAAATGGAT	TGGTGTGGGT	120
GGTAAGCTAG	AGAGAGGAGA	GACGCCCCAG	GAATGCGCGG	CGCGTGAAAT	CCTTGAAGAA	180
ACAGGGCTCA	AAGCCAAGCC	AGTTCTAAAA	GGTGTCATCA	CTTTTCCTGA	ATTTACACCA	240
GATTTAGACT	GGTACACCTA	TGTTTTTAAG	GTGACGGAGT	TTGAGGGCGA	CTTGATTGAC	300
TGCAATGAGG	GGATGCTAGA	ATGGGTTCCC	TATGATGAGG	TTTTGAGCAA	GCCGACTTGG	360
GAAGGTGACC	ACACCTTTGT	TGAGTGGCTT	TTAGAGGATA	AACCCCTCTT	TTCAGCCAAG	420
TTTGTATTATG	ATGGGGATAA	ATTGTTGGAT	ACCCAAGTTG	ATTTCTATGA	ATAA	474

(2) INFORMATION FOR SEQ ID NO:2011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...846

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2011:

GGAGGAAATA	TCGTGGGAAT	TCGTGTTTAT	AAACCAACAA	CAAACGGTCG	CCGTAATATG	60
ACTTCTTTGG	ATTTGCTGTA	AATCACAACA	AGCACTCCTG	AAAAATCATT	GCTTGTGCA	120
TTGAAGAGCA	AGGCTGGTCG	TAACAACAAC	GGTCGTATCA	CAGTTCGTCA	CCAAGGTGGT	180
GGACACAAAC	GTTTCTACCG	TTTGGTTGAC	TTCAAACGTA	ATAAAGACAA	CGTTGAAGCA	240
GTTGTTAAAA	CAATCGAGTA	CGATCCAAAC	CGTTCTGCAA	ACATCGCTCT	TGTACACTAC	300
ACTGACGGTG	TGAAAGCATA	CATCATCGCT	CCAAAAGGTC	TTGAAGTAGG	TCAACGTATC	360
GTTTCAGGTC	CAGAAAGCAGA	TATCAAAGTC	GGAAACGCTC	TTCCACTTGC	TAACATCCCA	420
GTTGGTACTT	TGATTCACAA	CATCGAGTTG	AAACCAGGTC	GTGGTGGTGA	ATTGGTACGT	480
GCTGCTGGTG	CATCTGCTCA	AGTATTGGGT	TCTGAAGGTA	AATACGTTCT	TGTTGCTCTT	540
CAATCAGGTG	AAGTTCGTAT	GATTCTTGGA	ACTTGCCGTG	CTACAGTTGG	TGTTGTCGGA	600
AACGAACAAC	ATGGACTTGT	AAACCTTGGT	AAAGCAGGAC	GTAGCCGTTG	GAAAGGTATC	660
CGCCCAACAG	TTCGTGGTTC	TGTAATGAAC	CCTAACGATC	ACCCACACGG	TGGTGGTGAA	720
GGTAAGGCAC	CAGTTGGTCG	TAAAGCACCA	TCTACTCCAT	GGGGCAAACC	TGCTCTTGGT	780
CTTAAACTC	GTAACAAGAA	AGCGAAATCT	GACAACTTA	TCGTTCGTCG	TCGCAACGAG	840
AAATAA						846

(2) INFORMATION FOR SEQ ID NO:2012:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1866 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2012:

ATTTTGAATA	TTATAGAGGA	AATCATGACA	AAATTAAGAG	AAGATATCCG	TAACATTGCG	60
ATTATCGCCC	ACGTTGACCA	CGGTAAAACA	ACCCTGGTTG	ACGAATTATT	GAAACAATCA	120
GAAACGCTTG	ATGCACGTAC	TGAATTGGCA	GAGCGTGCTA	TGGACTCAAA	CGATATCGAA	180
AAAGAGCGTG	GGATTACCAT	CCTTGCTAAA	AATACTGCCG	TTGCTTACAA	CGGAACTCGT	240
ATCAACATTA	TGGACACACC	AGGACACGCG	GACTTTGGTG	GAGAAGTTGA	GCGTATCATG	300
AAAATGGTTG	ACGGTGTGTG	CTTGGTCGTA	GATGCCATAT	AAGGAACCAT	GCCACAAACT	360
CGTTTCGTAT	TGAAAAAAGC	CTTGGAACAA	GACCTTGTC	CAATCGTGGT	TGTTAACAAA	420
ATCGATAAGC	CATCAGCTCG	TCCAGCAGAA	GATAGTGGAT	AAGTCTTGGA	ACTTTTCATC	480
GAGCTTGGTG	CAGATGACGA	CCAGCTTGAT	TTCCCAGTGG	TTTATGCTTC	AGCGATCAAC	540
GGAACCTCTT	CATTGTCAGA	TGATCCAGCT	GACCAAGAAG	CGACTATGGC	ACCAATCTTT	600
GACACGATTA	TCGACCATAT	CCCAGCTCCA	GATAGATAACT	CAGATGAGCC	TTTGCAGTTC	660
CAAGTGTGCG	TTTTGGACTA	CAATGACTTC	GTTGGACGTA	TCGGTATCGG	TCGTGTCTTC	720
CGTGGTACAG	TTAAGGTTGG	GGACCAAGTT	ACCCTTTCTA	AACCTGACGG	TACAACATAA	780
AACTTCCGTG	TTACAAAAC	CTTCGGTTTC	TTTGGTTTGG	AACGTCGTGA	AATCCAAGAA	840
GCCAAAGCGG	GTGACTTGAT	TGCCGTTTCA	GGTATGGAAG	ACATCTTTGT	CGGTGAAACC	900
ATCACTCCGA	CAGATGCAGT	AGAAGCTCTT	CCAATCCTAC	ACATCGATGA	GCCAACCTCT	960
CAAATGACTT	TCTTGGTCAA	CAACTCACCA	TTTGCTGGTA	AAGAAGGTAA	ATGGGTAACT	1020
TCTCGTAAGG	TGGAAGAACG	CTTGCAGGCA	GAATTGCAAA	CAGACGTTTC	CCTTCGTGTT	1080
GACCCAACTG	ATTACACAGA	TAAATGGACT	GTTTCAGGAC	GTGGAGAATT	GCACTTGTCA	1140
ATCCTTATCG	AAACAATGCG	TCGTGAGGGC	TATGAACCTC	AAGTATCTCG	TCCAGAAGTT	1200
ATCGTAAAAG	AAATCGACGG	TGTTAAATGT	GAACCATTTG	AACGTGTACA	AATCGACACT	1260
CCAGAAGAA	ACCAAGGGTC	TGTTATCCAA	AGCCTTTCTG	AACGTAAAGG	TGAAATGTTG	1320
GATATGATTT	CAACTGGTAA	TGGTCAAAC	CGTTTGGTCT	TCCTTGTTCC	AGCGCGTGGT	1380
TTGATTGGAT	ACTCAACTGA	GTTCTTGTCA	ATGACTCGTG	GTTACGGTAT	CATGAACCAT	1440
ACCTTCGACC	AGTACTTGCC	ATTGATTCCA	GGGGAAATTG	GTGGACGTCA	CCGTGGTGCC	1500
CTTGTTTCTA	TCGATGCTGG	TAAGGCTACA	ACTTACTCAA	TCATGTCTAT	CGAAGAACGT	1560
GGTACGATCT	TTGTCAACCC	AGGTACTGAG	GTTTATGAAG	GAATGATCAT	CGGCGAAAAC	1620
TCTCGTGAAA	ATGACTTGAC	AGTTAACATC	ACGAAGGCAA	AACAAATGAC	CAACGTTCTG	1680
TCAGCTACTA	AGGACCAAAC	AGCTGTTATC	AAGACGCCTC	GTATCTTGAC	ACTTGAAGAG	1740
TCTCTTGAGT	TCTTGAACGA	CGATGAGTAC	ATGGAAGTAA	CGCCTGAGTC	TATCCGTTTG	1800
CGTAAACAAA	TCCTTAACAA	AGCAGAGCGT	GAGAAAGCTA	ACAAGAAGAA	AAAATCAGCT	1860
GAATAA						1866

(2) INFORMATION FOR SEQ ID NO:2013:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2013:

CGTGTGAATA	TTAAATCTGC	CAGTGATTTG	TTGGGAATTT	CAGCGGATAC	GATTCGGTAT	60
TATGAACGGG	TTGGTCTTGT	GCCACCGATT	ACTCGTACTG	CTACTGGGAT	TCGTGATTTT	120
CAAGATCAGG	ATATCGAAGC	GCTGGAATTT	ATTAAGTGTT	TTCGTTCGGC	GGGTGTCTCT	180
G TAGATAGTT	TAGTTGACTA	TATGTCGCTC	TACCAAAGG	GAGATGAAAC	GAGAGAGGAG	240
AGGCTTGTA	TTT TAGAAGA	GGAAAAGCAA	AAATTAGAGG	AGCGCTTGTC	TCAGCTACAG	300
ACAGCTTTAA	ATCGTTTAAA	TCTCAAAATT	AACTTTTATA	AGGAAGGAAA	ATTTTAA	357

(2) INFORMATION FOR SEQ ID NO:2014:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1059 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2014:

GGAAAGAATA	TGACTGAATA	CAAAAATATT	ATCGTGACAG	GTGGAGCTGG	CTTTATCGGT	60
TCTAACTTTG	TCCATTATGT	TTACGAGAAC	TTTCCAGATG	TTCACGTGAC	AGTCCTAGAT	120
AAGTTGACTT	ATGCTGGAAA	CCGCGCGAAT	ATTGAGGAAA	TTT TAGGTAA	TCGTGTTGAG	180
TTAGTTGTTG	GTGACATTGC	TGATGCGGAG	TTGGTAGACA	AGTTGGCTGC	TCAAGCAGAT	240
GCTATCGTTC	ATTATGCAGC	GGAAAGCCAC	AATGATAATT	CGCTCAATGA	TCCATCGCCA	300
TTTATTCATA	CTAACTTCAT	TGGAACCTAT	ACTCTTTTAG	AAGCTGCTCG	TAAGTATGAT	360
ATTCGCTTCC	ACCATGTATC	GACAGATGAA	GTTTATGGGG	ATCTCCCTTT	ACGCGAAGAT	420

TTGCCAGGTC	ATGGAGAAGG	GCCGGGTGAG	AAATTTACGG	CTGAAACCAA	GTACAATCCA	480
AGCTCGCCTT	ACTCATCAAC	CAAGGCAGCC	TCAGATTTGA	TTGTCAAAGC	CTGGGTGCGT	540
TCTTTTGGAG	TCAAGGCAAC	GATTTCCAAC	TGTTCAAATA	ACTACGGTCC	TTATCAACAT	600
ATCGAAAAAT	TCATCCCACG	TCAGATTACT	AACATCCTAA	GTGGTATCAA	GCCAAAACCT	660
TACGGTGAAG	GTAAAAACGT	TCGTGACTGG	ATTCTATACCA	ATGACCATTC	TTCAGGAGTT	720
TGGACAATCT	TGACAAAAGG	GCAAATCGGT	GAAACCTACT	TGATTGGGGC	TGATGGTGAG	780
AAGAACAATA	AGGAAATTTT	GGAACCTTATC	CTTAAGGAAA	TGGGACAAGC	TGCGGATGCC	840
TATGATCATG	TGACTGACCG	TGCAGGACAT	GACCTTCGCT	ATGCGATTGA	TGCTAGCAAG	900
CTCCGTGATG	AGTTGGGGTG	GAAACCTGAA	TTTACCAACT	TTGAAGCTGG	GCTCAAGGCA	960
ACAATCAAGT	GGTATACAGA	TAACCAAGAA	TGGTGGAAAG	CAGAAAAAGA	AGCTGTTGAA	1020
GCCAATTATG	CTAAGACTCA	GGAGATTATT	ACAGTATAA			1059

(2) INFORMATION FOR SEQ ID NO:2015:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 963 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...963
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2015:

GATAGGAATA	TGGATTTTGA	AAAAATTGAA	CAAGCTTATA	CCTATTTTACT	AGAGAATGTC	60
CAAGTCATCC	AAAGTGATTT	GGCGACCAAC	TTTTATGACG	CCTTGGTGGA	GCAAAACAGC	120
ATCTATCTGG	ATGGTGAGAC	TGAGCTAGAA	CAGGTCAAAG	ACAACAATCA	GACCCTTAAG	180
CGTTTAGCAC	TACGCAAAGA	AGAATGGCTC	AAGACCTACC	AGTTTCTCTT	GATGAAGGCT	240
GGGCAACAG	AACCCTTGCA	GGCCAATCAC	CAGTTTACAC	CGGATGCTAT	TGCTTTACTT	300
TTGGTGTTTA	TTGTGGAAGA	GTTGTTTACA	GAGGAGGAAA	TTACTATCCT	CGAAATGGGT	360
TCTGGGATGG	GAATTCTAGG	CGCTACTTTC	TTGACCTCGC	TTGATAAAAA	GGTGGATTAC	420
TTGGGAATGG	AAGTGATGA	TTTGCTGATT	GATCTGGCAG	CTAGCATGGC	AGATGTAATT	480
GGTTTGCAAG	CTGGCTTTGT	CCAAGGAGAT	GCCGTTCCGC	CACAAATGCT	CAAAGAAAGC	540
GATGTGGTCA	TCAGTGACTT	GCCTGTTGGC	TATTATCCTG	ATGATGCCGT	TGCGTCGCGC	600
CATCAAGTTG	CTTCTAGCCA	AGAACATACT	TACGCTCATC	ACTTGCTCAT	GGAACAAGGG	660
TTTAAGTACC	TTAAGTCAGA	TGGATATGCT	ATTTTTCTAG	CTCCGAGTGA	TTTGTTGACC	720
AGTCCTCAAA	GTGATTTGTT	GAAAGTCTGG	TTGAAAGAGG	AGGCAAGTCT	GGTTGCTATG	780
ATTAGTCTGC	CTGAAAATCT	CTTTGCTAAT	GCCAAACAAT	CTAAGACTAT	TTTTATCTTA	840
CAGAAGAAAA	ATGAAATAGC	AGTAGAGCCT	TTTGTTTATC	CACTTGCTAG	CTTGCAAGAT	900
GCAAGTGTTT	TAATGAAATT	TAAAGAAAAT	TTTCAAAAAT	GGACTCAAGG	TACTGAAATA	960
TAA						963

(2) INFORMATION FOR SEQ ID NO:2016:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1866 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2016:

TCGAGGAATA	TTATGAAACA	AAGTAAATG	CCTATCCCAA	CGCTTCGCGA	AATGCCAAGC	60
GATGCTCAAG	TTATCAGCCA	TGCTCTTATG	TTGCGTGCTG	GTTATGTTTCG	CCAAGTTTCA	120
GCAGGTGTTT	ATTCTTATCT	ACCACTTGCC	AACCGTGTGA	TTGAAAAAGC	TAAAAACATC	180
ATGCGCCAAG	AATTGCAAAA	GATTGGTGCT	GTTGAGATGT	TGGCTCCTGC	CCTTCTTAGT	240
GCAGAATTGT	GGCGTGAATC	AGGTCGTTAC	GAAACCTATG	GTGAAGACCT	TTACAAACTA	300
AAAAACCGTG	AAAAATCAGA	CTTTATCTTA	GGTCCAACTC	ATGAAGAAAC	CTTTACAGCT	360
ATTGTCCGTG	ATTCTGTAA	ATCTTACAAG	CAATTGCCAC	TCAACCTTTA	TCAAATTCAG	420
CCCAAGTATC	GTGATGAAAA	ACGCCACGT	AATGGACTTC	TTCGTACACG	TGAGTTTATC	480
ATGAAGGATG	CTTATAGTTT	CCACGCTAAC	TATGATAGTT	TGGATAGTGT	TTATGATGAG	540
TACAAAGCAG	CCTATGAGCG	TATTTTCACT	CGTAGTGGTT	TAGACTTCAA	GGCTATTATT	600
GGTGACGGTG	GAGCCATGGG	TGGTAAGGAT	AGCCAAGAAT	TTATGGCCAT	TACATCTGCT	660
CGTACAGACC	TTGACCGCTG	GGTTGTCTTG	GACAAGTCAG	TTGCCTCATT	TGACGAAATT	720
CCTGCAGAAG	TGCAAGAAGA	AATCAAGGCA	GAATTGCTCA	AATGGATAGT	CTCTGGTGAA	780
GATACCAATTG	CTTACTCAAG	TGAGTCTAGC	TATGCAGCTA	ACTTAGAAAT	GGCAACAAAC	840
GAGTACAAAC	CAAGCAACCG	TGTTGTCGCT	GAAGAAGAAG	TTACTCGTGT	TGCAACGCCA	900
GATGTTAAAT	CAATTGATGA	AGTTGCAGCC	TTCTCAATG	TTCCAGAAGA	ACAAACGATT	960
AAAACCCCTCT	TCTACATTGC	AGATGGCGAG	CTTGTTGCAG	CCCTTCTAGT	TGGAAATGAC	1020
CAACTCAACG	AAGTCAAGTT	GAAAAATCAC	TTGGGAGCAG	ATTTCTTTGA	CGTTGCTAGC	1080
GAAGAAGAAG	TGGCGAATGT	TGTTCAAGCA	GGATTTGGTT	CACTTGGACC	AGTTGGTTTG	1140
CCAGAGAATA	TTAAATTAT	TGCAGATCGT	AAGGTACAAG	ATGTTGCGAA	TGCAGTTGTC	1200
GGTGCTAACG	AAGATGGCTA	CCACTTGANT	GGTGTGAACC	CAGGCCGTGA	TTTTACTGCA	1260
GAATATGTGG	ATATCCGTGA	AGTTCTGTAG	GGTGAAATTT	CCCCAGATGG	ACAAGGTGTC	1320
CTTAACCTTTG	CGCGTGGTAT	TGAGATCGGT	CATATTTTCA	AACTCGGAAC	TCGCTATTCA	1380
GCAAGCATGG	GAGCAGATGT	CTTGGATGAA	AATGGTCGTG	CTGTGCCAAT	CATCATGGGA	1440
TGTTACGGTA	TCGGTGTGAG	CCGTCTTCTT	TCAGCAGTGA	TGGAGCAACA	CGCTCGCCTC	1500
TTTGTTAACA	AAACGCCAAA	AGGTGAATAC	CGTTACGCTT	GGGGAATCAA	TTTCCCTAAA	1560
GAATTGGCAC	CATTTGATGT	GCATTTGATT	ACTGTCAATG	TCAAGGATGA	AGAAGCGCAA	1620
GCCTTGACAG	AAAAACTTGA	AGCAAGCTTG	ATGGGAGCTG	GTTATGAAGT	CTTGACAGAT	1680
GACCGTAACG	AACGTGTCGG	TGTTAAATTT	AGCGATAGTG	ACTTGATTGG	TCTTCCAATC	1740
CGTATCACTG	TTGGTAAAAA	AGCGGCCGAT	GGCATTGTAG	AAGTTAAGAT	CAAGGCAACT	1800
GGTGACACCA	TTGAGGTTCA	TGCAGATAAC	GTGCTTGAAA	CGCTTGAAAT	CCTAAGCAAG	1860
AAATAA						1866

(2) INFORMATION FOR SEQ ID NO:2017:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1185 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2017:

AAGTTTGATA	TAATGGTAGT	TATGAATAGA	ATAAGAGTCA	GCAAAAGGGT	TGAAAAGAAG	60
CTTGCTAAAG	GGCTAGTTTT	ACTAGAAGCC	AGTGATCTTG	AGAATGTCAA	TCTTAAGGAT	120
CAGGAAGTAG	AGGTGCAGGG	TCAGGAAGGA	AACTTTCTTG	GGACTGCCTA	CCTTTCTCAG	180
CAAAACAAGG	GCTTGGGCTG	GTTTGTTCAGC	AAAGACAAGG	TGGCCTTCAA	TCAAGCTTTC	240
TTTGAAACGT	TGTTTAGAAA	AGCCAAAAGAA	AAGAGAAAACG	CCTACTATCA	AGATGATTTG	300
ACAACCTGCCT	TTCGTCTCTT	TAATCAAGAG	GGAGATGGCT	TTGGGGGTCT	GACAGTGGAT	360
CTTTATGGCG	ACTACGCCGT	CTTTTCTTGG	TATAACTCTT	ATGTTTATCA	GATTCGTCAG	420
ACTATATCAG	AAGCCTTTAG	ACAGGTTTTC	CCTGAGGTTT	TAGGGGCTTA	TGAGAAAATC	480
CGCTTTAAGG	GTTTGGACTA	TGAATCTGCC	CATGTTTATG	GTCAAGAAGC	ACCTGACTTT	540
TTCACGTGTT	TAGAAAATGG	TGTCCTGTAT	CAAGTCTTTA	TGAATGATGG	CTTGATGACA	600
GGAATTTTCC	TAGACCAGCA	TGAGGTTCGC	GGTAGTTTAG	TTGACGGCTT	GGCTATGGGT	660
AAATCCTTGC	TCAATATGTT	TTCCTACACA	GCGGCTTTTT	CAGTAGCTGC	GGCCATGGGA	720
GGAGCTAGCC	AGACAACTTC	TGTTGATCTA	GCCAAACGTT	CACGAGAATT	GTCTCAAGCG	780
CATTTTTCAGG	CAAATGGGCT	CAGCACAGAC	GAGCATCATT	TTATAGTCAT	GGATGTCTTT	840
GAGTATTTCA	AATATGCCAA	ACGCAAAGAC	TTGACCTACG	ATGTGATTGT	CCTAGATCCG	900
CCTAGCTTTG	CTCGGAATAA	AAAACAAACT	TTCTCTGTGG	CCAAGGATTA	TCACAAGTTG	960
ATTTCCCAAG	GTCTTGAGAT	TTTAAATCCG	GGAGGGATTA	TCATTGCCAG	TACTAATGCT	1020
GCCAATGTTT	CCCGTCAGAA	ATTTACAGAA	CAAATTGATA	AAGGCTTTGC	AGGAAGAAGT	1080
TACCAGATTT	TAAACAAATA	TGGTCTTCCA	GCAGATTTTG	CCTATAATAA	AAAAGATGAA	1140
AGTAGTAATT	ACCTCAAGGT	GATTAGTATG	AAGGTTAGTA	AATGA		1185

(2) INFORMATION FOR SEQ ID NO:2018:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 828 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2018:

ACATTTCGATA	TTGATATTGC	CGACCTTCGA	GCACCGCTCG	ATGCGGAAGA	AATGTCTCGT	60
ATTACCATTG	AAGACGAGTA	TACCCTGATT	ATCGTAGACG	TGCCGGTCAC	GGAGGAAAGA	120
AATAACCGCA	CCTACTACGT	AACCATCCCG	CTTGGTATTA	TCATCACTGA	GGAAACCATT	180
ATCACTACGT	GTTTGGAACC	ACTACCTGTC	CTTGATGTCT	TTATCAACCG	TCGATTGCGT	240
AATTTCTATA	CCTTCATGCG	TTCACGTTTT	ATCTTTCAAA	TTCTTTATCG	CAATGCAGAG	300
CTTTACCTAA	CAGCCCTTCG	TTCAATCGAC	CGCAAGAGTG	AACAAATCGA	AAGTCAACTG	360
CATCAATCAA	CTCGTAATGA	AGAATTGATT	GAGCTCATGG	AATTGGAAAA	AACTATCGTC	420
TATTTCAAGG	CCTCCCTCAA	AACAAATGAG	CGCGTGATTA	AGAAATTGAC	CAGTTCAACC	480
AGCAATATCA	AGAAATACCT	TGAGGACGAA	GACCTGCTTG	AAGACACCCT	GATTGAAACC	540
CAACAGGCCA	TCGAGATGGC	AGATATTTAT	GGAAACGTCT	TGCATTCTAT	GACAGAGACC	600
TTTGCCTCTA	TCATTTCTAA	CAACCAGAAC	AACATCATGA	AAACCTTGGC	CCTTGTGACC	660
ATCGTCATGT	CCATCCCAAC	CATGGTCTTT	TCTGCCTACG	GGATGAACTT	TAAGGATAAT	720
GAAATCCCCC	TAAACGGAGA	GCCAAATGCC	TTCTGGTTAA	TCGTCTTTAT	CGCCTTTGCT	780
ATGAGTGTCT	CGCTCACTCT	CTATCTCATC	CATAAAAAAT	GGTTCTAA		828

(2) INFORMATION FOR SEQ ID NO:2019:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 597 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2019:

ACTAAAGATA	TGAAACATGA	TTTTAACCAC	AAAGCAGAAA	CTTTCGATTC	CCCTAAAAAT	60
ATCTTCCTCG	CAAACCTGGT	ATGTCAAGCA	GTCGAGAAAC	AGATTGATAT	TTTATCAGAC	120
AAAGTAATTT	TAGATTTTCG	TGGTGGCACG	GGTCTATTAG	CCTTGCCCTT	AGCCAAGCAG	180
GCTAAGTCAG	TCACTCTTGT	AGACATTTCT	GAGAAAATGT	TGGAGCAAGC	TCGTTTGAAA	240
GTGGAGCAGC	AAGCAATCAA	GAATATCCAG	TTTTTGGAGC	AAGATTTACC	GAAAAATCCC	300
TTGGAGAAAAG	AGTTTGATTG	CCTTGCTGTT	AGTCGGGTTC	TTTCATCATAT	GCCTGATTTG	360
GATGCGGCTC	TCTCACTGTT	TCATCAACAT	TTGAAGGAAG	ATGGGAAACT	CATCATTGCT	420
GATTTTACCA	AGACAGAAAG	TAATCATCAT	GGATTTGATT	TAGCTGAACT	GGAAAACAAG	480
CTAATTGAGC	ATGGTTTTTC	ATCTGTGCAT	AGTCAGATTC	TCTATAGCGC	TGAAGACCTG	540
TTTCAAGGAA	ATCACTCAGA	ATTCTTTTTA	ATAGTAGCCC	AAAAATCACT	CGCCTAG	597

(2) INFORMATION FOR SEQ ID NO:2020:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2020:

AATATGGATA	TCAAATCAGA	AGTTATTGAA	ATTATTGATG	AGTTGTTTAT	GGAAGATGTT	60
TCTGACATGA	TGGATGAAGA	TCTTTTGTGAT	GCAGGTGTCT	TGGATAGTAT	GGGAACGGTT	120
GAGTTGATTG	TGGAGATTGA	GAACCGTTTT	GACATTCGTG	TCCCTGTAAC	AGAGTTTGGT	180
CGTGACGACT	GGAATACAGC	TAATAAAATC	ATAGCTGGTA	TTGTGGAGCT	ACAAAATGCT	240
TAA						243

(2) INFORMATION FOR SEQ ID NO:2021:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2021:

ATAATGGATA	TTAAATTAAA	AGATTTTGA	GGACCCCTGG	ACTTACTCTT	GCATCTGGTT	60
TCTAAGTACC	AGATGGATAT	CTACGATGTG	CCCATTACGG	AAGTCATCGA	ACAGTATCTA	120
GCCTATGTCT	CAACCCTGCA	GGCCATGCGT	CTGGAAGTGA	CGGGTGAGTA	CATGGTCATG	180
GCTAGTCAGC	TCATGCTGAT	TAAGAGTCGT	AAACTCCTTC	CGAAGGTAGC	AGAAGTGACA	240
GACTTGGGGG	ATGACCTGGA	GCAGGACCTC	CTCTCTCAAA	TCGAAGAATA	TCGCAAGTTC	300

AAGCTCTTGG	GTGAGCACTT	GGAAGCCAAG	CACCAAGAAC	GGGCCCAGTA	TTATTCCAAA	360
GCGCCGACAG	AGTTGATTTA	CGAAGATGCG	GAGCTTGTGC	ATGACAAGAC	GACCATTGAC	420
CTCTTTTTTG	CTTTTTCAAA	TATCCTAGCC	AAGAAAAAAG	AGGAGTTTGC	ACAAAATCAC	480
ACGACGATCT	TGCGGGATGA	GTATAAGATT	GAGGACATGA	TGATTATCGT	GAAAGAGTCC	540
TTGATTGGAC	GAGATCAATT	GCGCTTGCAG	GATTTGTTCA	AGGAAGCCCA	GAATGTCCAA	600
GAGGTCATCA	CCCTCTTTTT	GGCAACCCTA	GAGTTAATCA	AAACCCAGGA	GCTGATCCTC	660
GTGCAAGAGG	AGAGTTTCGG	AGATATCTAT	CTCATGGAAA	AGAAGGAAGA	AAGTCAAGTG	720
CCTCAAAGCT	AG					732

(2) INFORMATION FOR SEQ ID NO:2022:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 948 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2022:

AAAAATGGATA	TAGTATATGC	GACAGATAAT	AATTTTGTAG	ATGTATTGAG	TGCATCTATC	60
AAGTCGCTTT	ACACTACTAA	TTCAGATTTG	GATTTAAATT	TATGGATTAT	TGCTGATAAA	120
GTTTCGGATA	GAAATAAAGA	AAAGATAAAT	AGATTATCAA	AACAATTTGC	GCAGAGAGAA	180
ATTAATTGGA	TAGAGAACGT	TGAGATTCCA	TTTAAATTAC	ATTTAGATAG	GGGATCAATT	240
AGTTCATTTA	GCAGATTATT	TCTGGGAAGT	GTTCTTCCAT	CTTCAATGAG	TAAAGTTCTC	300
TATCTTGATA	GTGATATTAT	TGTAATGGAT	TCTTTACGAA	GTATTCTTGA	TATTGATTTT	360
AAAGATAAAA	TTCTCTATGG	GGTAAATGAT	ACTTTTAATA	AAGAATACAA	GCAGGTGTTG	420
GGGATACCAA	TCGACAAACC	AATGTTTAAT	GCTGGAGTTA	TGCTGATTAA	TTTAGAGTTA	480
TGGAGAAATA	ATAACGTCGA	AGAAAAATTT	TTGCAAGTAA	TTCAAAAGTT	TAATGGTACT	540
ATATTACAAG	GTGATTTAGG	AGTTTTAAAT	GCAGTTTTAT	ATAACTCATT	TGGTGTACTT	600
CCTCCAGAAT	ATAATTATAT	GACCATATTT	GAAGATTTGA	CTTATGAAGA	AATGATAGTT	660
TTTAAAAAAC	CAATTAACTA	TTATTCAAAA	GAAGAAATTA	AAAATGCTAG	AGAACGTATA	720
GTCTTGCGCC	ATTTCACAAAC	GTGTTTCTTA	TCACTCAGAC	CTTGGCAAGA	AAATAGTGAG	780
GTGGCGCATG	TGGAAATATT	TAAAAAATAC	TATAGAGGAA	CATACAAACA	AGTATCTCCA	840
TCTAAGTTAT	CAAGAATTTA	TAAAATTTTA	CCGAAAAAAA	TGTCGCTCTA	TTTACTAGGT	900
TTTATTCAAT	CAAAAGTGCG	TCCAAAACCTG	TATAGAATTT	TGAAATAA		948

(2) INFORMATION FOR SEQ ID NO:2023:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...639
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2023:

ACTTTATGTA	TCTTTAGAAA	GTGTGTTAAC	TTGAAAGAAC	AAATTTT	GATGGGTGGG	60
AATCCCCAA	TGAAGAAATA	TAGTATTGTT	GATAAAATTG	TATTATCAAC	CAAGATTAAA	120
AGAATTATCA	TTTTTACAGT	TTTTTCGAGAA	AATTGGGAAC	CGTACATGAA	AAAAGTACACG	180
GAAGTTTTTC	AAAAGTCAATT	TCCTAATCTA	AACATTGATT	ACTTGCTCCT	GGACACTGAG	240
CAGATTGATC	TTGATAGCTA	TCTAGATGCT	GACATAATTA	TCATCGGTGG	TGGAAATACG	300
GAAAAATATA	TTGCTACTTA	TGTTAATCAG	GAGTTCAAAA	GTTATATCGA	TCATATGCTT	360
AATAAAGAGG	CAAAAATTAT	AGGATTTTCT	GCAGGAGCCC	TACTATTAGG	AGAAAAAGTC	420
TATGTCTCAC	CTAATGATAA	TTCAATCAT	CAGATAAAGA	TAAAAAATGG	ATTAGGACTC	480
TTTAGTCAGT	TTTAAATTAG	TGTCCATTAT	GATTCCTGGA	ATGATAAAGC	AAATAAGGAT	540
AGAGCTGAAG	AACTCGTTAA	TGTTCCCAT	ATTCCACTAA	ATGATCATTC	TTGTCTTGTA	600
TTGGATAAAC	TTGGAAACAT	CATAGAGAAA	ATTGACTAA			639

(2) INFORMATION FOR SEQ ID NO:2024:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1713 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1713
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2024:

TTGTTATGTA	TCCATTCTTC	CAAAAATACT	TTGATAAAGG	AATTATGGCT	GGTTCACTTA	60
AAGGATAAAA	AAAGAAAAAA	TAAAAGGAGT	TTTCTCATGA	AATTCAAAAC	ATTCTCAAAA	120
TCAGCAGTTT	TGTTGACAGC	TAGTTTAGCA	GTACTTGCGAG	CCTGTGGCTC	AAAAAATACA	180
GCTTCAAGTC	CAGATTATAA	GTTGGAAGGT	GTAACATTCC	CGCTTCAAGA	AAAAGAAAACA	240
TTGAAGTTTA	TGACAGCCAG	TTCAACGTTA	TCTCCTAAAG	ACCCAAATGA	AAAGTTAATT	300
TTACAACGTT	TGGAGAAGGA	AACTGGCGTT	CATATTGACT	GGACCAACTA	CCAATCCGAC	360
TTTGCAGAAA	AACGTAACCT	GGATATTTCT	AGTGGTGATT	TACCAGATGC	TATCCACAAC	420

GACGGAGCTT	CAGATGTGGA	CTTGATGAAC	TGGGCTAAAA	AAGGTGTTAT	TATTCCAGTT	480
GAAGATTTGA	TTGATAAATA	CATGCCAAAT	CTTAAGAAAA	TTTTGGATGA	GAAACCAGAG	540
TACAAGGCCCT	TGATGACAGC	ACCTGATGGG	CACATTTACT	CATTCCCATG	GATTGAAGAG	600
CTTGAGATG	GTAAAGAGTC	TATTCACAGC	GTCAACGATA	TGGCTTGGAT	TAACAAAGAT	660
TGGCTTAAGA	AACTTGGTCT	TGAAATGCCA	AAAACACTG	ATGATTTGAT	TAAAGTCCTA	720
GAAGCTTTCA	AAAACGGGGA	TCCAAATGGA	AATGGAGAGG	CTGATGAAAT	TCCATTTACA	780
TTTATTAGTG	GTAACGGAAA	CGAAGATTTT	AAATTCCTAT	TTGCTGCATT	TGGTATAGGG	840
GATAACGATG	ATCATTTAGT	AGTAGGAAAT	GATGGCAAAG	TTGACTTCAC	AGCAGATAAC	900
GATAACTATA	AAGAAGGTGT	CAAATTTATC	CGTCAATTGC	AAGAAAAAGG	CTTGATTGAT	960
AAAGAAGCTT	TCGAACATGA	TTGGAATAGT	TACATTGCTA	AAGGTCATGA	TCAGAAATTT	1020
GGTGTCTTACT	TTACATGGGA	TAAGAATAAT	GTTACTGGAA	GTAACGAAAAG	TTATGATGTT	1080
TTACCAGTAC	TTGCTGGACC	AAGTGGTCAA	AAACACGTAG	CTCGTACAAA	CGGTATGGGA	1140
TTTGCACGTG	ACAAGATGGT	TATTACCAGT	GTAAACAAAA	ACCTAGAATT	GACAGCTAAA	1200
TGGATTGATG	CACAATACGC	TCCACTCCAA	TCTGTGCAAA	ATAACTGGGG	AACTTATGGA	1260
GATGACAAAC	AACAAAACAT	CTTTGAATTG	GATCAAGCGT	CAAATAGTCT	AAAACACTTA	1320
CCACTAAACG	GAAGTGCACC	AGCAGAACTT	CGTCAAAGA	CTGAAGTAGG	AGGACCACTA	1380
GCTATTCTAG	ATTCATACTA	TGGTAAAGTG	ACAACCATGC	CAGATGATGC	CAAATGGCGT	1440
TTGGATCTTA	TCAAAGAATA	TTATGTTCCCT	TACATGAGCA	ATGACAATAA	CTATCCAAGA	1500
GTCTTTATGA	CACAGGAAGA	TTTGGACAAAG	ATTGCCCATTA	TCGAGGCAGA	TATGAATGAC	1560
TATATCTACC	GTAAACGTGC	TGAATGGATT	GTAAATGGCA	ATATTGATAC	TGAGTGGGAT	1620
GATTACAAGA	AAGAAGTTGA	AAAATACGGA	CTTTCTGATT	ACCTCGCTAT	TAAACAAAAA	1680
TACTACGACC	AATACCAAGC	AAACAAAAAC	TAG			1713

(2) INFORMATION FOR SEQ ID NO:2025:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2268 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2268
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2025:

GGTAGATGTA	TGCTTTGTCA	AAACTGTAAA	ATTAACGACT	CAACAATTCA	TCTTTACACC	60
AATCTCAATG	GAAAACAAAA	ACAAATTGAC	CTCTGTCAAA	ACTGCTATAA	GATTATCAAA	120
ACAGATCCTA	ACAATAGCCT	CTTCAAAGGT	ATGACGGATC	TGAACAATCG	TGACTTCGAT	180
CCCTTTGGTG	ATTTCTTCAA	TGATCTAAAC	AATTTTCAGAC	CTTCTAGCAA	TACTCCTCCT	240
ATTCCCCCAA	CCCAATCAGG	TGGAGGTTAC	GGTGGAAACG	GCGGTTATGG	TTCCCAAAAT	300
CGTGGATCTG	CTCAAACCTCC	GCCACCTAGC	CAAGAAAAAG	GCCTGCTGAA	AGAAATTTGGT	360
ATTAATGTAA	CTGAAATTGC	CCGTCTGTGA	GACATTGACC	CCGTTATTGG	GCGCGACGAT	420
GAGATTATCC	GTGTCATCGA	GATTCTCAAT	CGTAGAACCA	AGAATAATCC	TGTCCTTATC	480
GGTGAACCTG	GTGTCGGAAA	AACGGCCGTT	GTCGAAGGTC	TAGCTCAGAA	AATTGTCGAT	540
GGCGATGTGC	CACATAAACT	CCAAGGTAAA	CAAGTCATCC	GTCTGGATGT	GGTTAGCTTA	600
GTTCAAGGAA	CGGGGATTCTG	AGGACAATTT	GAAGAACGCA	TGCAAAAACT	CATGGAAGAA	660

ATTCGCAAAC	GTGAAGACAT	CATCCTCTTT	ATCGATGAAA	TCCATGAAAT	TGTTGGTGCT	720
GGTTCTGCGA	GTGATGGTAA	TATGGACGCA	GGAAATATCC	TCAAGCCAGC	CCTTGCTCGT	780
GGAGAAATGC	AACTAGTCGG	TGCTACTACC	CTCAATGAAT	ACCGTATCAT	TGAAAAGGAT	840
GCTGCCCTCG	AGCGTCGTAT	GCAGCCTGTT	AAAGTCGATG	AACCAACGGT	GGATGAAACA	900
ATCACTATTC	TCAAAGGGAT	TCAAAAGAAA	TACGAAGATT	ACCACCACGT	TCAATATACC	960
GATGCTGCGA	TTGAAGCAGC	TGCAACTCTT	TCCAATCGCT	ACATCCAAGA	TCGCTTCTTG	1020
CCTGACAAGG	CCATTGACCT	CCTAGATGAA	GCTGGTTCTA	AGATGAACTT	GACCTTGAAT	1080
TTTGTGGATC	CTAAAGTAAT	TGATCAGCGC	TTGATTGAGG	CTGAAAATCT	CAAGTCTCAA	1140
GCTACACGAG	AAGAAGATTT	TGAGAAGGCG	GCCTACTTCC	GCGACCAGAT	TGCCAAGTAT	1200
AAGGAAATGC	AAAAGAAAAA	GATCACAGAC	CAGGATACTC	CTATCATCAG	CGAGAAAACT	1260
ATTGAGCACA	TTATCGAGCA	GAAAACCAAT	ATCCCTGTTG	GTGATTTGAA	AGAGAAAGAA	1320
CAATCTCAAC	TCATCCATCT	AGCCGAAGAT	CTCAAGTCTC	ATGTTATTGG	CCAAGATGAT	1380
GCAGTCGATA	AGATTGCCAA	GGCTATTTCG	CGTAATCGTG	TCGGACTTGG	TACCCCTAAC	1440
CGCCCAATCG	GAAGCTTCC	CTTCGTTGGG	CCAAGTGGTG	TCGGTAAGAC	AGAACTTTCC	1500
AAACAACCTG	CTATCGAACT	TTTTGGTTCT	GCTGATAGTA	TGATTTCGCT	TGATATGAGT	1560
GAATACATGG	AAAAACATAG	TGTAGCTAAG	TTGGTCGGCG	CTCCTCCAGG	TTATGTTGGC	1620
TATGATGAGG	CTGGTCAATT	AACTGAAAAA	GTTTCGCCACA	ATCCATATTC	TCTCATCCTT	1680
CTCGATGAAG	TGAAAAAAGC	TCACCCAGAT	GTTATGCACA	TGTTTCTTCA	AGTCTTGGAC	1740
GATGGTCGTT	TGACAGACGG	GCAAGGACGC	ACCGTTAGCT	TCAAGGATGC	CATCATATATC	1800
ATGACCTCAA	ATGCAGGTAC	AGGAAAGACC	GAAGCTAGCG	TTGGATTTGG	TGCTACTAGA	1860
GAAGGACGTA	CCAATTCTGT	CCTCGGTGAA	CTCGGTAAC	TCTTTAGCCC	AGAGTTTATG	1920
AACCGTTTTG	ATGGCATTAT	CGAATTTAAG	GCTCTCAGCA	AGGATAACCT	CCTTCAGATT	1980
GTCGAGCTCA	TGCTAGCAGA	TGTTAACAAG	CGCCTCTCTA	GCAACAACAT	TCGTTTGGAT	2040
GTAAC TGACA	AGGTCAAGGA	AAAGTTGGTT	GACCTAGGTT	ATGATCCAAA	AATGGGAGCA	2100
CGCCCACTTC	GTCGGACTAT	TCAAGACTAT	ATTGAGGACA	CAATCACTGA	CTACTACCTT	2160
GAAAATCCAA	GCGAAAAAGA	TCTCAAAGCA	GTTATGACTA	GCAAGGGAAA	CATTTCAGATT	2220
AAATCTGCCA	AAAAAGCTGA	AGTTAAAAGT	TCTGAAAAAG	AAAAATAA		2268

(2) INFORMATION FOR SEQ ID NO:2026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2026:

CATAAGTGTA	TTATTCTTTA	TATAGATAAA	AATATAGATA	AAAGAAAGGA	TACTAATATG	60
GTATTAGCGA	TTATTTTAGT	AACATTCCCT	ATTCGATTGA	TTTTTTTAAA	GCGTTCGATA	120
GAGAA TGAGA	AACGAATCCT	TAGCAATGGC	GGGAAAGAAT	TTGGAGTTGA	GAATACAAAA	180
CGATTAACTG	TGGCTCATAT	TGTTTTTTAT	CTCTCTTGCC	TCGTTGAAGC	AATGGTGTCAT	240
AAGACAAATG	TTGATGGTAT	GAGCATGGTT	GGTTTAGTCT	TGCTTATTTT	TTCTATGCTG	300
ATGTTGATGT	TGGTGATTCA	CTTGTTGGGA	GATATTTGGA	CAGTGAAGCT	TATGCTTGTC	360

AATAATCACA	AATATGTAGA	TCATATCTTG	TTTAGGACAG	TAAAACATCC	TAATTACTTT	420
TTAAATATTT	TACCTGAGTT	GATTGGCTTG	ACCTTGTTGA	GTCATGCCTA	TATGACTTTT	480
GTTTTAGTCT	TTCCAGTTTA	TGCAGTTATT	TTGTATCGAC	GAATAGCTGA	AGAGGAAAAG	540
CTATTACATG	AAGTTATAAT	CCCAAATGGA	AGCATAAAGA	GATAA		585

(2) INFORMATION FOR SEQ ID NO:2027:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1176 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1176
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2027:

GGAGAGTGTA	TGAGATATTT	AACTGCAGGA	GAATCACACG	GCCCCCGTCT	AACAGCTATT	60
ATTGAGGGAA	TTCCAGCTGG	ACTTCCATTG	ACAGCTGAGG	ATATCAATGA	GGACCTTAGA	120
CGCCGTCAGG	GTGGCTACGG	TCGTGGTGGT	CGTATGAAGA	TTGAGAGTGA	CCAGGTTGTC	180
TTTACTTCGG	GCGTTCGCCA	CGGGAAGACG	ACAGGGGCGC	CTATTACTAT	GGATGTCATC	240
AATAAGGACC	ACCAGAAATG	GCTGGACATC	ATGTCTGCGG	AGGACATTGA	AGACCGCCTT	300
AAAAGCAAGC	GGAAAATTAC	TCATCCTCGC	CCAGGTCATG	CCGATTTGGT	TGGGGGGATT	360
AAGTACCGTT	TTGATGATTT	GCGAAATTCT	TTGGAGCGTT	CATCAGCTCG	TGAAACCACC	420
ATGCGGGTGG	CAGTTGGTGC	AGTAGCCAAA	CGCCTCTTGG	CTGAGCTGGA	TATGGAGATT	480
GCCAACCATG	TCGTGGTCTT	TGGTGGTAAG	GAAATAGATG	TTCTTGAAAA	TCTGACAGTC	540
GCTGAAATTA	AGCAAAGAGC	TGCCCAGTCT	GAAGTTTCTA	TTGTCAACCA	AGAACGAGAA	600
CAGGAAATCA	AGGACTATAT	TGACCAAATC	AAACGTGATG	GTGATACCAT	CGGTGGGGTT	660
GTGGAGACAG	TCGTCGGAGG	CGTTCCAGTT	GGTCTTGGTT	CCTATGTCCA	ATGGGATAGA	720
AAATTGGATG	CAAGATTGGC	TCAAGCTGTT	GTCTCTATCA	ATGCCTTTAA	AGGGGTGGAA	780
TTTGGTCTTG	GCTTTGAGGC	TGGTTATCGT	AAAGGCAGCC	AAGTTATGGA	TGAAATTCTC	840
TGGTCTAAAAG	AAGACGGTTA	TACTCGCCGT	ACCAATAATC	TAGGTGGTTT	TGAAGGTGGT	900
ATGACTAATG	GGCAACCCAT	CGTTGTTCGT	GGGGTCATGA	AACCCATTCC	TACTCTTTAT	960
AAACCTCTTA	TGAGTGTGGA	TATCGAAACC	CACGAACCTT	ACAAGGCAAC	CGTGGAGAGA	1020
AGTGATCCGA	CTGCTCTTCC	AGCTGCAGGA	ATGGTCATGG	AAGCAGTTGT	AGCAACGGTT	1080
CTGGCGCAAG	AAATCCTCGA	AAAATTCTCA	TCAGATAATC	TTGAGGAACT	AAAAGAAGCG	1140
GTAGCCAAAC	ACCGAGACTA	TACAAAGAAC	TATTAA			1176

(2) INFORMATION FOR SEQ ID NO:2028:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1476 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1476
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2028:

AGGAGGTGTA	TCGTGTCTAG	AAAACAAGAA	CAAATGGAAA	CGTTGTTGCT	CCTTTTGCGA	60
GATAGTAAGG	ATTATATATC	TGCTAAAGTA	TTGGGAGAAA	AATTAAATTG	CTCTGATAAA	120
ACGGTTTATC	GCCTTGTCAA	GGGAATCAAC	AAAGATTGTC	CGGTAGAAGC	ATTCAATTTTA	180
TCTGAAAAAG	GCAGAGGTTT	CAAATTAAT	CCAAGAAGTT	CCCTCGTGGA	CGTTGATGGG	240
AATTTTACAG	AGGCTTTTGA	TCCTGAAGTA	AGGCGTGAAA	AATTACTAGA	ACGTCTCTTG	300
TTGACTGCTC	CTAAGCCACA	TTCTATTTAT	GATTTAGGAG	AGGAATTCTA	CGTAAGCGAG	360
TCAGTAGTAC	TAAAAGATCG	TCAGATATTA	CAAGAGAGTC	TAGCAATTTA	TGGGTTAGAT	420
TTAAAAATGA	GACAACGAAA	GCTTTTTATT	GATGGGGATG	AGGCTCAAAT	TCGTTCAGCC	480
ATTCTAAATC	TACTGCCAAT	GTTTAATCAG	TTGGATTTAG	AGCAAATTAC	ACAGAATAAG	540
GTTCAGCCTC	TTGACGGAGA	ACTTGCTCAC	TTTTGTTTGG	GATTACTGAT	TACACTTGAG	600
AGAGAATTGG	GGGTAAACAT	TCCCTATCCA	TATAATATAA	ATATTTTCTC	TCACCTGTAT	660
ATTTTTATCA	GTAGGAATCG	TCGTAGTACT	AGTATTCATG	TTGTAGCACC	TTCAAAACCT	720
ACTATTGTTG	ATGAGAAAAT	TTACAGTGTC	TGTCAAAAAA	TTATTCAAGA	AATTGAACAA	780
TATTTTAGGA	TGAAGGTTGA	TGCAGTTGAG	ATTGACTATC	TTTATCAATA	CGTTGTATCT	840
TCGAGATTGC	AAAAACCATT	TTCTTCCGGG	AAGCTTCCTT	TTTCTCAGCG	AGTTTTAGAT	900
GTCACTCATT	ACTATTTTAG	CCGTATGTGT	ATGGACAATA	GAGAGATTGA	AACGACAGAT	960
CCTGACTTTG	TTGACTTGGC	GAGTCATATC	AGTCCCTTAC	TGAGGAGATT	AGATAATAGA	1020
GTACAGATTA	AGAATAGTCT	TTTATCACAA	ATTCTTTTAA	CCTATCCTAA	TCTGGTTAAA	1080
GAGTTAACAA	CTATTTCTAA	AGAAGTGAGT	CTAGTATTTG	GTTTTGCTTC	CTTGAGTCTG	1140
GACGAGATTG	GTTTTCTAGT	CTTATATTTT	GCACGGTTTC	AAGAAAAGCG	AGCACGTCCT	1200
CTAAAAACAG	TAGTGATGTG	TACATCAGGT	GTCGGAACCT	CAGAGCTTTT	ACGAGCACGA	1260
TTAGAAAAGC	AATTTTCTGA	ATTGGATATT	ATTGATGTAG	TTGCTTATCA	TCAATTAGAT	1320
GAGCTGATAA	ATCTATATCC	AGATTTAGAT	TTCAATTGTGA	CGACGGTAGC	TTTGCAGGAA	1380
CCAGCAAGTG	TCCCGTTTGT	CCTAGTTAGT	GTTTTTCTAA	CCGAGGGTGA	TAAACAACGT	1440
CTTCAAGCAA	AAATTCAGGA	GATAAACTAT	GAATAA			1476

(2) INFORMATION FOR SEQ ID NO:2029:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 654 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2029:

GGACAGCTCT	TATGCAGGCA	GAAAATGTGG	CCCAGAGAAT	CAAGGAGTTG	CAGATTGACA	60
AAGGTTAAAA	TTTGTGGACT	ATCGACCAAA	GAAGCGGTGG	AAACAGCCGT	TTCAGCAGGA	120
GCCGACTATA	TCGTTTTTGT	CTTTGCACCT	AGTAAAAGAC	AGGTGACTTT	AGAAGAGGCA	180
GCTGAGTTGG	CAAAGCTTAT	TCCTGCAGAT	GTGAAAAAGG	TTGGAGTATT	TGTTTCACCA	240
AGTCGGGTAG	AACTGCTGGA	AGCGATTGAC	AAAGTTGACT	TGGACTTGGT	TCAAGTTCAC	300
GGTCAGGTGG	CAGATGATTT	ATTTGAGAAT	TTGCCTTGTT	CCAGTATTCA	GGCTGTGCAG	360
GTAGATGGAA	ATGGGCATGT	CCCCAATTCT	CAGGCAGATT	ATCTACTCTT	TGATGCCCCCT	420
GTGGCAGGAA	GTGGCCAGTC	CTTTGATTGG	GGTCAACTGG	ATACGACTGG	ACTAGCACAG	480
CCCTTCTTTA	TCGCAGGTGG	CCTTAATGAA	GATAATGTAG	TAAAAGCAAT	TCAACATTTT	540
ACTCCCTATG	CAGTAGATGT	ATCGAGCGGA	GTGGAGACAG	ATGGACAAAA	AGATCATGAA	600
AAGATTAGAA	GATTTATAGA	GAGGGTAAAG	CATGGCATAT	CAGGAACCAA	ATAA	654

(2) INFORMATION FOR SEQ ID NO:2030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2030:

GAGAAATAGTA	TGGAAATCAA	ATTTACAATT	AAACAAGTTG	TTGCTGTCGG	AATTGGCGCT	60
GCCCTCTTTG	TCGTCATCGG	GATGATCAAC	ATTCCAACCC	CTGTTCCAAA	TACAAGCATC	120
CAGCTTCAGT	ATGCGGTACA	AGCGCTACTT	TCTATTATTT	TTGGACCGAT	TATCGGTTTG	180
CTTGTCGGGT	TGATTGGTCA	TGCAATCAAA	GACTCTCTTG	TTGGTTATGG	TCTATGGTGG	240
ACTTGGATTA	TCTCTAGCGG	ACTCTTTGGT	TTAGTTGTGG	GACTTTTTTAG	AAAGTACGTT	300
CGCGTGATCA	ATAGTGTTTT	TGACTGGAAA	GATATTCTTA	TTTTTAATCT	CATTCAACTA	360
CTTGCAAATG	CCCTTGTTTT	GGGTGTCTTG	GCACCACTTG	GAGATGTTGT	GATTTATCAA	420
GAAGCGGCAG	AAAAAGTATT	TGCACAAGGG	ATTGTTGCGG	GAATTGCCAA	TGGTGTATCT	480
GTAGCTATTG	CAGGAACCTCT	TCTCTTACTT	GCCTATGCAG	GAACCCAAAC	TCGTGCAGGA	540
AGTTTGAAAA	AGGACTAA					558

(2) INFORMATION FOR SEQ ID NO:2031:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2031:

GGGAATAGTA	TGATTTATTT	AAGAAAGTTA	AAGAGAGAAG	ATTTGATGTC	TTTATGGGAA	60
ATGGCTTATT	CACAACTTAA	TCCAGTTTGG	AAACAGTATG	ATGCTCCCTA	TTATGATGAT	120
TATCAGTATT	TTTCAAATTT	TAAAGAATTC	GAACACAAA	AATCAGAATC	CATTTTAAGC	180
AACTCAAATC	GCCTTGGTAT	TTTTGTTGAT	GATAAACTAG	TTGGGACTGT	TTCGCGTTAT	240
TGGGTATGTA	AACAAACAAG	ATGGATGGAA	TTGGGAATTG	GTATTTATGA	TAAAAAATTC	300
TGGAACACTG	GTATTGGGAA	AGTTGCTATG	TTGCAGTGGA	TAGATAGGAC	GTTTCAGGAT	360
TACTTGGAGT	TGGAGCATCT	GGGTTTGACA	ACTTGGTCAG	GAAATCTTGG	TATGATGAAA	420
CTTGCTGAAA	AATTAAGAAT	GAAAAAAGAA	GCTCATATTC	CAAAAGTTCT	TTATTATCAA	480
GGTAAATATT	TTGATAGTAT	TAAATATGGT	ATTTTGAGAG	AAGACTGGGA	GAAAATGAAT	540
GACGGTTATT	ATCAAATCAA	TGGAAACTCC	TGA			573

(2) INFORMATION FOR SEQ ID NO:2032:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 795 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2032:

ATGGATAGTA	TGATTTTAGG	GCGTTATATC	CCAGGGGATT	CGATTGTTCA	CCGATTGGAT	60
CCACGTAGCA	AATTGCTTGC	TATGATGCTA	CTGATTTTGA	TTGTGTTTTG	GGCTAATAAC	120
CCCTTGACGA	ATCTGATTCT	TTTATAGCG	ACAGGGATAT	TTATTGCCTT	GTCAGGAGTA	180

TCTCTTTTCAT	TTTTTATTCA	GGGCTTGAAG	TCTATGTTTT	TCTTGATTGC	CTTCACAACT	240
ATTTTTCAAC	TATTTTTTCAT	TTCTAATGGG	AATGTTTTAT	TTGAGTTTTC	GTTTGTGAGA	300
ATCACGGATT	ATGCTTTGCA	ACAAGCTGGG	ATTATTTTTT	GTCGCTTTGT	ATTGATTATT	360
TTCTTTTCAA	CTTTGTTAAC	CTTAACAACC	ATGCCTTTAA	GTTTGGCATC	AGCTGTCGAA	420
GCTTTATTAG	CACCTTTAAA	GCGTGTGAAA	GTTCCAGTTC	ATGAAATTGG	ATTGATGCTG	480
TCTATGAGTT	TGCCTTTTGT	CCCAACCTTG	ATGGATGATA	CGACGCGGAT	TATGAATGCA	540
CAGAAAGCTC	GTGGAGTGGA	TTTTGGAGAA	GGAAGCATCG	TTCAAAAAGT	AAAGGCGATG	600
ATTCCCATTT	TGATTCCTCT	TTTTGCGACA	AGTTTAAAC	GTGCAGATTC	CTTGGCTATC	660
GCTATGGAAG	CGCGTGGCTA	TCAGGGTGGA	AAAGGCAGAA	GTCAATACCG	ACAATTGAAA	720
TGGACTCTAA	AGGATACGCT	GACCATTCCT	GTTATTCTCG	TACTTG GTTG	TTGTTTATTT	780
TTCTTAAAAAT	CTTAG					795

(2) INFORMATION FOR SEQ ID NO:2033:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...267
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2033:

TATTACAGTA	TCTGGGAGAA	GATGATGCCA	GCTAATACGA	AAGTTATTTT	TCAAGAAATG	60
TTTGCGGATT	TTCAGAACTA	TTATGTTCTG	ATTGGGGGAA	CTGCTACCTC	TATCGTATTG	120
GATTTCGCAAG	GATTTAAAAAG	TCGCACAACA	AAAGATTATG	ATATGGTCAT	CATTGATGAA	180
GTAAAAAATA	AGGAATTTTA	TACTACCTGG	AATCATTTTT	TAGAATTGGG	AGAGTATCAA	240
GGAAGTCAGA	AAGATGAGAA	AGCGTAG				267

(2) INFORMATION FOR SEQ ID NO:2034:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2034:

TNAGTAAGTA	TTATTGCTAC	TATATTAGTT	TTATTTTTTA	ATAAAAGACT	AGAAATTATT	60
GAAC TTGGTG	AAGAAATAGC	AATCGGACTT	GGAGCAAATC	CCGAGCTTTC	AAGGCTTGTT	120
TTAATTTTTT	GCGCTGTATC	TTTAACTGCT	TTTTCTACTT	CAATTACAGG	ACCAATAGCT	180
TGTATATCTT	TTTTAGCTGG	CCCAATAGCC	TTAAATATTG	GCAAGAAAAG	AAGTCCAATA	240
TTAGCTGGAT	TGGTTGGAAT	TTTACTAGTT	TTGTTATCAG	ACATATTCTC	TCAAAATATT	300
TTACCAGCTA	GATATCCAGT	AGGTGTTGTA	ACTGCATTGT	TAGTTTCACA	ATACTTAATA	360
TACTTACTAA	TAAAAATGAA	CAGGAGGAAT	ATATAA			396

(2) INFORMATION FOR SEQ ID NO:2035:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2035:

GACAAAAGTA	TAATATTAAA	TATAAAAAGC	GAACAAAATC	AGTTATCTGA	CACTCAGAAT	60
TCTGTCTTGT	TCGCTTTTTT	GTCTAATCTA	TCGATTTTAA	AAATTTATAA	TAAAGAATTC	120
CTAAAATCAA	AATCTTTTTA	TCCCAGACTC	TTTTCTTTTA	AGCCGAATAC	TTTTTACAAA	180
CATTTTTGA						189

(2) INFORMATION FOR SEQ ID NO:2036:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1488 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2036:

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ATGAAAAGTA TAAAATTAAA TGCTCTATCT TACATGGGAA TTCGTGTCTT GAATATTATT      60
TTTCCCATCC TAACTGGAAC CTATGTCGCG CGTGTCTTGG ACCGAACTGA CTATGGTTAC      120
TTCAACTCAG TCGACACTAT TTTGTCATTT TTCTTGCCCT TTGCAACTTA TGGTGTCTAT      180
AGCTACGGTT TAAGGGCTAT CAGTAATGTC AAGGATAACA AAAAAAGATCT TAACAGAACC      240
TTTTCTAGTC TTTTTTATTT GTGCATCGCT TGTACGATTT TGACCACTGC TGTCTATATC      300
CTAGCCTATC CTCTCTTCTT TACTGATAAT CCAATCGTCA AAAAGGTCTA CCTTGTTATG      360
GGGATTCAAC TCATTGCCCA GATTTTTCAT ATCGAATGGG TCAATGAAGC TCTGGAAAAT      420
TACAGTTTTT TCTTTTACAA AACTGCCCTT ATCCGTATCC TGATGCTGGT CTCTATTTTC      480
TTATTTGTTA AAAATGAACA CGATATTGTT GTCTATACAC TTGTGATGAG TTTATCGACG      540
CTGATTAACT ACCTGATTAG TTATTTTTGG ATTAAGAGAG ACATCAAAC TGTAAAAATT      600
CACCTAAGTG ATTTTAAACC ACTCTTTCTC CCTCTGACAG CCATGTTAGT CTTTGCCAAT      660
GCCAATATGC TCTTCACTTT TTTAGATCGC CTCTTCCTCG TTAAAACAGG GATTGATGTC      720
AACGTTAGTT ACTATACCAT AGCTCAGCGA ATTGTGACCG TTATAGCTGG GGTGTAACA      780
GGTGCAATTG GAGTGAGTGT GCCTCGTCTC AGTTACTATC TGGGGAAAGG AGACAAAGAA      840
GCCTATGTTT CTCTGGTTAA TAGAGGTAGT CGAATCTTTA ACTTCTTTAT CATTCCACTG      900
AGTTTTGGAC TCATGGTTTT AGGACCAAAT GCCATCCTAC TTTACGGTAG TGAAAAATAT      960
ATCGGAGGCG GCATCTTGAC CTCTCTCTTC GCTTTTCGTA CGATTATCCT GGCCCTTAGAT     1020
ACCATTCTTG GTTCCCAAAT TCTCTTTACC AATGGCTATG AAAAAACGTAT CACAGTCTAT     1080
ACAGTCTTTG CTGGGCTACT CAATTTGGGC TTGAATAGTC TCCTTTTTTT CAACCATATC     1140
GTGGCTCCTG AATACTACTT ACTGACAACT ATGCTATCAG AGACTTCTCT ACTTGTTTTT     1200
TATATCATT TCAATCCATAG AAAACAACCT ATCCACTTGG GACATATCTT TAGCTATACT     1260
GTTGATACT CTCTCTTTTC ACTTTCCTTT GTAGCAATTT ATTTCTTGAT TAATTTCTGT     1320
TATCCTGTAG ATATGGTCAT TAATTTGCCA TTTTGTGATTA ATACTGGTTT GATTGTCTTG     1380
CTATCAGCTA TCTCTTATAT TAGTCTACTT GTCTTCACAA AAGATAGCAT TTTCTATGAA     1440
TTTTTAAACC ATGTCCTAGC CTTAAAAAAT AAATTTAAAA AATCATAG      1488
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(2) INFORMATION FOR SEQ ID NO:2037:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1473 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2037:

AAGGAAAGTA	TGTCAATTAC	ATCATTTGTA	AAAAGAATTC	AAGATATCAC	TCGAAACGAT	60
GCTGGTGTTA	ATGGTGATGC	TCAACGTATT	GAGCAAATGT	CTTGGTTATT	ATTCTTAAAA	120
ATTTATGATA	GCCGTGAAAT	GGTTTGGGAA	TTAGAAGAAG	ACGAGTATGA	GTCAATTATC	180
CCAGAGGAAT	TAAAATGGCG	AAATTGGGCT	CATGCTCAAA	ATGGGGAACG	GGTATTGACA	240
GGCGATGAAT	TACTTGATTT	TGTCAATAAC	AAGTTATTCA	AAGAGTTGAA	AGAGCTTGAA	300
ATAACTTCAA	ATATGCCTAT	TCGAAAAACG	ATTGTTAAAT	CAGCTTTTGA	AGATGCGAAC	360
AACTATATGA	AAAAATGGCGT	CTTGTTACGC	CAAGTCATCA	ATGTTATTGA	TGAAGTTGAT	420
TTCAATAGCC	CTGAAGATCG	TCATTGCTTT	AATGATATTT	ACGAAAAAAT	TCTTAAAGAT	480
ATTCAAAAATG	CTGGGAACTC	AGGAGAATTT	TATACGCCAC	GTGCAGCGAC	TGATTTTATT	540
GCCGAAGTTC	TTGACCCAAA	ACTTGGAGAA	TCAATGGCAG	ACCTTGCTTG	CGGAACAGGA	600
GGCTTCTTGA	CTTCGACTCT	GAACCGTTTA	AGTAGTCAAC	GTAAAACTAG	TGAAGATACC	660
AAAAAATATA	ATACAGCTGT	TTTTGGTATT	GAAAAGAAAG	CATTTCTCTA	TCTTTTAGCA	720
GTTACAAATC	TGTTTCTTCA	CGAAATTGAT	GACCCTAAAA	TTGTTTCATGG	AAATACTTTG	780
GAGAAAAATG	TTCTGTAATA	TACGGATGAT	GAAAAATTTG	ACATTATTAT	GATGAATCCA	840
CCTTTTGGAG	GGTCAGAATT	AGAAACAATA	AAAAATAACT	TTCCAGCAGA	ATTACGGAGT	900
TCTGAAACAG	CTGATTTATT	TATGGCTGTC	ATTATGTATC	GTTTGAAAGA	AAATGGTCGT	960
GTGGGAGTTA	TTTTACCTGA	TGGTTTTCTA	TTTGGTGAAG	GTGTAAAAAC	TCGCTTGAAA	1020
CAAAAACTGG	TAGATGAGTT	CAACTTACAT	ACGATTATTA	GGTTGCCTCA	TAGTGTCTTT	1080
GCACCGTATA	CAGGAATCCA	TACGAACATT	CTTTTCTTTG	ATAAAACAAA	GAAAACAGAA	1140
GAACTTGGT	TTTATCGTTT	AGATATGCCA	GATGGTTATA	AAAATTTCTC	GAAAACTAAG	1200
CCGATGAAGT	CAGAACTT	CAATCCTGTT	CGTGAATGTT	GGGAAAATCG	TGAAGAGATT	1260
CTGGAAGGTA	AGTTCTACAA	ATCTAAATCA	TTTACACCTA	GTGAATTGGC	TGAGTTGAAT	1320
TATAATTTAG	ACCAGTGTGG	CTTTCCAAAA	GAGGAAGAGG	AAATCTTAAA	TCCCTTTGAG	1380
TTGATTTCAGA	ATTATCAAGC	GGAAAAGAGCA	ACTTTAAATC	ATAAGATTGA	TAATGTATTA	1440
GCTGATATTT	TGCAGTTGTT	GGAGGACAAA	TAA			1473

(2) INFORMATION FOR SEQ ID NO:2038:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 996 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2038:

GAGGAAAGTA	TTATGATCCA	ACATCCACGT	ATTGGGATTC	GTCCGACTAT	TGATGGTCGT	60
CGTCAAGGTG	TACGCGAATC	ACTTGAAGTA	CAAACAATGA	ACATGGCTAA	AAGTGTGGCA	120
GATTTGATTT	CAAGCACATT	GAAATATCCA	GATGGGGAAC	CTGTGGAATG	TGTGATTTCT	180
CCATCTACCA	TTGGTCGTGT	TCCAGAGGCT	GCAGCTTCCC	ATGAGTTGTT	TAAAAAATCA	240
AATGTTTGCG	CAACAATTAC	AGTTACACCA	TGCTGGTGTT	ATGGTAGTGA	AACTATGGAT	300
ATGTCTCCAG	ATATTCCTCA	TGCTATTTGG	GGATTTAATG	GGACAGAACG	CCCAGGAGCT	360
GTCTATCTTG	CAGCTGTACT	AGCTTCACAT	ACTCAAAAAG	GGATTCCAGC	CTTTGGGATT	420

TATGGTAGAG	ATGTTTCAGGA	AGCTAATGAT	ACAGCTATTC	CAGAAGATGT	CAAAGAAAAA	480
CTTTTACGTT	ATGCGCGGGC	AGCTCTTGCA	ACTGGCTTGA	TGAGAGACAC	TGCTTACCTA	540
TCAATGGGTA	GTGTTTCGAT	GGGGATTGGT	GGTTCATTG	TAAATCCAGA	TTTCTTCCAA	600
GAATACTTAG	GAATGCGAAA	TGAATCGGTA	GATATGACGG	AGTTCACGCG	CCGTATGGAC	660
CGTGGTATTT	ACGACCCTGA	AGAGTTCGAA	CGTGCGCTCA	AATGGGTGAA	AGAAAACGTA	720
AAAGAAGGAT	TCGACCATAA	CCGTGAAGAC	CTTGTTTAA	GCCGTGAAGA	AAAAGATAGA	780
CAATGGGAAT	TTGTTATTAA	GATGTTTCATG	ATTGGACGTG	ACTTAATGGT	TGGTAACCCA	840
AGACTTGCTG	AACTTGTTTT	TGAGGAAGAA	GCAGTTGGTC	ACCATGCTTT	AGTAGCTGGT	900
TTCCAAGGTC	AACGTCAGTG	GACAGACCAT	TTTCCAAATG	GGGACTTTAT	GGAAACTTTC	960
CTCAATACTC	AGTTTGACTG	GAATGGTATT	CGATAA			996

(2) INFORMATION FOR SEQ ID NO:2039:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2039:

TATGGAAGTA	TGATAAGGAA	TAAAAAACAA	GATTATGTAC	TGGCCTACAA	GCAACCAGCT	60
TCAACCACTT	ACATGGGTTG	GGAAGAAGAA	GCTTTACCGA	TAGGTAATGG	TTCTTTAGGA	120
GCAAAAAGTAT	TTGGCCTTAT	AGGGTCTGAA	CGGATTCAAT	TTAATGAAAA	AAGTCTCTGG	180
TCTGGAGGTC	CACTTCCTGA	TAGTTCAGAT	TATCAGGGTG	GAAATCTTCA	GGATCAGTAT	240
GTTTTTTTAG	CTGAGATTCG	GCAGGCTTTG	GAGAAGAGAG	ATTACAATCT	GGCTAAGGAA	300
CTGGCTGAGC	AGCACCTAAT	TGGGCCAAAA	ACGAGTCAAT	ATGGGACCTA	TCTGTCTTTT	360
GGGGATATTC	ACATTGAGTT	CAGCCAGCAA	GGTACGACTT	TGTCTCAGGT	GACGGACTAT	420
CAGAGACAGT	TGAATATTAG	TAAGGCACCT	GCGACGACTT	CTTATGTCTA	TAAGGGAACG	480
CGATTTGAAC	GTGAAGCTTT	TGCGAGTTTT	CCAGATGATC	TCTTGTTTCA	ATGTTTTACT	540
AAGGAAGGGT	TGGAAACTCT	AGATTTTACT	ATAGAACTAT	CCTTGACCTG	TGATTTGGCT	600
TCTGATGGAA	AGTATGAGCA	GGAAAAATCT	GATTACAAGG	AGTGTAAGTT	GGATATTACT	660
GATTCTCATA	TCTTGATGAA	GGGAAGAGTT	AAGGATAATG	ATCTGCGGTT	TGCTAGTTAT	720
CTAGCTTGGG	AAACGGATGG	AGATATTAGA	GTTTGGTCAG	ATAGGGTTCA	GATATCAGGA	780
GCCAGTTATG	CCAATCTCTT	CTTGCCCGCT	AAGACGGATT	TTGCCCAAAA	TCCTGCTAGC	840
AATTATCGCA	AGAAACTAGA	TTTAGAGCAA	CAGGTGATAG	ACTTGGTGGA	CACAGCTAAA	900
GAAAAGGGCT	ATACCCAATT	GAAATCAAGG	CATATCGAGG	ACTACCAAGC	CTTATTCCAG	960
CGTGTTC AAT	TGGATTTGGA	AGCTGATGTT	GACGCATCCA	CTACAGATGA	TTTGT TAAAA	1020
AATTATAAGC	CACAAGAAGG	GCAGGCTTTG	GAGGAGCTGT	TCTTCCAGTA	TGGACGGTAT	1080
TTATTGATTA	GTTTCGTCCAG	AGACTGCCCCA	GATGCTCTAC	CAGCTAACCT	ACAGGGAGTC	1140
TGGAATGCGG	TCGACAATCC	TCCTTGGAAT	TCGGACTATC	ACTTAAATGT	CAATCTGCAG	1200
ATGAATTATT	GGCCAGCCTA	TGTTACCAAT	CTCCTAGAGA	CGGTCCTTCC	AGTCATCAAC	1260
TATGTAGATG	ATTTGCGTGT	CTATGGTTCGT	CTAGCGGCTG	TAAAGTATGC	AGGAATCGTC	1320
TCTCAGAAAG	GTGAGGAAAA	TGGTTGGTTG	GTTTCATACTC	AAGCGACTCC	CTTTGGTTGG	1380

ACGGCACCTG	GTTGGGATTA	CTATTGGGGT	TGGTCACCAG	CTGCCAATGC	GTGGATGATG	1440
CAAACCGTTT	ATGAAGCCTA	TTCATTTTAT	AGGGACCAAG	ACTATCTTAG	GGAGAAAATT	1500
TATCCCATGT	TGAGGGAAAC	GGTTCGTTTT	TGGAATGCCCT	TTTTACATAA	GGATCAGCAG	1560
GCGCAGCGTT	GGGTGTCTTC	TCCGTCTTAT	TCCCCAGAAC	ATGGGCCGAT	TTCGATTGGC	1620
AATACCTATG	ACCAATCTCT	GATTTGGCAG	TTATTTTCATG	ATTTTATTCA	GGCTGCTCAG	1680
GAATTGGGAC	TGGATGAGGA	CTTGTTGACT	GAGGTTAAGG	AGAAGTCTGA	TTTACTAAAT	1740
CCTTTGCAAA	TCACTCAATC	TGGTCGAATC	AGGGAGTGGT	ATGAGGAGGA	AGAGCAGTAT	1800
TTTCAAAATG	AGAAAGTGGA	GGCCCAGCAT	CGGCACGCTT	CCCATCTAGT	GGGACTCTAT	1860
CCTGGCAATC	TCTTTAGCTA	CAAGGGACAA	GAGTATATTG	AAGCGGCGCG	TGCTAGCCTC	1920
AATGATCGTG	GAGATGGCGG	CACAGGCTGG	TCCAAGGCTA	ATAAGATCAA	TCTCTGGGCG	1980
CGTTTGGGAG	ATGGCAATCG	AGCCCATAAA	TTATTGGCAG	AGCAGTTAAA	GACATCCACC	2040
TTGCAAAATC	TTTGGTGTAG	CCATCCTCCT	TTTCAGATAG	ATGGTAATTT	TGGTGCTACT	2100
AGTGGCATGG	CAGAAATGTT	ACTCCAGTCT	CATGCAGCTT	ATCTGGTACC	TCTAGCTGCC	2160
CTACCTGATG	CTTGGTCAAC	AGGTTCTGTT	TCAGGCTTAA	TGGCACGTGG	ACATTTTGAA	2220
GTGAGCATGA	GCTGGGAAGA	TAAAAAATC	TTACAGTTGA	CCATTTTATC	AAGGAGTGGA	2280
GGAGATTTGC	GAGTTTCTTA	TCCAGATATT	GAGAAGAGTG	TGATTAAAAAT	GAATCAAGAA	2340
AAAATAAAAAG	CGAAATGCAT	GGGGAAAGAT	TGTATTTCGG	TGGCAACAGC	AGAAGGTGAT	2400
CTTGTTC AAT	TTTATTTT A					2421

(2) INFORMATION FOR SEQ ID NO:2040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2040:

GTGGGGAGTA	TAGTTATGAA	ATTGAAGTTT	CTTATAACAA	ATTTGTTTCA	TGTTCTTTTG	60
TCTAATCTGA	TTACAAATCT	TACATCAGTT	ATAGTTGTAC	TAATTTTACC	AAAAATTATG	120
GGAGTAACTG	AGTATAGTTA	TTGGCAACTA	TATATTTTTT	ACCTAACATA	TATTGGTTTT	180
TTTCATCTGG	GATGGATTGA	TGGAATTTAT	CTTAAATATG	GCGGATTAGA	GTACCAGAAC	240
TTAGATAAGA	AACAGTTTTA	TTCTCAAATA	CTTCAATTTT	CCAGTTTTTT	AATTTTAATT	300
TCTTTTCTAT	TATTTGGTTT	TAACTTATTG	ACTGTGACAG	ATCAAAATGC	AAAATATATT	360
TATAACATGA	CTATTATTAG	TATGATAGTT	ACAAATTTAA	GAATGTTATT	CGTTTATATT	420
TTGCAGATGA	CAAAATCGATT	AAAGGATAGT	TCCATCATTC	TAATCAGTGA	TCGCGTTATA	480
TATGTTATTG	TTTTATTCTT	GTTTATTATA	TTTAAATGGC	ATGAATACAA	GGTAATGATT	540
TGGGCAGATG	TTTTGGGAAG	GACATTTTCT	CTCCTACTTT	CTTTTTTGGAT	TTGTAAAGAT	600
ATTGTTTTTC	AATCCTTATC	CGAGTTTATA	TTGGATCTGA	GAGAGTCTTT	TGACAATATC	660
CGTGTGGGAA	TCAATTTAAT	GTTATCCAAT	ATTGCAAGTA	GTATGATTAT	TGGTATTGTT	720
CGAATGGGAA	TTCAATGGAA	TTGGAATATC	GAAACATTCG	GGAAAGTATC	ACTGACGCTA	780
AGCATCTCTA	ATTTATT AAT	GACTTTTATT	AATGCGATTG	GTTTAGTTGT	TTTTCTTTTG	840
TTAAAACGGA	CAAAAACGGA	AAATTTATCT	AAAATTTATT	CCAACCTAAA	AAATGTATTG	900

ATGCTTATCA	TGTTGCGGAT	ATTGCTCATT	TACTATCCTT	TAAAAATTGT	GTTATACCTC	960
TGGTTGTCAG	CCTATCAAGA	TGCCTTGATT	TTCATGAACC	TTATTTTCCC	TATGTCAGTC	1020
TATGAAAGAA	AAATGGCATT	GGTCATTAAT	ACTTACTTAA	AGGGCTTAAA	AATGGAGAGA	1080
GATATTCTCA	AAATAAATAC	TTTGATTATG	TTGTTGAGTA	TGTTAGTTTA	CCTAAATAAC	1140
TACTCTATTA	TTAAATAG					1158

(2) INFORMATION FOR SEQ ID NO:2041:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 984 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2041:

AATTATGGTA	TAATATTAGC	AATAAAAGAA	ATCTGGAGGA	TTAGAATCAT	GGTATCAACG	60
AAAACACAAA	TTGCTGGTTT	TGAGTTTGAC	AATTGCCTGA	TGAATGCAGC	AGGTGTGGCT	120
TGTATGACGA	TAGAGGAGTT	AGAAGAGGTC	AAAAACTCAG	CGGCAGGAAC	CTTTGTTACT	180
AAGACAGCGA	CCTTGGACTT	CCGTCAGGGG	AATCCTGAGC	CACGCTACCA	AGATGTTCCA	240
CTTGTTTCCA	TCAACTCTAT	GGGCTTGCCA	AATAATGGCT	TAGACTATTA	TTTGGATTAT	300
CTTTTAGATT	TGCAGGAAAA	AGAGTCGAAC	CGAACTTTCT	TCTTATCTCT	GGTCGGCATG	360
TCTCCAGAGG	AAACCCATAC	TATTTTGAAA	AAAGTCCAAG	AGAGTGATTT	TCGTGGTCTG	420
ACTGAGCTAA	ATCTTTCCTG	TCCAAATGTT	CCAGGTAAAC	CTCAGATTGC	CTATGATTTT	480
GAGACAACAG	ACCGGATTTT	GGCAGAAGTG	TTTGCTTACT	TCACCAAACC	TCTTGGAATT	540
AAATTGCCAC	CTTATTTTGA	TATTGTTTCA	TTTGATCAAG	CGGCAGCTAT	TTTCAACAAA	600
TATCCGCTCA	AGTTTGTCAG	CTGCGTTAAC	TCTATCGGAA	ACGGCCTCTA	TATAGAAGAC	660
GAATCTGTCT	TTATTCGGCC	TAAGAATGGT	TTTGGTGGAA	TTGGTGGAGA	ATACATCAAA	720
CCGACTGCTC	TAGCCAATGT	TCACGCCTTT	TATCAACGTT	TAAATCCTCA	AATCCAAATT	780
ATCGGAACAG	GTGGCGTTCT	GACTGGTCGA	GATGCCTTTG	AAACATCCCT	CTGTGGAGCA	840
AGTATGGTGC	AGGTGGGAAC	GACCC TTCAC	AAAGAAGGCG	TCAGTGCTTT	TGACCGCATT	900
ACCAATGAAC	TGAAAGCAAT	CATGGTGGAA	AAAGGCTACG	AGAGCTTAGA	AGATTTCCGT	960
GGGAAATTGC	GCTATATTGA	CTAA				984

(2) INFORMATION FOR SEQ ID NO:2042:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2042:

ATCTACGGTA	TCCATGTTGC	CAAGATTGCT	GGCTTGCCAG	CAGACCTTTT	AGCAAGGGCG	60
GATAAGATTT	TGACTCAGCT	AGAGAATCAA	GGAACAGAGA	GTCCTCCTCC	CATGAGACAA	120
ACTAGTGCTG	TACTGAACA	GATTTCACTC	TTTGATAGGG	CAGAAGAGCA	TCCTATCCTA	180
GCAGAATTAG	CTAAACTGGA	TGTGTATAAT	ATGACACCTA	TGCAGGTTAT	GAATGTCTTA	240
GTAGAGTTAA	AACAGAAACT	ATAA				264

(2) INFORMATION FOR SEQ ID NO:2043:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2043:

ATAATAGGTA	TTTTCATAGG	CAACAGGATT	CACGGTTTTA	TGGATTTTCA	TACTAGCTCC	60
AATCTCAAAG	AATGTACTAA	TACTCTTCGA	AAATCTCTTC	AAACCGCGTC	AACTTTATCT	120
GCAACTTCAA	AGCAGTGCTT	TGAACAGCCT	GCGGCTAGCT	TTCTAGTTTG	CTCTTTGATT	180
TTCATTGAGT	ATAAATTAAG	TATAGCACAG	TTAGGGAGAA	TAGGTAAGGA	TTTAAAATGA	240

(2) INFORMATION FOR SEQ ID NO:2044:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2044:

GATAGGGGTA	TGAATCTGAA	AGTGAAACAA	AAAATACCAT	TAAAAATCAA	GCGCATGGGA	60
ATTAACGGTG	AGGGAATCGG	CTTTTACCAA	AAAACATTAG	TCTTTGTACC	AGGAGCTCTC	120
AAAGGCGAAG	ATATCTATTG	TCAGATTACT	TCTATTAGAC	GCAACTTTGT	TGAAGCAAAA	180
TTACTGAAGG	TCAACAAGAA	GTCTAAATTT	CGAATTGTGC	CATCTTGTAC	TATTTATAAT	240
GAATGCGGAG	GCTGCGCAAA	TCATGCACCT	GCATTATGA			279

(2) INFORMATION FOR SEQ ID NO:2045:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1884 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2045:

GGTACTATCT	TTCCCTACTT	TTTTTGCTAT	AATGGAACTA	TGAACAACTT	GATTAAATCA	60
AAACTAGAGC	TCTTGCCGAC	CAGCCCTGGT	TGCTACATTC	ATAAGGATAA	AAATGGCACC	120
ATTATCTATG	TAGGAAAGGC	TAAAAATCTG	CGTAATCGAG	TACGGTCCTA	TTTTCGTGGA	180
AGTCATAATA	CCAAGACAGA	GGCTCTGGTG	TCTGAAATTG	TGGATTTTGA	ATTTATTGTT	240
ACGGAGTCTA	ATATTGAGGC	ACTTCTCCTA	GAAATTAACC	TGATCAAGGA	AAACAAGCCC	300
AAGTACAATA	TCATGCTCAA	GGATGACAAG	TCCTATCCTT	TCATCAAAAT	CACCAATGAG	360
CGCTATCCAC	GCTTGATTAT	CACTCGTCAG	GTCAAAAAGG	ACGGAGGTCT	TTATTTTGGA	420
CCCTATCCCG	ATGTGGGGGC	AGCCAATGAA	ATCAAGCGGT	TGCTGGATCG	GATATTCCCT	480
TTTCGTAAGT	GTACCAACCC	GCCCTCTAAG	GTCTGTTTTT	ATTACCATAT	CGGTCAATGC	540
ATGGCCCACA	CCATCTGTAA	GAAGGATGAG	GCTTATTTCA	AGTCTATGGC	TCAGGAGGTG	600
TCTGATTTTC	TGAAAGGTCA	GGATGACAAA	ATCATCGATG	ATCTCAAGAG	TAAAATGGCA	660
GTAGCAGCAC	AAAGTATGGA	GTTTGAACGT	GCGGCGGAAT	ACCGTGACCT	GATTCAGGCT	720
ATTGGAACGC	TTCGAACCAA	GCAACGGGTC	ATGGCGAAAAG	ATTTGCAAAA	TCGCGATGTC	780
TTTGGCTACT	ATGTGGATAA	GGGCTGGATG	TGTGTGCAGG	TTTTCTTTGT	CCGTCAGGGT	840

AAGCTTATCG	AGCGCGATGT	CAATCTCTTC	CCCTACTTCA	ATGATCCAGA	TGAGGATTTT	900
TTGACCTATG	TAGGACAATT	CTATCAAGAA	AAATCTCATC	TAGTTCCCAA	TGAGGTACTG	960
ATTCCGCAGG	ATATTGACGA	AGAGGCTGTC	AAGGCCTTGG	TGGATTCCAA	GATTCTTAAG	1020
CCTCAACGTG	GAGAGAAAAA	ACAAC TGGTC	AATCTAGCCA	TAAAAAATGC	TCGTGT TAGT	1080
CTAGAGCAGA	AGTTCAATCT	GCTAGAAAAA	TCTGTGCGAA	AGACTCAAGG	AGCTATTGAA	1140
AATCTAGGGC	GTTTGCCTCCA	AATCCCGACC	CCAGTACGTA	TCGAGTCCTT	CGATAACTCT	1200
AATATCATGG	GAAC TAGCCC	TGTTTCGGCT	ATGGTGGTCT	TTGTCAACGG	TAAACCGAGT	1260
AAGAAGGATT	ACCGTAAGTA	CAAGATAAAA	ACGGTTGTTG	GACCAGACGA	CTATGCCAGC	1320
ATGAGAGAGG	TCATTGCGAG	ACGCTATGGT	CGAGTACAGC	GTGAGGC'TTT	GACTCCTCCA	1380
GATTTGATTG	TGATTGATGG	GGGGCAAGGT	CAAGTCAATA	TCGCTAAGCA	GGTTATCCAA	1440
GAGGAACTGG	GCTTGGATAT	TCCAATTGCT	GGGCTGCAAA	AGAATGATAA	GCACCAAACC	1500
CATGAATTGC	TCTTTGGAGA	TCCGCTTGAG	GTGGTGGACT	TGTCTCGCAA	TTCTCAGGAA	1560
TTTTTCCCTCC	TCCAACGCAT	CCAAGATGAG	GTGCACCGCT	TTGCTATCAC	TTTCCACCGC	1620
CAACTGCGCT	CCAAAAATTC	TTTCTCATCT	CAATTGGATG	GGATTGACGG	TCTGGGACCT	1680
AAACGCAAGC	AGAATCTTAT	GAAGCATTTT	AAGTCTTTGA	CCAAAATCAA	GGAAGCCAGT	1740
GTGGATGAGA	TTGTGCAAGT	TGGGGTACCT	AGAGTCGTTG	CAGAGGC'TGT	GCAAAGAAAG	1800
TTGAACCCGC	AGGGAGAAGC	CTTGCC'TCAA	GTAGCAGAAG	AAAGAGTAGA	TTACCAAACG	1860
GAAGGAAACC	ACAATGAACC	ATAA				1884

(2) INFORMATION FOR SEQ ID NO:2046:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2046:

CTCCAAATCT	TCCAAGGTTT	TATTAGCCAA	TTTAGCATAG	TTGTGGGATT	TTTCTACACG	60
GAAATAGACA	TCCCCTTGAC	TCTCATAGGC	AAAGCCTTTT	TCGATCAAGT	CTTCCACAAA	120
ACGGATGATG	TCTGCCATAA	ACTCCACTAC	ACGCGGATGG	CGAGTCGCAG	GTTTCACGCC	180
CAATGCCGTC	ACATCCTCAC	GAAAGGCAGC	GATGTACTTA	TCCGCAACCT	CCTGAGGTGT	240
GATGCCTTCT	TCCCTGGCAC	GGTTGATAAT	CTTATCATCC	ACATCTGTAA	AATTGGAAAT	300
ATAGGCAACC	TTATACCCAC	GGTACTCAAA	ATAGCGACGA	ATCGTATCAA	AAGCTACCGT	360
CGAACGGGCG	TTTCCCACGT	GAATATAGTT	GTACACGGTT	GGCCCACAAA	CATACATCTT	420
GATCTTGCCG	TCCTCAATCG	GGACAAATTC	TCGCAAATCA	CGAGACATGG	TGTCATAGAT	480
TTTAATCATA	AATCATAA					498

(2) INFORMATION FOR SEQ ID NO:2047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1368 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2047:

GGAAAAATCT	TAATGTATCA	AGCACTTTAT	CGAAAAATATA	GAAGTCAAAA	CTTCTCCCAG	60
TTAGTTGGTC	AAGAAGTTGT	GGCTAAGACT	CTTAAACAAG	CGGTGGAGCA	AGAGAAAATA	120
AGTCACGCTT	ATCTTTTTTC	TGGTCCTCGT	GGAACGGGAA	AAACCAGTGT	TGCTAAAATC	180
TTTGCCAAGG	CTATGAACTG	TCCCAATCAA	GTGGGTGGCG	AACCTTGCAA	TAAC TGCTAT	240
ATTTGTCAAG	CAGTGACGGA	CGGTAGTTTA	GAAGATGTCA	TTGAAATGGA	TGCAGCTTCT	300
AATAATGGGG	TAGATGAAAT	TCGCGAAATT	CGTGATAAAT	CTACCTATGC	GCCTAGCCTT	360
GCTCGTTATA	AGGTTTATAT	CATAGATGAG	GTTTCACATGC	TGTCTACAGG	GGCTTTTAAAT	420
GCCCTCCTAA	AGACGCTGGA	AGAACCAACA	CAGAATGTAG	TCTTTATTTT	GGCCACTACT	480
GAATTGCACA	AGATTCCCTGC	TACTATTCTA	TCCCGTGTGC	AACGTTTTGA	GTTTAAATCA	540
ATTAAGACAC	AGGATATTAA	GGAACATATT	CACTATATCT	TAGAAAAAGA	AAATATCAGT	600
TCTGAACCAG	AGGCTGTGGA	AATCATTGCC	AGACGGGCGG	AAGGTGGAAT	GCGGGACGCC	660
TTGTCTATTT	TGGATCAAGC	CCTGAGTTTG	ACACAGGGAA	ATGAGCTGAC	GA CTGCTATC	720
TCTGAAGAAA	TTACTGGCAC	CATTAGCCTA	TCAGCCTTGG	ATGATTATGT	GGCGGCCCTTG	780
TCTCAACAGG	ATGTTCCCAA	AGCTTTGTCT	TGCTTGAATC	TTCTTTTTGA	CAATGGTAAG	840
AGCATGACTC	GTTTTGTGAC	CGATCTTTTG	CACTATTTAA	GAGACTTGTT	AATTGTTCAA	900
ACAGGGGGAG	AAAATACTCA	TCATAGTTCA	GTCTTTGTAG	AAAATTTGGC	ACTTCCTCAA	960
AAAAATCTGT	TTGAAATGAT	TCGCTTAGCA	ACAGTGAATT	TAGCAGATAT	TAAGTCTAGT	1020
TTGCAGCCCA	AGATTTATGC	TGAAATGATG	ACCGTCCGTT	TGGCGGAAAT	CAAGCCCGAA	1080
CCAGCTCTAT	CAGGAGCGGT	TGAAATGAA	ATTGCTACGC	TGAGACAGGA	AGTTGCCCGT	1140
CTCAAACAAG	AGCTTTCTAA	TGCAGGTGCG	GTTCTTAAAC	AAGTTGCACC	AGCTCCTAGT	1200
CGACCAGCTA	CGGGCAAAAC	AGTCTATCGT	GTCGATCGCA	ATAAAGTGCA	ATCTATCTTA	1260
CAAGAGGCCG	TCGAAAATCC	TGATTTAACA	CGTCAAAATC	TAATTCGTTT	GCAGAATGCA	1320
TGGGGAGAGG	TAATTGAAAG	TCTAGGTGGG	CCGGACAAGC	TCTGCTAG		1368

(2) INFORMATION FOR SEQ ID NO:2048:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2048:

GTCCCTTTCA TTATACCACA AACTAGCCAC CCTGACCAGT TTGTTCTACA CTTTCAGGGA	60
TGGAATAGAC AGCAAAAAGA ACCCTGCTTT TCTGAAAAAG AGGTCTCCTT GCTAAGTTTA	120
TACTCAATGA AAATCAAAGA ACAAAC TAGG AAGCTAGCCA CAGGTTGCTC AAAGCACCGC	180
TTTGAGGTTG CAGATAAAAC TGACACGGTT TGA	213

(2) INFORMATION FOR SEQ ID NO:2049:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 348 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2049:

AGTATTATCA TTGTTATTAA CATAGAGGAG GAAAACATAA TGGTGAAGAT TGGTTTGTTT	60
TGTGCAGCAG GTTTTTCTAC TGGTATGCTT GTAAATAATA TGAAAATTGC AGCGCAAGCT	120
AGTGGAGTTG AGGCAGAAAT AGAGGCGTTT TCTCAGTCTA AATTAGCGGA TTATGCGCCA	180
AATATAGATG TTGCACTATT GGGTCCACAA GTTGCTTATA CATTAGATAA ATCAAAAGAA	240
ATTTGTGATA AGTGTGATGT TCCGATAGCT GTTATTCCGA TGATGGACTA TGGTATGTTA	300
GATGGGAAAA AAGTATTAGA TTTGGCCCTA TCTTTGATTA GTGGGTAA	348

(2) INFORMATION FOR SEQ ID NO:2050:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 714 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2050:

```
GCGGTTATCA TGCCCAATCA CGAGGGGCTG GACTTGCACT TGCCAAAGAA GTGTGTTTAT      60
GCATTGGTAG GTGAGGAGAT TGACCGCTAT GCAAGGGAAG TAGGGGCGGA TTGTGTCGGC      120
GAATTCGTTT CTGCTACCAA GACCTATCCA GTCTATGTCA TCAACTACAA GGGTGAGGAG      180
GTCTGTCTGG CTCAGGCTCC TGTGGGCTCC GCTCCAGCAG CCCAGTTTAT GGATTGGTTG      240
ATTGGCTATG GTGTGGAGCA GATTATCTCT ACTGGGACCT GTGGTGTCCCT AGCTGATATA      300
GAGGAAAATG CCTTTCAGT CCCTGTTTCG GCTTTGCGAG ATGAGGGAGC CAGTTACCAC      360
TATGTGGCAC CTGTGCGTTA TATGGAAATG CAGCCAGAGG CTATTGCTGC TATTGAGGAA      420
GTTTTGGAAG ACAGAGGGAT TCCTTATGAA GAAGTCATGA CCTGGACGAC AGACGGTTTT      480
TACCGAGAAA CGGCTGAAAA GGTGGCTTAT CGTAAGGAAG AAGGCTGTGC TGTGTGGAG      540
ATGGAGTGTT CTGCTCTTGC GGCAGTAGCT CAATTGCGTG GGGTTCTCTG GGGTGAATTG      600
TTGTTACAG CAGATTCTCT AGCGGACTTG GACCACTACG ACAGTCGTGA CTGGGGCTCG      660
GAAGCTTTTA ATAAGGCGCT AGAACTGAGT TTAGCAAGTG TTCACCACCT TTAG      714
```

(2) INFORMATION FOR SEQ ID NO:2051:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 555 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2051:

```
GAGCCTATCA TGGAGTTTGA AGAAAAAACG CTTAGCCGAA AAGAAATCTA TCAAGGACCA      60
ATATTTAAAC TGGTCCAAGA TCAGGTTGAA TTACCAGAAG GCAAGGGAAC TGCCCCACGG      120
GATTTGATTT TCCACAATGG GGCTGTCTGT GTTTTAGCAG TAACGGATGA AAAAAAATT      180
ATCTTGGTCA AGCAGTACCG CAAAGCTATC GAGGCTGTCT CTTACGAAAT TCCAGCCGGA      240
AAATTGGAAG TAGGAGAAAA CACAGCCCCT GTGGCAGCTG CCCTTCGTGA ATTAGAGGAA      300
GAAACAGCCT ATACAGGGAA ATTAGAATCT TTGTACGATT TTTATTCAGC TATTGGCTTT      360
TGTAATGAGA AGTTAAAACT ATATTTAGCA AGCGATTTGA CAAAAGTGGA AAATCCGCGT      420
CCGCAGGATG AGGATGAAAC CTTGGAAGTC CTTGAAGTGA GCTTAGAAGA AGCGAAAGAA      480
TTAATCCAAT CAGGTCATAT CTGTGATGCC AAGACAATTA TGGCTGTTCA GTATTGGGAG      540
TTGCAGAAAA AATAG      555
```

(2) INFORMATION FOR SEQ ID NO:2052:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2052:

GGGACTATCA	TATGCGGCTT	TTTTAGGTAT	TTTATTCCAA	AGTATGTAAG	CGAGTCTCGT	60
GTACTGTATT	TGGATTGAGA	TATTGTTGTA	AGAAAATCGA	TAGATGAGCT	GTGGGATTTG	120
GACTTGACGG	CTATACCCCT	AGCTGCAGTT	AGAGATGATT	TTTATACACA	TAATTTTAAT	180
TCTGGTGTTT	TGTTAATCAA	CGATGGCATG	TGGAGAGCAG	AAAATGTCAC	GCAAGACCTG	240
ATTTAA						246

(2) INFORMATION FOR SEQ ID NO:2053:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2053:

AGGGATATCA	TGAAATACAT	TATCAATCAT	TCAAATGACA	CTGCTTTTAA	TATTGCCTTG	60
GAAGAATACG	CCTTTAAACA	CCTTTTGGAT	GAGGATCAAA	TCTTCCTACT	TTGGATTAAC	120
AAGCCATCTA	TCATTGTTGG	TCGTCACCAG	AACACTATCG	AAGAAAATCAA	CCGTGATTAT	180
GTTCGCGAAA	ATGGTATTGA	GGTAGTTCGC	CGTATTAGTG	GTGGTGGAGC	TGTTTACCAC	240

GATTTAAATA	ACCTCAACTA	CACGATCATC	TCCAAAGAAG	ATGAAAATAA	GGCATTGAC	300
TTCAAGAGCT	TCTCAACTCC	GGTTATCAAT	ACCCTGGGCTC	AACTCGGGGT	TAAAGCTGAG	360
TTCACAGGTC	GTAATGACCT	TGAGATTGAT	GGTAAGAAGT	TCTGTGGCAA	TGCCCAAGCC	420
TATATCAACG	GCCGTATCAT	GCACCACGGT	TGCTTGCTCT	TTGACGTTGA	TTTGTGAGTC	480
CTCGCAAATG	CCCTTAAGGT	TTCAAAAGAT	AAATTTGAAT	CAAAAGGTGT	GAAATCCGTC	540
CGTGCCCGTG	TAACTAATAT	TATCAATGAA	TTACCAAAAA	AAATCACAGT	CGAAAAATTC	600
CGTGATTTAC	TCTTGGGAATA	CATGAAAAAA	GAGTACCCAG	AGATGACTGA	ATACGTCTTT	660
TCAGAAGAAG	AATTGGCCGA	AATCAATCAC	ATCAAGGATA	CTAAGTTTGG	AACTTGGGAC	720
TGGAACATATG	GTAAATCACC	TGAATTTAAC	GTCCGTCGTG	GAACCAAATT	CACTAGTGGT	780
AAGGTTGAAG	TCTTTGCTAA	CGTTACTGAA	TCAAAAATCC	AAGACATCAA	GATTTATGGT	840
GACTTCTTTG	GTATTGAAGA	CGTTGCTGCA	GTAGAAGATG	TCCTTCGTGG	GGTGAAATAC	900
GAACGCGAAG	ATGTTCTTAA	GGCGCTAAAA	ACCATTGATA	TCACACGCTA	CTTCGCTGGT	960
ATTAGCCGTG	AAGAAATCGC	TGAAGCGGTA	GTTGGATAA			999

(2) INFORMATION FOR SEQ ID NO:2054:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...213
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2054:

TTTTTCATCA	TAAGAATATT	TTTGATATCC	AGCATTGGGC	CAATGACGAG	AAAAGCCAGA	60
ACTGGAGCCA	AACCGAAACT	CGAGAGTAGA	GAAGCCCCGA	TAAAGGCATC	CGCCTCACTA	120
CAGAGCGAAA	GAAGAAAGGC	CAAAATCATC	AAGAGCAGGA	TGGCAAAAAG	AGGAGTCGCA	180
CTGATAGAGG	TCAGAATCCG	AGTCGGAACA	TAA			213

(2) INFORMATION FOR SEQ ID NO:2055:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1047 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2055:

GAGGTCATCA	TGGATATTAG	ACAAGTTACT	GAAACCATCG	CCATGATTGA	GGAGCAAAAC	60
TTCGATATTA	GAACCATTAC	CATGGGGATT	TCTCTTTTGG	ACTGTATCGA	TCCAGATATC	120
AATCGTGCTG	CGGAGAAAAT	CTATCAAAAA	ATTACGACAA	AGGCGGCTAA	TTTAGTAGCT	180
GTTGGTGATG	AAATTGCGGC	TGAGTTGGGA	ATTCCCTATCG	TTAATAAGCG	TGTATCGGTG	240
ACACCTATTT	CTCTGATTGG	GGCAGCGACA	GATGCGACGG	ACTACGTGGT	TCTGGCAAAA	300
GCGCTTGATA	AGGCTGCGAA	AGAGATTGGT	GTGGACTTTA	TTGGTGGTTT	TTCTGCCCTTA	360
GTACAAAAAG	GTTATCAAAA	GGGAGATGAG	ATTCTCATCA	ATTCCATTCC	TCGCGCTTTG	420
GCTGAAACGG	ATAAGGTCCTG	CTCGTCAGTC	AATATCGGCT	CAACCAAGTC	TGGTATTAAT	480
ATGACGGCTG	TGGCAGATAT	GGGACCAATT	ATCAAGGAAA	CAGCAAATCT	TTCAGAGATC	540
GGAGTGGCCA	AGTTGGTTGT	ATTTCGCTAAT	GCTGTTGAGG	ACAATCCATT	TATGGCGGGT	600
GCCTTTTCATG	GTGTTGGGGA	AGCAGATGTT	ATCATCAATG	TCGGAGTTTC	TGGTCCCTGGT	660
GTTGTGAAAC	GTGCTTTTGA	AAAAGTTCGT	GGACAGAGCT	TTGATGTAGT	AGCCGAAACA	720
GTTAAGAAAA	CTGCCTTTAA	AATCACTCGT	ATCGGTCAAT	TGGTTGGTCA	AATGGCCAGT	780
GAGAGACTGG	GTGTGGAGTT	TGGTATTGTG	GACTTGAGTT	TGGCACCAAC	CCCTGCGGTT	840
GGAGACTCTG	TGGCACGTGT	CCTTGAAGAA	ATGGGGCTAG	AAACAGTTGG	CACGCATGGA	900
ACGACGGCTG	CCTTGGCCCT	CTTGAACGAC	CAAGTTAAAA	AGGGTGGAGT	GATGGCCTGT	960
AACCAGGTCG	GTGGTCTATC	TGGTGCCTNT	ATCCCTGTTT	CTGAGGGTGA	AGGAATGATT	1020
GCTGCAGTGC	GCAAATGGCT	CTCTTAA				1047

(2) INFORMATION FOR SEQ ID NO:2056:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2056:

TTTCCCATCA	TCATGGGCTC	AAAATCCGAC	TGGGCAACCA	TGCAAAAAAC	AGCAGAAGTC	60
CTAGACCGCT	TCGGTGTAGC	CTACGAAAAG	AAAGTTGTTT	CCGCACACCG	TACACCAGAC	120
CTCATGTTCA	AACATGCGAG	AGAAGCCCGT	AGTCGTGGCA	TCAAGATCAT	CATCGCAGGT	180
GCTGGTGGCG	CAGCGCATTT	GCCAGGCATG	GTAGCTGCCA	ANACAACCTA	TCCAGTCATT	240
GGTGTGCCAG	TCAAGTCTCG	TGCTCTTAGT	GGAGTGGATT	CACTCTATT	TATCGTTCAG	300
ATGCCGGGTG	GGGTGCCTGT	TGCGACCATG	GCTATCGGTG	AAGCTGGAGC	GACTAACGCA	360
GCTCTCTTTG	CCATCCGTCT	CCTCTCTGTA	GAAGATAAGT	CCATTGCGGA	TGCACTTGCC	420

AACTTTGCTG AAGAACAAGG AAAAATCGCA GAGGAGTCGT CAAATGAGCT CATCTAA

477

(2) INFORMATION FOR SEQ ID NO:2057:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 561 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...561
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2057:

GGTAGCATCA	TGAAATCTAT	TGGTACGCAA	ATATTACAGA	CAGAACGTTT	GATTTTAAGA	60
AGATTTGTGG	AGAGTGATGC	AGAAGCCATG	TTTCAAAATT	GGGCTTCATC	CGCTGAGAAT	120
CTGACCTATG	TTACCTGGAA	TCCCCATCCT	GATGTCGAAA	TCACTCGAAA	CTCGATTTCGC	180
AATTGGGTTG	CTTCCTATAC	TAATCTCAAC	TATTACAAAT	GGGCCATTTG	TCTAAAAGAA	240
AACCCAGAGC	AAGTGATAGG	AGATATCAGC	ATCGTTAAGA	TAGACGAGGC	TGATTTAAGC	300
TGTGAAATCG	GCTATGTGCT	AGGCAAGGCT	TACTGGGGAC	ATGGTATGAT	GACAGAGGCC	360
TTGAAAGCTG	TCTTGACTT	TTGTTTTACT	CAAGCAGGTT	TTCAAAAGGT	CAGAGCACGT	420
TATGCCAGTC	TCAACCCAGC	TTCAGGTCGT	GTCATGGAAA	AGGCTGGAAT	GTCCTATCTA	480
CAAACCATTG	TTAATGGTGT	AGAGAGAAAA	GGCTATCTTG	CGGATCTTAT	TTATTATGGT	540
ATAAGTAGGG	AAGAATGTTG	A				561

(2) INFORMATION FOR SEQ ID NO:2058:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1455 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2058:

GTGTTAATCA	TGAGTAGACG	TTTTAAGAAA	TCAGGTTTAC	AGAAAGTGAA	GCGAAGTGTT	60
AATATAGTTT	TGTTGACTAT	TTATTTATTG	TTAGTTTGTT	TTTTATTGTT	CTTAATCTTT	120
AAGTACAATA	TCCTTGCTTT	TAGATATCTT	AATCTAGTGG	CAACTGCCCTT	TGTTCTACTA	180
GTTGCCTTAA	TAGGGCTACT	CTCGATTATC	TATAAAAAAG	CTGAAAAGTT	TACCATTTTTT	240
CTGTTGGTGC	TCTCTATTCT	TGTCAGCTCA	GTGTCGCTCT	TTGCAGTACA	GCAGTTTGTT	300
GGACTGACCA	ATCGTTTAAA	TGCGACTTCT	AATTACTCAG	AATATTGCTT	CAGTGTGCTT	360
GTTTTAGCAG	ATAGTGAGAT	TGAGAATGTT	ACGCAACTGA	CGAGTGTGAC	AGCACCGACT	420
GGGACTGATA	ATGAAAACAT	TCAAAAACTA	CTAGCTGATA	TCAAATCAAG	TCAGAATATC	480
GATTTGACGG	TTAATCAAAG	TTCGTCTTAC	TTGTCAGCTT	ACAGGAGTTT	GATTGCAGGA	540
GAGACTAAGG	CCATTGTCTT	AAATAGTGTC	TTTGAAAATA	TCATTGAATC	GGAGTATCCA	600
GATCACGCAT	CGAAGATAAA	AAAGATTTAT	ACCAAGGGAT	TCATTAAAAA	AGTAGAAGCT	660
CCTAAGACGT	CTAAGAATCA	GTCTTTCAAT	ATCTATGTTA	GTGGAATTGA	TACTTATGGT	720
CCAATTAGTT	CGGTGTCGCG	TTCAGATGTC	AATATCTTGA	TGACTGTCAA	TCGAGATACC	780
AAGAAAATTC	TCTTGACCAC	AACGCCACGT	GATGCTTATG	TACCAATCGC	AGATGGTGGA	840
AATAATCAAA	AAGATAAATT	GACTCATGCG	GGCATTATATG	GAGTTGATTG	GTCCATTAC	900
ACCTTAGAAA	ATCTCTATGG	AGTGGATATC	AATTACTATG	TGCGATTGAA	CTTCACCTCG	960
TTTTTGAAAT	TGATTGATTT	GTTGGGTGGG	GTAGATGTTT	ATAATGATCA	GGAATTCACA	1020
GCTCTTGCTA	ATAAAAAACA	CTATTCTATT	GGTAATGTCC	ATTTAGATTG	AGAAGAGGCA	1080
CTCGCTTTTG	TTCGTGAGCG	CTATTCCCTA	GCGGATGGTG	ATCGTGACCG	TGGGCGCAAT	1140
CAACAAAAGG	TGATTGTGGC	TATCCTTCAA	AAATTAACCT	CGACCGAAGT	ACTGAAAAAT	1200
TATAGTACGA	TCATTGATAG	CTTGCAAGAT	TCTATCCAAA	CAAACATGCC	ACTTGAGACC	1260
ATGATAAACT	TGGTCAATGC	TCAGTTAGAA	AGTGGTGGAA	CGTACAAAGT	AAATTCGCAA	1320
GACTTGAAGG	GTAGGGGACG	GACGGATCTT	CCTTCCTATG	CGATGCCAGA	TAGTAACCTC	1380
TATGTGATGG	AAATTAACGA	CAGTAGCCTT	GCATCTGTCA	AAACGGCTAT	TCAGGACGTG	1440
TTGGAGGGCA	GATGA					1455

(2) INFORMATION FOR SEQ ID NO:2059:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2059:

TGTAGAATCA	TGAAAAAATT	TGAAATGATT	TCTATCACAG	ATATACAAAA	AAATCCCTAT	60
CAACCCCGAA	AAGAATTTGA	TAGAGAAAAA	CTAGATGAAC	TAGCACAGTC	TATCAAAGAA	120
AATGGGGTCA	TTCAACCGAT	TATTGTTTCGT	CAATCTCCTG	TTATTGGTTA	TGAAATCCTT	180
GCAGGAGAGA	GACGCTATCG	GGCTTCACTT	TTAGCTGGTC	TACGGTCTAT	CCCAGCTGTT	240
GTTAAACAGA	TTTCAGACCA	AGAGATGATG	GTCCAGTCCA	TTATTGAAAA	TTTACAGAGA	300
GAAAAATTAA	ACCCAATAGA	AGAAGCACGC	GCCTATGAAT	CTCTCGTAGA	GAAAGGATTC	360

ACCCATGCTG	AAATTGCAGA	TAAGATGGGC	AAGTCTCGTC	CATATATCAG	CAACTCCATT	420
CGTTTACTTT	CCTTGCCAGA	ACAGATTCTT	TCAGAAGTAG	AAAATGGCAA	ACTATCACAA	480
GCCCATGCGC	GTTCCCTAGT	TGGGTAAAT	AAGGAACAAC	AAGACTATTT	CTTTCAACGG	540
ATTATAGAAG	AAGATATTTT	TGTAAGGAAA	TTAGAAGCTC	TTCTGACAGA	GAAAAACAA	600
AAGAAACAGC	AAAAAACTAA	TCATTTTATA	CAAAATGAAG	AAAAACAGTT	AAGAAAACTA	660
CTCGGATTAG	ATGTAGAAAT	TAAACTATCT	AAAAAAGACA	GTGGAAAAAT	CATTATTTCT	720
TTTTCAAATC	AAGAAGAATA	TAGTAGAATT	ATCAACAGCC	TGAAATAA		768

(2) INFORMATION FOR SEQ ID NO:2060:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 825 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...825
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2060:

AAAGGAATCA	TTATGGATCA	ACTGCAGATT	AAGGATTTGG	AAATGTTTGC	CTATCATGGT	60
CTTTTTCTTA	GTGAGAAAGA	ATTGGGGCAG	AAATTTGTCT	TTTCAGCCAT	CCTATCCTAT	120
GATATGACCA	AGGCAGCTAC	AGACTTGGAT	TTAACAGCCT	CTGTCCATTA	CGGAGAAATG	180
TGTCAGCAGT	GGACGACTTG	GTTTCAGGAA	ACGAGTGAAG	ATTTGATTGA	AACGGTAGCC	240
TATAAACTGG	TGGAACGTAC	CTTTGAGTCT	TATCCTCTTG	TCCAAGAAAT	GAAGTTGGAA	300
CTGAAAAAAC	CTTGGGCACC	GGTGCATTTG	TCAC TAGATA	CTTGCTCGGT	AACCATTCAT	360
CGCCGCAAGC	AACGAGCCTT	TATCGCCCTA	GGAAGCAATA	TGGGAGATAA	ACAAGCAAAC	420
TTGAAGCAAG	CCATTGACAA	ACTGCGAGCT	CGTGGCATCT	ATATTCTCAA	AGAGTCCAGT	480
GTCTTAGCGA	CGGAGCCTTG	GGGTGGAGTG	GAGCAGGATA	GCTTTGCCAA	TCAAGTGGTT	540
GAGGTGGAAA	CCTGGCTACC	AGCACAAAGC	TTGTTAGAAA	CCTTGTTAGC	CATTGAGTCA	600
GAGCTGGGAC	GGGTGAGAGA	AGTGCATTGG	GGACCTCGTT	TGATTGATTT	GGACTTGCTC	660
TTTGTGGAGG	ACCAGATCCT	TTATACAGAC	GACCTCATAT	TGCCTCATCC	TTACATAGCG	720
GAACGCCTTT	TTGTCCCTGA	GTCCTTACAG	GAAATTGCGC	CTCATTTTAT	CCATCCGATA	780
TTAAAACAAC	CGATCCGTAA	CTTGTATGAT	GCTTTGAAAA	AATAG		825

(2) INFORMATION FOR SEQ ID NO:2061:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2061:

TCTACGATCA	TAGTCTTCTT	CAGCTTGTTG	ATCAGCTGGT	TTTTCTGCTT	TTGGTTGTTT	60
AGCTGGCTTC	TCTGGTTTTG	GTGCGGGAGC	TGGTTGAGGA	GCCGGCGCTG	GTTTTGGTTG	120
TTCAGCTGGT	GCTTCTGGGG	CTGGAGTTTC	TGGAGCTGGA	GCTGGTTTTT	CTGGCTCATT	180
AACTGCTTTC	TTAAGGTCAG	CTTCAGTTTT	TTCTAA			216

(2) INFORMATION FOR SEQ ID NO:2062:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 285 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2062:

TCCTGGATCA	TTCTCATCAG	GATTACTCTT	TACTGCTATT	TTAGAAACTG	GGGTGGTTTG	60
ATGGAAAGTA	TTGGTCTTGT	TATCGTTTCA	CATTCCAAAC	ACATTGCAGA	AGGTGTTGTT	120
GCACTAATTA	GTAAAGTAGC	TAAAGATGTT	CCGATTACTT	ATGTAGGAGG	AAACCGAGGGC	180
GGAGGAATTG	GAACGAGTTT	TGATCAAGTA	GATAGGGTTG	TTTCCGAAAA	TCCAGCAGAT	240
ACTTTACTTG	CCTTTTTTTGA	CCTAGGTTCT	GCTATAAAAT	GTTAA		285

(2) INFORMATION FOR SEQ ID NO:2063:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1017 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2063:

GCAGGGATCA	TAGCCTTATC	CAGTTTTGTA	TTGATGGCAC	TTCGTTTTTC	GAGTATGGTT	60
TATGATACAA	ATGGGGAGCA	GGTCAAGCAG	TTATTTGGCG	GCGCAATACC	ATTTTTTAGC	120
CTGAATGCAT	CTTCTTTGTT	TATGGCGATT	ACTATTGGAT	TGGTTACAGC	AGAGATTTAT	180
CGTATGTTTA	TCCAGCGCGG	AATTACGATA	AAAATGCCAA	GTGGTGTCCC	AGATGTAGTA	240
AGTAAATCAT	TTTCAGCTCT	TTTACCTGGT	TTTACTACTT	TTGTTTTGTG	GGCTTTGGTC	300
TTAAAAGGTC	TTGAAGCGGC	AGGAGTTGCA	GGAGGTCTCA	ACGGATTCCCT	AGGTGCAATT	360
GTTGGAACAC	CGCTTAAGTT	AATTGCAGGA	ACGCTTCCAG	GTATGATTCT	ATGTGTTATT	420
GTAAACTCAT	TCTTTTGTTT	CTGTGGAGTT	AATGGGGGAC	AAGTTTTAAA	TGCTTTTGTA	480
GACCCAGTTT	GGTTACAATT	TACTACAGAA	AACCAAGAAG	CTGTGGCTGC	AGGACAAACA	540
CTCCAACACA	TTATTACATT	ACCGTTTAAA	GATTTATTTG	TATTTATAGG	TGGCGGTGGA	600
CGGACTATTG	GTCTTGCGAT	TTGTCTCTTC	CTATTTAGTA	AGAGTCGTGC	GAATAAAACA	660
TTAGGTAAGC	TAGCTATTAT	ACCGTCTATT	TTTAATATCA	ATACAGCTAT	TCTATTTACG	720
TTTCCAACAG	TTTTAAATCC	GATTATGCTG	ATTCCGTTTA	TTGCTACTCC	TACAAATCAAT	780
GCCTTGATTA	CCTATGTATC	AATGGCTGTA	GGATTAGTAC	CCTATACAAC	AGGTGTAATC	840
CTTCCGTGGA	CAATGCCACC	GATTATAGGA	GGCTTCCTTG	CAACAGGGGC	TAGTTGGCGA	900
GGAGCTCTAT	TACAAGTTGT	TTTGATTTTG	GTTTCTGTAG	CAATTTATTA	TCCATTCTTC	960
AAAATTGCAG	ATAAACGCAA	TCTTGAAAAA	GAAAAAGCTA	CTGTTGGAGG	GAAATAA	1017

(2) INFORMATION FOR SEQ ID NO:2064:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 723 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2064:

AATACTGTCA	TTTTGAATAT	AAAGGAGTTT	GATATGGAGT	GGATTAGATT	AATAGGAATA	60
GCAATCATTG	TTGTGGGTTT	TATTTTAAAA	TTTGATACAA	TTGCAACAGT	AGTCTTAGCT	120
GGTTTGTTTA	CAGCTTTAGT	TTCAGGTGTT	TCTCTCGTTG	AATTTTTTGA	GATTTTGGA	180

AAAGAATTTA	GCAATCAGCG	AGTGCTCACG	ATTTTTATGG	TTACCTTGCC	TCTTGTGGGG	240
CTGTCAGAAA	CCTTTGGACT	CAAGCAACGA	TCAATCGATT	TGATTCGAAA	GATTAAAGGT	300
CTGACAGTTG	GAAACTTCTA	TACAGTTTAT	TTCTTTATTC	GAGAGTTAGC	TGGTTTCTTT	360
TCAATTCGTC	TAGGAGGACA	CCCTCAGTTT	GTCAGACCTT	TGGTTCAGCC	TATGGGAGAA	420
GCAGCTGCAG	AGTCTCAATT	AGGTAGAAA	TTAACAGAGG	TTGAAGATGA	GACAATAAAA	480
GCGCGTGC	CTGCCAATGA	AAATTTTGGA	AATTTCTTTG	CTCAAAATAC	GTTTGTAGGT	540
GCTGGGGGAG	TCCTCTTGAT	AGGGGGAACA	TTAGATCAGT	TAGGCTATGA	AAGCAATTAT	600
GCAGGGATTG	CTTCTACATC	TATTATTGTT	GCTGTTATAA	CACCTATTGT	AGTGGGGATT	660
TACAATTATT	TATTTGATAA	AAAATTGATA	TCAAAAAGA	CTAGGGGAGG	AGAACAAAAA	720
TGA						723

(2) INFORMATION FOR SEQ ID NO:2065:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2065:

AATAGTGTCA	TGAGTAAAT	GTATTATGCA	GAAAATCCTG	ACGCTGCTCA	CGACATTCAT	60
GAGTTGAGAG	TGGACTTGTT	GGGACAAAAA	ATGACCTTTT	TAACGGATGC	GGGTGTTTTT	120
AGCAAGAAAA	TAGTTGACTT	TGGAAGTCAA	CTATTGCTCA	AGTGTCTTGA	GGTCAACCAA	180
GGAGAACTG	TCCTTGATGT	AGGCTGTGGT	TACGGACCTT	TGGGTTTGTC	CTTAGCTAAG	240
GCTTATGGAG	TTCAGGCTAC	TATGGTTGAT	ATCAACACTC	GTGCCTTGGA	TTTAGCTCGG	300
AGAAATGCTG	AAAAAATAA	TGCAAAAGCG	ACGATTTTCC	AGTCCAACAT	CTATGAACAA	360
GTTGAAGGAC	ATTTTGATCA	TGTCATTTCC	AATCCTCCTA	TCCGTGCGGG	CAAGCAAGTC	420
GTTTCATGAA	TCATTGAGAA	AAGTAAAGAT	TTCTTGGA	CTGGTGCGGA	TTTGACAATC	480
GTCATCCAGA	AAAAACAAG	GGGCTCCAAG	TGCTAA			516

(2) INFORMATION FOR SEQ ID NO:2066:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2066:

GGATTAGTCA	TGGA AAAATTT	ACAGTTTAAA	GCCTTACCGA	AGGAGTTTTT	ATTAGGAGCT	60
GCTACCGCTG	CTTATCAAGT	AGAGGGTGCA	ACTAGGGTAG	ATGGTAAAGG	AATAAATATG	120
TGGGATGTTT	ATTTGCAAGA	AAATAGTCCG	TTCTTACCAG	ATCCAGCTAG	TGATTTTTTAT	180
TATCGTTACG	AAGAGGATAT	AGCTTTGGCG	GCAGAACATG	GTTTGCAGGC	TTTGC GTTTA	240
TCTATTTCTT	GGGTTCGTAT	ATTTCCCTGAT	ATAGATGGAG	ATGCTAATAT	ATTGGCTGTT	300
CGTTATTACC	ATAGAGTCTT	TCAGTCTTGC	TTAAAACATA	ATGTGATTCC	GTTTGT TCT	360
TTACATCATT	TTGATTCCGC	TCAGAAAATG	TTAGAAACAG	GGGATTGGTT	GGATAGAGAG	420
AATATTGATC	ATTTCATACG	ATATGCTCGC	TTTTGT TTTCC	AAGAATTTAC	AGAAGTCAAG	480
CATTGGTTTA	CAATCAATGA	ACTGATGTCT	CTTGCTGCAG	GTCAATATAT	AGGAGGTCAG	540
TTTCCTCCAA	ATCATCATTT	TCAATTATCT	GAAGCAATTC	AAGCGAATCA	TAATATGTTG	600
TTGGCGCATG	CTCTTGCAGT	CCTCGAATTT	CATCAATTAG	GAATTGAGGG	AGAGATAGGT	660
TGTATTCATG	CTTTAAAGCC	AGGCTATCCT	ATTGATGGGC	AAAAAGAAAA	TATTTTGGCA	720
GCTAAACGGT	ATGATGTTTA	TAATAATAAA	TTTCTATTAG	ATGGAAC TTT	TTTGGGCTAC	780
TACAGTGAGG	ACACGCTTTT	TCAC TTGAAT	CAAATATTGG	AAGCTAATAA	TTCTAGCTTT	840
ATTATTGAAG	ATGGTGATTT	AGAAATTA TG	AAGAGAGCTG	CACCTCTTAA	TACGATGTTT	900
GGGATGAATT	ATTATCGTTC	AGAATTTATT	CGTGAATACA	AAGGTGAAAA	TAGACAAGAA	960
TTTAATTCAA	CAGGAATAAA	AGGACAGTCT	TCTTTTAAAT	TAAATGCTCT	AGGTGAATTT	1020
GTAAAAA AAA	CTGGTAT TCC	GACAAACAGAT	TGGGATTGGA	ATATTTATCC	TCAAGGGTTA	1080
TTTGATATGT	TGCTTCGTAT	CAAAGAAGAA	TATCCTCAAC	ATCCGGTCAT	TTATTTAACT	1140
GAAAAATGGTA	CAGCCCTTAA	AGAAGTTAAG	CCAGAGGGCG	AGAATGATAT	TATTGATGAC	1200
AGTAAGAGAA	TCCGTTATAT	TGAGCAACAT	TTACACAAAG	TTTTAGAGGC	TCGAGATAGA	1260
GGAGTCAATA	TTCAAGGCTA	TTTTATATGG	TCTTTGCAAG	ATCAATTTTC	TTGGGCGAAT	1320
GGCTACAATA	AGCGATATGG	TCTTTTCTTT	GTTGATTATG	AAACACAGAA	GAGATATATT	1380
AAGAAAAGTG	CTCTTTGGGT	AAAAGGGCTA	AAACGGAATT	AA		1422

(2) INFORMATION FOR SEQ ID NO:2067:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2067:

AAGCAAGTCA	TCAAAACAAG	AGAGTGTTC	CACACTTTAA	CTGCTAAAA	AGAAAATGTT	60
GCTCCTCGTG	ACCAAGAATT	TTATGATAAA	GCATATAATC	TGTTAACTGA	GGCTCATAAA	120
GCCTCGTTTG	AAAATAAGGG	TCGTAATTCT	GATTCCAAAA	CCCTTAGACA	AATTATTAGA	180
ACGCTTGAAT	GA					192

(2) INFORMATION FOR SEQ ID NO:2068:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2068:

AATAGAGTCA	TGAAAATTAA	AGTTGTAACA	GTTGGGAAAC	TGAAAGAAAA	GTATTTAAAA	60
GATGGTATCG	CAGAGTATTC	AAAACGAATT	TCTAGATTTG	CTAAGTTTGA	AATGATTGAG	120
TTATCAGATG	AAAAACACC	AGATAAGGCC	AGTGAATCAG	AAAATCAAAA	GATTTTAGAA	180
ATAGAAGGTC	AGAGAATTTT	ATCAAAAATT	GCTGACCGTG	ATTTCTGTTAT	TGTGTTAGCC	240
ATTGAAGGGA	AAACTTTCTT	CTCAGAAGAA	TTTAGTAAGC	AGTTAGAAGA	AACTTCTATA	300
AAAGGATTTT	CTACTCTTAC	TTTTATTATT	GGGGGAAGTT	TAGGATTGTC	ATCATCTGTA	360
AAAAATAGAG	CCAATCTTTC	TGTCAGTTTT	GGTCGCCTAA	CCTTACCCCA	TCAGTTAATG	420
AGACTAGTTC	TTGTTGAACA	AATCTATCGC	GCTTTTACGA	TTCAGCAGGG	ATCCCCCTAC	480
CATAAATAG						489

(2) INFORMATION FOR SEQ ID NO:2069:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 864 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2069:

AAGTTGGTCA	TCGAGAGAT	ATTTATTAAA	TTAAAGCTGA	GTAATAACAG	TATAGAAAGT	60
AAGGAGAGTA	AAAAATTTGAA	GAAAAAATGG	TTTTTTGCAG	ATTATTATGA	CACAACAATT	120
ATTTTACTTG	CTTTAATCTC	TGTTATTCTG	GTATTACTTG	GATTTGCTGA	AATGATTGAT	180
TTGGACAATC	CGCCTTATAG	TATTATTGAT	TTAGTAATCT	GGGGTGTTTT	TGTAATTGAC	240
TATAGTTGGC	GCTTTTTTAC	GACTAAAAGA	AAATGGCGCT	TTATTCTTGA	AAATATTTTT	300
GATTTATTGG	CTATTCTCCC	TTTAAATGCT	ATTTTTACAG	TGTTTCGATT	AGGGCGTATC	360
TTTCGTTTTAG	CTAAACTAAC	AAAATTACTG	AAACTGACTC	GTTTACTTAG	AATAATTGGA	420
CTTACAGGTA	AATTAGAAAG	AAAAATTAGT	AGATTCTTAC	GGACAAATGG	CCTGATTTAT	480
ATCTTGTATG	TTAATATCTT	TATTGTTCTA	GTAGGGAGTT	CGATTTTATC	CGTTGTTGAA	540
GAAAAATCCT	TCTCAGATAG	TCTTTGGTGG	GCTCTTGTTA	CAGTAACTAC	TGTTGGATAT	600
GGGGATATTG	TTCTTGCTTC	CATTTTTTGGG	AAATGGCTAG	CAGTTTTTACT	GATGCTTGTC	660
GGTATTGGAA	CAATAGGGAT	GTTAACAAGT	GCCTTGACGA	ACTTTTTTGT	AAAGGATAAT	720
CCAGATGAAC	AGATAAAACT	TGATAAACTC	AAAGATGAAT	TATCGAGCCA	AAGAATATTA	780
CTAGAGAAAC	AATCTACAAA	GATAGAAGAA	CTACCTTTAA	TGATACCCGA	TCTGATTGAT	840
AAAACCTTAT	CCATATCAAG	ATGA				864

(2) INFORMATION FOR SEQ ID NO:2070:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 891 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2070:

TGGGAGGTCA	TTCTTATGAC	TGAAAACTA	ATCAATTCAA	AACCAAATGG	TGTATTGCGA	60
TTGATTCTCA	TTGAGTTGAC	AATCGTACTT	GGTGTCTTTA	TATTTATAAT	GGGTGTTGGT	120
TCGGAAAACA	TTTTTGGAAT	TATTATCGGA	CCTTTACTAA	TCGTAATTGC	AGCGCTAACT	180
CATGCTGGTT	TAAAAGTTGT	CAAACCTCAG	GAAGCTCTGG	TTCTGACACT	CTTTGGTAAT	240
TATACAGGTA	CCATCAAAGA	ACCTGGTTTT	TACTTTGTCA	ATCCCTTCAG	CGTAGCAGTC	300
AACCTTGCAA	ACCACACTCG	ACTTGGACAA	AGTGGTGATG	TTAGCACAAA	ATCTCCTTTT	360
TTAGGAGCTA	AATCATCAAA	TGACAAATGAT	GTAAATCTTG	AAATTGGCAA	GAAACACATT	420
TCCCTCAAAG	TCATGACCTT	GAGCAATTCT	CGTCAAAAAA	TCAATGATTG	CTTAGGAAAC	480
CCTGTAGAAA	TCGGTATCGC	GGTAACTTGG	AGAGTTGTCT	ATACCGCTAA	GGCAGTCTTC	540
AACGTTGATA	ACTACAAAAG	ATATCTTTCA	TTGCAATGTG	ATAGCGCCCT	CCGTAATATT	600
GTCCGCATCT	ATCCTTACGA	TGTGTCTCCT	AATGTGGATA	CTACGGGTGA	ACGGCAAGCA	660
AATGAAAGTA	GTCTCCGTGG	CTCTAGCGAA	ATTGTTGCTA	ACCGTATTTC	TGAAAAAATC	720

CAAAGTCGTG TTGAAGATGC TGGCTTGGAA ATCCTTGAAG CACGTATCAC TTACCTACCT	780
AATGCTCCAA AAATTGCTGC CGTTATGCTT CAACGCCAAC AAACATCTGC CATTATTGAT	840
GCACGAAAAA TAAATGTAAA TGGTGCTGTA GGAATGGTTA AAATGGCATA A	891

(2) INFORMATION FOR SEQ ID NO:2071:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 438 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...438
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2071:

AGACGGGTCA TTATTATCCT TCTTGGTTCG CACCAAATGG AGATTCTACA CTTTAAGGAG	60
CTTTATAAGG AAAAGAGGCT ACAACTGCAA GGACAGGGGC AAAATGGTAA GGGCTATAGT	120
CAGGCATTTT TATTGGGCTT GACCTTTAGT TTTGCTTGGG CGCCTTGCGT GGGGCCGGTT	180
CTGGGGTCTG TTTTGGCCTT GCGGGCTTCA GGTGGTTCAN GAGCTTGGCA GGGAGCTGGT	240
CTCATGTTGG TGTATACGCT GGGCTTGGCG CTACCATTCT TGCTTCTAGC TCTGACCTCT	300
AGTTATGTTT TGAAACATTT CCGAAAACCT CATCCCTATC TCGGAATCCT CAAAAAAGTG	360
GGTGGTTTTT TCATTATTGT GATGGGACTC TTGGTTCTGT TTGGAAATGC TTCAATTTTA	420
AGTCAATTAT TTGAATAA	438

(2) INFORMATION FOR SEQ ID NO:2072:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2072:

GGTGATTCCA	TGAAAATAGA	TATAACAAAT	CAAGTTAAAG	ATGAATTTCT	TATATCATTA	60
AAAACCTTGA	TTTCCTATCC	TTCAGTACTC	AATGAAGGAG	AAAATGGAAC	ACCTTTTGGG	120
CAAGCAATCC	AAGATGTCCT	AGAAAAAACT	TTAGAGATTT	GTCGAGACAT	AGGTTTCACT	180
ACCTATCTTG	ACCCTAAAGG	TTATTACGGA	TATGCAGAAA	TCGGTCAGGG	AGCAGAGCTT	240
CTGGCCATTG	TCTGTCAATTT	GGATGTTGTT	CCATCAGGTG	ATGAAGCAGA	TTGGCAGACA	300
CCGCCATTTG	AAGCAACTAT	CAAAGACGGC	TGGGTATTCTG	GACGTGGTGT	CCAAGATGAT	360
AAAGGTCCTT	CGCTTGCAGC	TCTCTATGCA	GTAAAAAGCT	TGCTGGACCA	AGGTATTCAG	420
TTCAAAAAGC	GCGTACGCTT	TATCTTTGGT	ACCGATGAGG	AAACCCCTCTG	GCGCTGCATG	480
GCACGCTACA	ATACCATCGA	AGAACAGGCC	AGCATGGGCT	TTGCACCTGA	CTCATCTTTT	540
CCTCTGACCT	ATGCTGAAAA	AGGGCTTCTA	CAGGTCAAAC	TTCATGGCCC	TGGATCGGAT	600
CAACTAGAGC	TTGAAGTAGG	AGGCGCTTTT	AACGTTGTAC	CAGACAAGGC	CAACTACCAA	660
GGTCCCCTCT	ATGAACAGGT	TTGTAACGAT	CTCAAAGAAG	CTGGTTATGA	TTACCAATCC	720
ACTGAACAAA	CCGTAACGGT	TCTCGGAGTG	CCAAAGCATG	CTAAGGATGC	TAGTCAAGGT	780
ATCAATGCTG	TCATCCGACT	AGCTACCATT	CTTGCTCCTC	TCCAAGAACA	CCCTGCTCTC	840
AGCTTTCTTG	CAACACAAGC	AGGTCAAGAC	GGCACAGGAA	GACAAATCTT	TGGTGATATA	900
GCAGATGAAC	CTTCTGGTCA	CCTATCCTTT	AATGTCGCAG	GTCTCATGAT	CAATCATGAA	960
CGTTCTGAAA	TCCGTATTGA	CATTCGGACT	CCTGTCTTAG	CTGACAAGGA	AGAACTAGTA	1020
AAGTTGCTTA	CAAGATGTGC	ACAAAACCTAC	CAACTCCGCT	ACGAAGAGTT	TGACTATCTA	1080
GCGCCTCTAT	ACGTCGCAAA	AGACAGTAAA	CTCGTTAGCA	CACTGATGCA	AATCTACCAA	1140
GAAGAGACTG	GCGATAACAG	TCCTGCTATT	TCATCCGGTG	GTGCCACTTT	TGCTCGCACC	1200
ATGCCAAATT	GTGTAGCCTT	CGGCGCCTTA	TTCCCAGGAG	CGAAGCAGAC	AGAACATCAG	1260
GCAATGAAT	GTGCCGTTCT	AGAAGATTG	TACCGTGCTA	TGGATATTTA	TGCCGAAGCC	1320
GTCTATCGAC	TTGCAACTTA	A				1341

(2) INFORMATION FOR SEQ ID NO:2073:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2073:

GGGTGCTCCA	TATTATGCCG	AGGACCGGAA	TCGAACCGGT	ACGATCGTTA	CCAATCGCAG	60
GATTTTAAGT	CCTGTGCGTC	TGCCAGTTCC	GCCACCCCGG	CCTCTCTAAG	CGAACGACGG	120
GATTGGAACC	CGCGACCCCC	ACCTTGGCAA	GGTGGTGTTT	TACCACTGAA	CTACGTTTCG	180
ACTGTTTTCT	TCTATCTAAA	AATGCCGGCT	ACATGA			216

(2) INFORMATION FOR SEQ ID NO:2074:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2074:

GGGTGCTCCA TATTATGCCG AGGACCGGAA TCGAACCGGT ACGATCGTTA CCAATCGCAG	60
GATTTTAAGT CCTGTGCGTC TGCCAGTTCC GCCACCCCGG CCTCTCTAAG CGAACGACGG	120
GATTCGAACC CGCGACCCCG ACCTTGGCAA GGTGGTGTTC TACCACTGAA CTACGTTTCG	180
ACTGTTTTCT TCTATCTAAA AATGCCGGCT ACATGA	216

(2) INFORMATION FOR SEQ ID NO:2075:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2075:

GATGTTCCCA TGGAATTTCC AATTAAGATC ATTCAGGCAA GCAAGTCTGA TTTGCCTGAG	60
ATAGGGGCAC TTCAGACCTC GTCTTTTCCA GCTGAAAAGC AGCAACTTTC CCATATTTTA	120
GAAGAAAGTA TCCGTAAGTG TGCGGATACC TTTCTTCTAG CTAGGGATGA AAATCAACTT	180
TTAGGCTATA TTTTATCAAG TCCCCAGTCA GACAATCCGC AATGTCTAAA AGTACATTCT	240
TTAGTCATCG AGTCTGACCA TCAGAGACAG GGCTTGGGAA CACTTCTTCT TGCAGCCTTG	300
AAAGAGGTGG CAGTTGAGCT GGATTACAAA GGATTCGTTT GGAGATCATG TGGAGTCTTC	360

(2) INFORMATION FOR SEQ ID NO:2076:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...351
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2076:

GCAAATCCCA	TTGGAACAAA	AGTACTATCA	AATCCAATAG	TAATAGACTT	GTTAGACTGG	60
TACTTTGACC	AATTATCTCC	ACTAGTTTCG	CTAGAATTTT	TCCCACAAGC	TACTAAGAAC	120
AAAGCAGTCA	TCAGACTGAC	TAATACAAGC	ATCCATTTTT	TCATCCATTT	TTTCATCCAT	180
TTTTCTCCT	ATTTAGGTC	TACTTTCAAT	AATACATCTG	CGATATTTTC	AGCAAAGTGC	240
AAATCATGGG	TAACCACAAT	CTGGGTCATC	CCAAGTCCCC	TATTTTGCAA	GATTAGCTTC	300
TCCACTTCCA	AACGTAATTC	TGGATCCAGG	GCAGAAAGTTG	GTTTCATCGTA	G	351

(2) INFORMATION FOR SEQ ID NO:2077:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1500
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2077:

GAGGATCCCA	TGTCTACAGA	ACATATGGAA	GAATAAATG	ACCAGCAGAT	TGTTCCGCGT	60
GAAAAAATGG	CTGCGCTCCG	CGAACAAGGA	ATCGATCCTT	TCGGAAAAACG	TTTGAAACGT	120
ACTGCAAATT	CACAAGAATT	AAAAAGATAAA	TATGCCAACCC	TCGATAAAGA	ACAAATTACAC	180
GATAAAAAACG	AAACAGCTAC	TATCGCAGGA	CGCTTGGTAA	CCAAACGTGG	TAAAGGAAAA	240
GTTGGTTTTG	CCCACCTTCA	AGACCGCGAA	GGCCAGATTC	AGATCTACGT	TCGTAAGGAT	300
GCTGTCCGGT	G	AAGAAAACTA	CGAAATCTTC	AAAAAAGCAG	ACCTTGGTGA	360

GTCGAAGGTG	AAGTGATGCG	TACGGATATG	GGAGAACTCT	CTATCAAGGC	AACCCACATC	420
ACACACTTGT	CTAAGGCTCT	TCGTCCCTCT	CCTGAGAAAT	TCCATGGTTT	GACAGATGTT	480
GAAACAATTT	ACCGTAAACG	TTACCTTGAC	TTGATTTCTA	ATCGTGAAAG	CTTTGAACGC	540
TTTGTCACTC	GTTCAAAAAT	CATCTCTGAA	ATCCGTCGTT	ACCTTGACCA	AAAAGGATTC	600
CTTGAAGTGG	AAACACCTGT	TCTTCATAAT	GAAGCCGGTG	GTGCTGCTGC	CCGTCCATTT	660
ATCACCCACC	ACAATGCCCA	AAACATTGAC	ATGGTGCTTC	GTATCGCGAC	TGAGCTTCAC	720
TTAAAACGCC	TTATCGTGGG	TGGTATGGAA	CGTGTCTATG	AAATTGGCCG	TATCTTCCGT	780
AACGAAGGAA	TGGACGCTAC	TCATAACCCT	GAGTTTACTT	CTATCGAAGT	TTACCAAGCT	840
TATGCAGACT	TCCAAGACAT	CATGGACTTG	ACGGAAGGCA	TTATCCAACA	CGCTGCTAAA	900
TCAGTTAAGG	GCGATGGCCC	AGTCAACTAC	CAAGGTACTG	AAATCAAGAT	TAACGAACCA	960
TTTAAGCGTG	TTCATATGGT	GGATGCTATC	AGAGAAATTA	CTGGTGTCGA	TTTCTGGCAA	1020
GACATGACTT	TAGAAGAAAG	TAAAGCTATC	GCTGCTGAGA	AGAAAGTTCC	AGTTGAGAAA	1080
CACTACACTG	AGGTTGGTCA	CATCATCAAT	GCCTTCTTTG	AAGAGTTTGT	TGAAGAAACT	1140
TTAATCCAAC	CAACCTTTGT	CTATGGACAT	CCAGTAGCTG	TATCTCCACT	CGCTAAGAAA	1200
AATCCTGAAG	ACCAACGCTT	TACTGACCGT	TTCTGAGCTCT	TTATCATGAC	TAAGGAGTAC	1260
GGTAATGCCT	TTACTGAACT	CAACGACCCA	ATCGACCAAC	TTAGCCGTTT	TGAAGCCCAA	1320
GCTAAAGCCA	AAGAACTTGG	TGATGATGAA	GCGACAGGAA	TCGACTATGA	CTACATTGAA	1380
GCTCTTGAAT	ACGGTATGCC	ACCAACAGGT	GGTTTGGGAA	TCGGTATCGA	CCGTCTCTGC	1440
ATGCTCCTCA	CTGATACAAC	AACTATCCGT	GATGTATTGC	TCTTCCCAAC	AATGAAATAA	1500

(2) INFORMATION FOR SEQ ID NO:2078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2078:

GTACACCCCA	TCCATTATCA	TTGCCCTGAA	AATATCTCAA	ATTTTCAACG	AAACAGTCGA	60
ATCGGTATTT	CGTTTGGAGG	AGGACGAGTG	ATGAACAAAGT	ATAAAGTGAT	TTATTATGTA	120
GTGGTCATAG	CTTTATTAGT	CAGCGTATTT	CTACTGATTG	GGATGGACCT	AAGCTGGTTT	180
AATCCCTATC	AAAGCGACCA	ATTTGTTTGG	GTCTACTTTG	CTCTCATCCC	AGTAATTGAA	240
TGGATTGAAA	AGAAATCCAA	AAATCTAGCA	AGTGAAAAAG	GAGAAATGA		288

(2) INFORMATION FOR SEQ ID NO:2079:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...594
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2079:

GAGAATACCA	TGAGTTATAA	AGATACGGTA	CAAAAAATCC	TCGATGTAAT	TGGAGGTGAA	60
AAAAATGTCA	ATAGAGTTAC	CCATTGTGTA	ACACGTTTAA	GATTAGAATT	AAAAGATGAA	120
AATTTTAGTCA	ATGATGATGA	TGTGAAGAAG	ATACCAGGTG	TAATAGGTAT	TATGAAAAAG	180
AATGGACAAT	ATCAAAATTAT	ACTTGGTAAT	GATGTAGCTA	ATTATTATAA	AGAATTCGTT	240
AAACTTGGCA	ATTTTGAATC	CGATTTCAGTT	GTTCAAGGGC	ACAAAGGGAA	TATTTTAGAA	300
AGAATCATTG	AGTATATCGC	TGGTTCCATG	ACTCCAATCA	TTCCAGCAAT	GTTAGGGGGA	360
GGTATGCTGA	AAGTCTTGGT	AATTATTTTA	CCAATGCTTG	GTATATTGCA	ATCAGATTCT	420
CAGACTATTG	CTTTTTTGAC	ATTTTTTGGG	GATGCTCCAT	ATTATTTCTT	ACCGCTGTTA	480
TTAGCTTATT	CTGCATCACA	AAAATTAAAA	GTAACATCTA	CAATAGCTAT	GTCTGTAGCA	540
GGTGACTTCT	CCATCCAAAT	TTTGTTCAAA	TGGTGCAATC	AGGAATCCTC	TTAG	594

(2) INFORMATION FOR SEQ ID NO:2080:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...225
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2080:

CGGCCAACCA	TTCTCGTGCA	TGTTTGCTGT	GCCCCTTGTA	GTACCTATAC	ACTAGAATAT	60
TTGACCAAGT	ATGCAGATGT	GACCATCTAT	TTTGCCAAAT	CTAATATCCA	TCCCAAGGCA	120
GAATACCATA	AGCGGGTCTA	TGTCACCAAG	AAATTTGTTA	GTGATTTTAA	TGAGCGGACA	180
GGAAATACGG	TTCAGTACCT	AGAAGCTCCC	TACGAACCCA	ATTAA		225

(2) INFORMATION FOR SEQ ID NO:2081:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2081:

GAGAGAACCA	TGCTCTTAAA	AGATAGATTC	GATAGATTTA	TAGATTATTT	TACGGAGGAT	60
GAGGATTCAA	GTCTCCCTTA	TGAAAAAAGA	GATGAGCCTG	TGTTTACTTC	AGTAAATTCT	120
TCACAGGAAC	CGGCTCTCCC	AATGAATCAA	CCTTCACAGT	CGGCTGGTAC	AAAAGAGAAC	180
AATATCACCA	GACTTCATGC	AAGACAACAG	GAATTGGCAA	ATCAGAGTCA	GCGTGCAACG	240
GATAAGGTCA	TTATAGATGT	TCGTTATCCT	AGAAAAATATG	AGGATGCAAC	AGAAATTGTT	300
GATTTATTGG	CAGGAAACGA	AAGTATCTTG	ATTGATTTTC	AGTATATGAC	AGAGGTGCAG	360
GCTCGTCGTT	GTTTGGACTA	TTTGGATGGA	GCTTGTCTATG	TTTTAGCTGG	AAATTTGAAA	420
AAGGTAGCTT	CTACCATGTA	TTTGTTAACA	CCAGTGAACG	TTATTGTAAA	TGTTGAAGAT	480
ATCCGTTTAC	CAGATGAAGA	TCAACAGGGT	GAGTTCGGTT	TTGATATGAA	GCGAAATAGA	540
GTACGATAA						549

(2) INFORMATION FOR SEQ ID NO:2082:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2082:

CCGGGAACCA	TTGGGCCCCG	TTTGGGATTT	GGGCTGCGAC	CCAGGGGGTC	TTCGGGATTT	60
AAAACAAAGG	GATTCGGGAA	TTTGGAGGGT	TGGAGAATTT	TTAACCTTGG	AAAGGAGGAA	120
GGGGTGTATT	TTAAACAAC	CAAAAAGGT	TTGAAATCCG	GGGTTCCGGG	CAATTTTGGT	180

(2) INFORMATION FOR SEQ ID NO:2083:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1083 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1083

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2083:

TTGCTTGCCA	TCCTGAAAAA	GAACTTTGTA	CCAAGCTATG	ACGTTGAAAG	TTTTGTAAAC	60
TCAATCGAAA	AACCTCGTCG	TATCATGCTG	ATGGTTCAAG	CTGGACCTGG	TACAGATGCT	120
ACTATCCAAG	CCCTTCTTCC	ACACCTTGAC	AAGGGTGATA	TCTTGATTGA	CGGAGGAAAC	180
ACTTTCTACA	AAGATACTAT	CCGTCGTAAT	GAAGAATTGG	CAAACTCAGG	TATCAACTTT	240
ATCGGTA CTG	GAGTTTCTGG	TGGTGAAAAA	GGTGCCCTTG	AAGGTCCTTC	TATCATGCCT	300
GGTGGACAAA	AAGAGGCCCTA	CGAATTGGTT	TCGGATGTTC	TTGAAGAAAT	CTCAGCTAAA	360
GCACCAGAAG	ATGGCAAACC	ATGTGTGACT	TATATCGGTC	CTGATGGAGC	TGGTCACTAT	420
GTGAAAATGG	TTCACAACGG	TATCGAGTAC	GGTGATATGC	AATTGATCGC	AGAAAGCTAT	480
GACTTGATGC	AACACTTGCT	AGGCCTTTCT	GCAGAGGATA	TGGCTGAAAT	CTTTACTGAG	540
TGGAACAAGG	GTGAATTGGA	TAGCTACTTG	ATCGAAATCA	CAGCTGATAT	CTTGAGCCGT	600
AAAGACGATG	AAGACCAAGA	TGGACCAATC	GTAGACTACA	TCCTTGATGC	TGCAGGTAAC	660
AAGGGA ACTG	GTAAATGGAC	GAGCCAATCA	TCTCTTGACC	TTGGTGTACC	ATTGTCACTG	720
ATTACTGAGT	CAGTGTTTGC	ACGCTACATT	TCAACTTACA	AAGAAGAACG	TGTACATGCT	780
AGCAAGGTGC	TTCCAAAACC	AGCTGCCTTC	AACTTTGAAG	GAGACAAGGC	TGAATTGATT	840
GAAAAAATCC	GTCAAGCCCT	TTACTTCTCA	AAAATCATTT	CATACGCACA	AGGATTGCT	900
CAATTGCGTG	TAGCCTCTAA	AGAAAACAAC	TGGA ACTTGC	CATTTGCAGA	TATCGCATCT	960
ATCTGGCGTG	ATGGCTGTAT	CATCCCGTCC	TCGTTTCTTG	CAAAAGATTA	CAGATGCCTA	1020
CAACCGCGAT	GCAGATCTTG	CCCACCTTCT	TTTGGACGAG	TACTTCTTGG	ATGTTACTGC	1080
TAA						1083

(2) INFORMATION FOR SEQ ID NO:2084:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2084:

GAGGCTGCCA	TGTTAGAATT	ACGAAATATC	AATAAAGTCT	TTGGAGACAA	ACAAATCCTG	60
TCTAATTTCA	GTCTAAGTAT	TCCTGAAAAG	CAAATCCTGG	CTATCGTTGG	ACCTTCTGGT	120
GGAGGTAAGA	CAACTCTTTT	ACGTATGCTT	GCAGGTCTTG	AAACCATTGA	TTCAGGGCAA	180
ATCTTTTATA	ATGGACAACC	TTTAGAGCTG	GATGAATTGC	AGAAGCGCAA	TCTACTGGGA	240
TTTGTCTTCC	AAGATTTTCA	ACTATTTTCT	CATCTATCAG	TTCTGGAAAA	TTTGACTTTA	300
TCGCCGTGTA	AGACCCATGG	GAATGAAGCA	GGAAGAGGCT	GA		342

(2) INFORMATION FOR SEQ ID NO:2085:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2085:

TTAAGTGCCA	TAATATCCCT	CTTTTTTTCT	TCATTAAATT	TATTTAATTA	TAGCATAAAT	60
ATTGATTTCA	TTCAATCTTA	CATTGATTTA	GTGATTTGTT	TTAGAGAATT	TGTTGTGTTA	120
TTCCGTCCTT	ATTTTGCCAT	AAATTGTTTT	AAGTGGGACC	TCTTATCCTT	ACCATTTTTA	180
CCTCCTAATT	TTGAGTATAA	AAAAGACGAT	AGAGTTTTTA	ATTTCTATCG	TCTGAGATTT	240
ACATATTAA						249

(2) INFORMATION FOR SEQ ID NO:2086:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2086:

TTAATAGTCT	TCGAAAATCT	CTTCAAACCA	CGTCAGCGTC	GCCTTACCGT	ATATATGTTA	60
CTGACTTCGT	CAGTTCTATC	TGCAACCTCA	AAACCATGTT	TTGAGCTGAC	TTCGTCAGTT	120
TCATCTGCAA	CCTCAAAACC	ATGTTTTGAG	CTGACTTCGT	CAGTTTCATC	TACAACCCTCA	180
AAACCATGTT	TTGAGCTGAC	TTCGTCAGTT	CTATCCACAA	CCTCAAAACA	GTGTTTTGAG	240
CAACCTGCGG	CTAGCTTCCT	AGTTTGCAC	TTGATTTTCA	TTGAGTATAA	AAAGATCTTG	300
GGAAAAGACT	CAATTTTCAGT	AGAAAAGGAA	GTAAATCTTC	CCACAATAAA	ACGCATAGTA	360
TCAAGTTTTT	TCAATACCTG	A				381

(2) INFORMATION FOR SEQ ID NO:2087:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2087:

AAAAAAGTCT	TTAAAATTAT	AAAACGCATC	ATATCAAGTT	TTTTCAAAAA	CCTTGATATG	60
ATGCGTTTTA	TTGTGGGAAT	ATTTATTTCA	TTTTCTACTA	AAATTATGTT	TTTGAATAAC	120
CTCTATCTTA	GTAGTTTGTA	TAATCCCCCT	CAATCAGCTT	TTACGATAAG	CTTTAATACT	180
ATGACTATAC	CATTCTTGCA	TTTCTTTTGA				210

(2) INFORMATION FOR SEQ ID NO:2088:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 627 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...627
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2088:

GGAGTTTACA	TGTCACAGGA	TAAACAAATG	AAAGCTGTTT	CTCCCCTTCT	GCAGCGAGTT	60
ATCAATATCT	CATCGATTGT	CGGTGGGGTT	GGGAGTTTGA	TTTTCTGTAT	TTGGGCTTAT	120
CAGGCTGGGA	TTTACAAATC	CAAGGAAACC	CTCTCTGCCT	TTATCCAGCA	GGCAGGCATC	180
TGGGGTCCAC	CTCTCTTTAT	CTTTTACAG	ATTTTACAGA	CTGTCTGCC	TATCATTCCA	240
GGGGCCTTGA	CCTCGGTGGC	TGGGGTCTTT	ATCTACGGGC	ACATCATCGG	GACTATCTAC	300
AACTATATCG	GCATCGTGAT	TGGCTGTGCC	ATTATCTTTT	ATCTAGTGCG	CCTATACGGA	360
GCTGCCTTTG	TCCAGTCTGT	CGTCAGCAAG	CGCACCTACG	ACAAGTACAT	CGGCTGGCTA	420
GATAAGGGCA	ATCGTTTGA	CCGCTTCTTT	ATTTTATGA	TGATTTGGCC	CATTAGCCCA	480
GCTGACTTTC	TCTGTATGCT	GGCTGCCCTG	ACCAAGATGA	GTTTCAAGCG	CTACATGACC	540
ATCATCATT	TGACCAAACC	CTTTACCCTC	GTGGTTTATA	CCTACGGTCT	GACCTATATT	600
ATTGACTTTT	TCTGGCAAAT	GCTTTGA				627

(2) INFORMATION FOR SEQ ID NO:2089:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 639 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...639
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2089:

GAGAATTACA	TGACCAAATC	AGATACGATT	ATTGAACTAA	AAAAACAGAA	AATTGTCGCT	60
GTCATTCGAG	GAAATACAAA	GGAAGAAGGA	CTACAAGCCT	CGATTGCTTG	TATCAAGGGC	120
GGTATCAAAG	CTATTGAAAT	CGCCTATACC	AATCAGTATG	CAGGACAAAT	CATCAAGGAA	180
CTTGTAAGCT	TGTATCAGGA	CGATCAGAGT	GTTTGTATCG	GTGCAGGTAC	TGTGCTTGAT	240
GCCGTAAGT	CTAGAGATGC	CATTCTAGCT	GGAGCAAATT	ACGTTGTTTC	TCCATCTTTC	300
CATGCTGAAA	CTGCGAAAAT	GTGCAATCTC	TACAGCACAC	CGTACATTCC	AGGCTGTATT	360

ACCCTCACAG	AGATCACGAC	TGCACTTGAA	GCCGGTAGTG	AAATCATCAA	ACTCTTCCCA	420
GGTAGTACTC	TCAGTCCAGC	ATATATCTCT	GCAGTCAAGG	CACCGATCCC	ACAAGTTTCC	480
GTAATGGTAA	CCGGAGGAGT	CGGCCTAAAC	AACATCCCTC	AATGGTTCGC	TGCTGGTGCA	540
GATGCCGTTG	GAATTGGTGG	CGAACTCAAT	AAACTCGCTT	CCCAAGGCAA	CTTTGACCGC	600
ATCAGCGAGA	TTGCCCAACA	GTATATTACA	CTCAGATAA			639

(2) INFORMATION FOR SEQ ID NO:2090:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1167 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1167
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2090:

TTCTTGGTCT	TTTTGTTTGC	GCTTTCGCAT	TATATAATAA	ACTTACAAAA	ACAATTCAAA	60
AGGAGAACAA	TTATGGAAGT	CGTTTCAAGT	GTTCTAAATT	GGTTTTCTAG	CAATATTTTG	120
CAGAAATCCG	CATTTTTCGT	AGGTTTATTG	GTGTTGATAG	GATATGCACT	TTTGAAAAAA	180
CCTGCCCATG	ACGTTTTTTC	AGGGTTTGTT	AAAGCAACAG	TAGGGTATAT	GTTGCTTAAC	240
GTGGGTGCTG	GTGGTTTGGT	TACAACCTTT	CGTCCAATCT	TAGCAGCTCT	TAACTACAAA	300
TTCCAAATTG	GTGCAGCGGT	TATCGACCCT	TACTTTGGAC	TTGCTGCAGC	AAACAACAAA	360
ATTGTAGCAG	AGTTTCCAGA	TTTTGTTTGA	ACTGCAACTA	CAGCTCTATT	GATTGGTTTT	420
GGAATAAATA	TCTTGCTCGT	AGCTCTTCGA	AAGATTACGA	AGGTAAGAAC	CCTCTTTATT	480
ACTGGTCACA	TCATGGTACA	ACAAGCTGCA	ACAGTATCTC	TTATGGTTCT	ATTCTTAGTA	540
CCACAATTGC	GCAATGCTTA	CGGTACAGCA	GCGATTGGTA	TCATCTGTGG	ACTTTACTGG	600
GCAGTTAGTT	CAAAATATGAC	TGTTGAGGCA	ACTCAACGCT	TGACTGGTGG	TGGCGGATTT	660
GCGATTGGTC	ACCAACAGCA	ATTTGCAATC	TGGTTTGTAG	ATAAAGTAGC	AGGACGCTTT	720
GGTAAGAAAG	AAGAAAGTTT	AGACAATCTT	AAATTACCTA	AGTTCCTCTC	AATCTTCCAC	780
GATACAGTTG	TTGCATCTGC	TACCTTGATG	CTCGTATTCT	TCGGAGCCAT	TCTTTTAATC	840
TTGGGTCCAG	ACATTATGTC	TAATAAAGAA	GTCATCACTT	CAGGAACCTCT	ATTCAATCCT	900
GCTAAACAAG	ATTTCTTTAT	GTACATTATC	CAAACAGCCT	TTACCTTCTC	AGTTTACTTG	960
TTTCGTTTTGA	TGCAAGGTGT	CCGAATGTTT	GTATCTGAGT	TGACAAACGC	CTTCCAAGGT	1020
ATTTCAAACA	AATTGTTGCC	AGGTTTATTC	CCAGCGGTTG	ACGTTGCAGC	TTCTTATGGA	1080
TTTGGTTCTC	CAAAATGCTGT	CTTGTGAGGA	TTTACCTTTG	GTTTTGATTG	GTCAATTGAT	1140
TACAATTGTT	TTGCTCATCG	TCTTTAA				1167

(2) INFORMATION FOR SEQ ID NO:2091:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 633 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2091:

ATAATGGTCT	TGTCAAAAAA	ACGAGCACGA	AAGGTGCTAG	AAGAAATCAT	TGCCCTCTTC	60
CCAGATGCCA	AGCCTAGTCT	TGATTTTACC	AATCATTTTG	AACTCCTGGT	TGCGGTCATG	120
TTATCAGCCC	AGACGACAGA	TGCAGCGGTA	AATAAGGCCA	CACCAGGTCT	CTTTGTTGCC	180
TTTCCAACAC	CCCAAGCTAT	GTCTGTAGCG	ACAGAGAGTG	AGATTGCTTC	ACATATTTCT	240
CGCTTGGGAT	TGTATCGGAA	TAAAGCTAAA	TTCCTTAAAA	AATGTGCCCCA	ACAGTTACTA	300
GACGATTTTG	ATGGTCAAGT	CCCTCAGACA	CGTGAAGAAT	TGGAGAGTTT	GGCAGGTGTT	360
GGTCGCAAGA	CAGCCAATGT	TGTCATGAGT	GTAGGATTTG	GGATTCCAGC	CTTTGCAGTG	420
GATACTCATG	TGGAGCGTAT	TTGCAAACAC	CACGATATTG	TCAAAAAATC	AGCGACGCCA	480
CTTGAGGTGG	AAAAGCGGGT	CATGGATATC	TTGCCGCCTG	AGCAGTGGTT	AGATGCCCCAT	540
CAGGCCATGA	TTTATTTTGG	AAGAGCCATT	TGCCATCCAA	AAAATCCAGA	GTGTGACCAG	600
TACCCACAAT	TATATGATTT	TAGCAATTTG	TAA			633

(2) INFORMATION FOR SEQ ID NO:2092:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2092:

GGAGAACACA	TGATACAGGC	AGTCTTTGAG	AGAGCCGAAG	ATGGCGAGCT	GAGGAGTGCG	60
GAAATTA CTG	GACACGCCGA	GAGTGGCGAA	TACGGCTTAG	ATGTCGTGTG	TGCATCGGTT	120
TCTACGCTTG	CCATTAACTT	TATCAATTCT	ATTGAGAAAT	TTGCAGGCTA	TGAACCAATC	180
CTAGAATTAA	ACGAAGATGA	AGGTGGCTAT	CTGATGGTTG	AAATACCAAA	AGATCTTCCT	240
TCACACCAGA	GAGAAATGAC	CCAGTTATTC	TTTGAATCAT	TTTTCTTAGG	TATGGCAAAC	300
TTATCGGAGA	ACTCTTCTGA	GTTCGTCCAA	ACCAGAGTTA	TCACAGAAAA	CTAA	354

(2) INFORMATION FOR SEQ ID NO:2093:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...372
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2093:

AAAGTTAACA	TTCCTAATTC	TGAAAGTACA	AAACCTAAGA	CTTTTGAAAT	TGATTGTTTA	60
GTCGAGAGAAA	AACACGCATA	CGAAATAAAA	TGGTGGGATG	CAACTACAGA	TGGAGACCAT	120
ATAACTAAAAG	AACACACTAG	AATAAAAAGTT	ATTCTATAACA	AAGGATATAT	ACCAATTCGG	180
TTAATGTTCT	ACTATCCAAA	TAGAACTCAA	GCTATAAAAA	TTCAGCAAAC	TTTAGAAAACA	240
TTGTATAACG	GTATTGGAGG	GAAATATTAT	GGAGATTCTG	CCTGGGAACA	TTTAAGAGCA	300
GTGACCGGTA	TTGATTACT	TAGTATTCTA	ACAGATATTG	CAAATAAAAA	AACAGGGGTA	360
AAATCAAAAT	GA					372

(2) INFORMATION FOR SEQ ID NO:2094:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...216
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2094:

GTGTGTAACA	TGCAACTAAA	AAATCGTCTA	AAAGAGCTTC	GAGCTCGCGA	GTGGTCTCAA	60
TCAAACCGAC	CTAGCCAAAC	TGGCAGGGGT	TTCAGACAGA	CCATTAGCCT	ACTAGAGCGG	120

GATGAGTACA	CCCCATCCAT	TATCATTGCC	CTGAAAATAT	CTCAAATTTT	CAACGAAACA	180
GTCGAATCGG	TATTTTCGTTT	GGAGGAGGAC	GAGTGA			216

(2) INFORMATION FOR SEQ ID NO:2095:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1623 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1623

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2095:

GGTAAAAACA	TGGAAATCAT	GTCGCTTGCG	ATTGCTGTTT	TTGCCGTCAT	CATTGGTTTA	60
GTCATTGGAT	ATGTCAGCAT	CTCAGCTAAG	ATGAAATCAT	CTCAGGAAGC	TGCAGAGTTG	120
ATGCTTTTAA	ATGCTGAACA	AGAAGCAACT	AATTTACGTG	GACAAGCTGA	GCGTGAAGCG	180
GATTTACTTG	TTAATGAAGC	CAAACGTGAA	AGCAAGTCTC	TTAAAAAAGA	AGCACTATTG	240
GAGGCCAAAG	AAGAAGCCAG	AAAATACCGT	GAAGAAGTGG	ACGCTGAATT	CAAATCAGAA	300
CGTCAAGAAC	TCAAACAAAT	CGAAAGTCGT	TTGACAGAGA	GAGCTACTAG	CCTTGACCGT	360
AAGGACGACA	ATTTGACGAG	TAAAGAACAA	ACACTTGAAC	AAAAAGAACA	AAGTATTTCT	420
GATAGAGCGA	AAAACCTTGA	TGCGCGTGAA	GAGCAATTAG	AGGAAGTCGA	AAGACAAAAA	480
GAAGCAGAAC	TAGAGCGTAT	TGGTGCTCTG	TCTCAGGCAG	AAGCACGAGA	TATTATCTTG	540
GCTCAGACAG	AGGAAAACCT	GACCAGGGAG	ATTGCCAGTC	GCATTCGCGA	AGCTGAGCAA	600
GAGGTCAAGG	AACGTTCTGA	CAAAATGGCC	AAGGACATCT	TGGTTCAAGC	TATGCAACGT	660
ATCGCTGGTG	AATATGTAGC	GGAGTCAACA	AACTCAACAG	TTCATCTGCC	AGACGATACT	720
ATGAAGGGAC	GCATTATTGG	TCGTGAAGGT	CGTAACATTC	GTACCTTTGA	AAGTTTGACA	780
GGGGTCGATG	TGATTATCGA	CGATACACCA	GAAGTGGTGA	CCTTGTTCAGG	ATTTGATCCG	840
ATTCGTCTGT	AGATTGCCCG	TATGACTATG	GAAATGTTGC	TCAAAGATGG	TCGTATACAT	900
CCAGCTCGTA	TCGAAGAGTT	GGTTGAGAAA	AACCGTCAAG	AGATTGACAA	TAAGATTCGT	960
GAATACGGTG	AGGCTGCTGC	CTATGAAATT	GGTGCGCCAA	ACCTTCATCC	AGACTTGATG	1020
AAGATTATGG	GACGTTTGCA	GTTCCGTACT	TCATATGGAC	AAAATGTTTT	GCGCCATTCTG	1080
ATTGAGGTTG	CTAAGTTGGC	TGGTATCATG	GCGAGCGAAC	TTGGTGAAAA	TGCGGCTCTT	1140
GCCCCGTCGT	CTGGATTCCCT	TCACGATATC	GGGAAAGCCA	TTGACCATGA	GGTTGAAGGT	1200
AGCCACGTTG	AAATCGGTAT	GGAATTGGCC	CGTAAGTACA	AGGAACCCCC	AGTTGTGGTG	1260
AATACGATTG	CTAGTCACCA	CGGAGATGTT	GAAGCTGAGA	GCGTGATAGC	AGTTATCGTC	1320
GCTGCAGCAG	ATGCCCTTGAG	CGCAGCCCGT	CCAGGTGCTC	GTAGTGAGTC	TCTTGAAAGC	1380
TACATCAAGC	GTCTCCATGA	TTTGGAAGAA	ATTGCTAACG	GCTTTGAAGG	AGTGCAAACCT	1440
AGCTTTGCCC	TTCAAGCAGG	ACGTGAAATT	CGTATCATGG	TCAATCCAGG	AAAAATCAAG	1500
GACGACAAAG	TCACAATCTT	GGCTCACAAA	GTTCGTAAGA	AAATTGAAAA	CAATCTCGAT	1560
TATCCAGGAA	ATATCAAGGT	AACCGTGATT	CGCGAGCTTC	GTGCAGTAGA	TTATGCTAAA	1620
TAA						1623

(2) INFORMATION FOR SEQ ID NO:2096:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1257 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1257
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2096:

GAAAAAACA	TAGAAAGTAA	GTATATGGCA	CTAACAACAC	TCACGAAAGA	AGAGTTTCAG	60
ACTTATTCTG	ATCAGGTTTC	TTCTCGTTCC	TTTATGCAAT	CTGTCCAGAT	GGGGGATTTC	120
CTAGAAAAAA	GAGGGGCTCG	AATTGTTTAT	CTTGCTTTGA	AACAAGAAGG	AGAAATTCAA	180
GTTGCAGCTC	TGGTTTATAG	CTTGCCCATG	CTGGGTGGTC	TGCATATGGA	ACTCAATTCG	240
GGGCCGATTT	ATACCCAACA	AGATGCTCTT	CCAGTTTTTT	ATGCAGAGTT	AAAAGAAATAT	300
GCCAAGCAAA	ATGGTGTTAT	AGAGTTGCTT	GTAACACCTT	ATGAAACTTA	TCAAACTTTT	360
GATAGCCAAG	GTAATCCAAT	AGATGCTGAG	AAAAAAAAGTA	TTATTCAAGG	TTTGACTGAT	420
TTAGGTTATC	AATTTGATGG	CTTAACAACA	GGTTACCCAG	GTGGAGAACC	AGATTGGTTA	480
TACTATAAAG	ATTTAACTGA	ATTAAGTAA	AAGAGTTTGC	TTAAAAGTTT	TAGCAAAAAG	540
GGTAAACCTT	TGGTGAAAAA	GGCTGAAACC	TTTGGCATTC	GGTTGAAAAA	GTTAAAACGT	600
GAAGAACTAT	CGATTTTTAA	GAATATAACA	AAAGAAACCT	CTGAACGTAG	AGAATATAGT	660
GATAAAAGTT	TAGAATATTA	TGAGCATTTT	TATGATACTT	TTGGAGAACA	AGCGGAGTTT	720
CTCATAGCAA	GCTTGAATTT	TTTCGAGTAT	ATGAGCAAAT	TGCAAGGTGA	ACAAAGTAAA	780
CTAGAAGAAA	AATTGGACAA	GTTGCGACTT	GATTTGAGTA	AAAATCCTCA	TTCTGAGAAA	840
AAACAAAATC	AACTGAGAGA	ATATTCTAGT	CAATTTGAAA	CGTTTGAAGT	TCGAAAAGCA	900
GAAGCGCGAG	ACTTGATTGA	AAAATATGGA	GAAGAAGATA	TTGTTTTAGC	TGGGAGTTTA	960
TTTGTTTATA	TGCCTCAGGA	AACGACTTAT	CTCTTTAGTG	GTTCTTACAC	TGAGTTTAAT	1020
AAGTTCTATG	CCCCTGCACT	GCTTCAAAAA	TATGTTATGT	TGGAAAGCAT	AAAACGTGGA	1080
ATACCTAAAT	ACAACCTCCT	AGGCATTCAA	GGGATTTTTC	ATGGAAGTGA	TGGTGTTTTG	1140
CGTTTTAAAC	AGAATTTTAA	TGGCTATATT	GTACGCAAAG	CAGGTACTTT	CCGTTACCAT	1200
CCATCGCCTT	TAAAATACAA	AGCTATCCAG	TTACTCAAAA	AAATAGTAGG	ACGTTAA	1257

(2) INFORMATION FOR SEQ ID NO:2097:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1005 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2097:

GGAAAAACA	TGAATGTCAA	AAAGATAATG	TCAATTTTTC	AATCCTTTTA	TGTTGATGTC	60
AGTATTGAGG	AACTGACTTT	GACTTTACCA	ATCAGTTTTC	TAAAAAGGTT	TGAGTATACT	120
CAAATGACTT	TTCATAAGGA	ATCATTTTTC	TTGATTAAAG	AAAAGAGAAG	GGGGAGTTTG	180
AGTTCATTTG	TTACTCAGGC	TCGCACTATG	GGTGAAAAAG	CCAATATGGA	TGTTGTTTTG	240
GTGTTTTTCG	AGTTATCAGA	CAGTGAAAAA	AAGCAATTAC	TTCAAGCTAG	AGTTCCGTTT	300
GTAGACTTTA	AGGGAAACCT	CTTCTTCCCT	CCATTGGGAC	TAGTACTCAA	TGCGAATGAT	360
ACTGAAATCC	CTAAGGAATT	AACACCTAGC	GAACAATTAA	CGTGGATTGC	CTTTTTATTG	420
CCAAAAGGTC	AAAAAGTAGT	AAATGTTGAT	TTGCTTTCAC	ACGTCCTGG	ACTTCCAAAC	480
TCAACAATTT	ATAGGTGTTT	GAGGACTTTT	AAAGCTTTAT	ATTGGTTAAA	CAAGCAAAAT	540
AAGCTTTTACA	CATATACGGT	GTCAAAGAAA	GAATTATTCT	TAAAAATCCGT	GTCATGTTTA	600
TTTAATCCCA	TCAAAAAACG	GATTTTATTG	CCAGATGGCG	ATATAAAGCA	GATAAAATCT	660
GTTTCTAACC	TTCTATATGG	TGGTGCTTAT	GCTTTGTGCG	ATTCAACTTT	TTTAGCTGAA	720
ACGGATGAAA	ATACTAGCTA	TGTCATATGG	CAGAGAAAAT	TCAATCAGTT	ATCCTTGCCA	780
CTTTCTCAGC	ATGTTTTAAA	AGGAAAGATG	CTAGAGATAT	GGAAATATCG	TCCTTTTGTA	840
TCTGAGTTTT	GGAATGATTT	TAAAAATAAT	CATGATAAAC	AATTTGTAGA	TCCGATTCT	900
CTTTATTTGA	CCTTAAAAGA	TGATGATGAC	CCACGTATAG	AGGAAGAGAG	TGAAGCACTA	960
GAAAATATGA	TATTACAGTA	TCTGGGAGAA	GATGATGCCA	GCTAA		1005

(2) INFORMATION FOR SEQ ID NO:2098:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1095 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2098:

ACAGAAAACA	TTCCAGAGTC	AGACAAGACT	TTGGAATGTT	TTGGCTCTAT	AATTTCTGTA	60
GTGGGTAAATC	CCACCCAGG	AATTATAGGG	TCGTTTCTTG	TAGAAAAAAA	GCCCCATATG	120
ACCTATAATG	AAAAGCGTCT	AACCAACTCA	TTAGAAAGGG	TTCAATATGGA	ACAACCTAAG	180
AATACCACAG	ATTTGCTCGG	ATTGGAAGAC	AAAAATATCA	AAATCTTGTC	TGTTCTGAAA	240
TACCAAAACC	ATCTAGTCGT	TCAGCCAAAAG	TTGGATTCCC	CCGCTCCTCC	TTGTCCTCAT	300
TGTCAAGGGA	AGATGATCAA	ATACGACTTC	CAGAAAGCCT	CTAAAAATTC	GCTTCTCGAC	360
TGTCAGGGTT	TACCCACGGT	ACTGCATCTC	AAAAAGCGCC	GCTTTCAGTG	CAAGAATTGC	420

CTTAAGGTGG	TCGTTTCTCA	AACATCCATT	GTCAAGAAAA	ATTGCCAGAT	TTCCAACATG	480
GTGAGACAAA	AAATCGCTCA	GCTCCTCCTT	GAAAAAGCAGT	CTATGACTGA	GATTGCCCAC	540
AGATTGGCGG	TCTCAACTTC	CACCGTCATC	CGAAAACTGA	GGGAATTTAA	GTTTGAAACC	600
GATTGGACCA	AGTTGCCAAA	AGTTATGAGT	TGGGATGAGT	ATAGCTTCAA	AAAGAGCAAA	660
ATGAGCTTCA	TTGCCCAAGA	TTTTGAGTCC	AAATCCATCC	TCGCAATTTT	AGACGGGCGA	720
ACTCATGCGG	TGATTGCAAA	CCATTTCCAA	CGCTATCAGA	GAGAGGTTTCG	GGAGCTGGTC	780
GAGGTCATCA	CCATGGACAT	GTACAGCCCT	TATTATCGGC	TCGCTAAGCA	ACTCTTTCCA	840
AAGGCGAAGA	TTGTTCCTGA	CCGCTTCCAC	ATTGTCCAAC	ATCTGAGCCG	AGCTATGAAC	900
CGAGTACGAA	TCCAAATCAT	GAACCAATTT	GACCGAAAAAT	CCTTGGAGTA	TCGGGCGCTC	960
AAGCGCTTTT	GGAACCCTCG	CTTTTTTCGTT	TCTAGGCTCG	GGCTAAATCA	GTCCACTGGA	1020
CTGATTTACT	ACACCAGGAT	AGCTTCAAGC	TCTGTCAGAA	ACGATTCTAT	CAGCCCACGT	1080
TTCGAATGCA	CTTAA					1095

(2) INFORMATION FOR SEQ ID NO:2099:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1923 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2099:

GAGAGAAACA	TGATTTATCA	TTTTACTGAA	GAATACGATA	TTATTGTAAT	TGGTGCGGGA	60
CACGCTGGGG	TTGAGGCTTC	CTTGGCCGCT	AGCCGTATGG	GCTGTAAGGT	CCTGCTTGCG	120
ACCATCAATA	TTGAAATGCT	GGCTTTCATG	CCTTGTAATC	CCTCTATCGG	TGGTTC TGCC	180
AAGGGGATTG	TCGTACGTGA	AGTCGATGCC	CTCGGTGGCG	AGATGGCCAA	GACTATTGAC	240
AAGACTTACA	TCCAGATGAA	GATGCTCAAC	ACAGGGAAGG	GGCCAGCTGT	CCGTGCTCTT	300
CGTGCGCAGG	CTGACAAGGA	ACTTTACTCT	AAGGAGATGC	GCAAGACAGT	TGAAAATCAA	360
GAAAATCTGA	CCCTTCGTCA	AACCATGATT	GATGAGATTT	TGGTGGAAGA	TGGCAAGGCT	420
GTCGGTGTGC	GTACAGCCAC	CCATCAAGAA	TATGCTGCTA	AGGCTGTTAT	TGTGACGACA	480
GGGACTGCTC	TCCGTGGGGA	AATTATCATC	GGAGACCTCA	AGTACTCATC	AGGTCCTAAC	540
CACAGCTTGG	CTTCTATTAA	CCTAGCTGAC	AATCTCAAGG	AACTGGGTCT	CGAAATCGGT	600
CGTTTCAAGA	CAGGAACCCC	TCCACGTGTC	AAGGCTTCTT	CTATCAATTA	CGATGTGACA	660
GAAATTCAGC	CAGGAGACGA	AGTGCCTAAT	CATTTCTCAT	ACACTTCACG	TGATGAGGAT	720
TATGTCAAGG	ACCAAGTACC	ATGCTGGTTG	ACCTATACCA	ATGGTACCAG	TCATGAGATT	780
ATCCAAAACA	ACCTCCACCG	TGCGCCTATG	TTTACAGGTG	TGGTCAAGGG	AGTGGGACCT	840
CGTTACTGTC	CATCGATTGA	GGACAAGATT	GTGCGCTTTG	CGGACAAGGA	ACGTCACCAA	900
CTCTTCTTTC	AGCCAGAAGG	ACGCAATACA	GAGGAAGTCT	ATGTTCAAGG	ACTTTCAACC	960
AGTCTGCCTG	AGGATGTCCA	ACGTGACTTG	GTTTATTTCCA	TCAAAGGTCT	GGAAAATGCA	1020
GAGATGATGC	GAACAGGTTA	TGCTATTGAG	TATGATATGG	TCTTGCCTCA	TCAGTTGCGT	1080
GCGACTTTGG	AAACCAAGAA	AATCTCAGGT	CTCTTCACTG	CTGGTCAGAC	AAATGGAACG	1140
TCAGGTTACG	AAGAGGCAGC	AGGCCAAGGG	ATTATCGCGG	GTATCAATGC	GGCTCTGAAA	1200
ATCCAAGGCA	AGCCTGAATT	GATTCTAAAA	CGAAGTGACG	GTTACATTGG	GGTCATGATC	1260

GACGACTTGG	TGACCAAGGG	AACCATTGAA	CCTTACCGTC	TCTTGACCAG	TCGTGCTGAA	1320
TATCGTCTCA	TTCTTCGCCA	TGACAATGCT	GATATGCGCT	TGACTGAGAT	GGGCCGTGAG	1380
ATTGGCCTTG	TGGACGATGA	ACGCTGGGCT	CGTTTTGAAA	TCAAGAAAAA	TCAATTTGAT	1440
AATGAGATGA	AGCGTCTAGA	CAGTATCAAA	CTCAAGCCAG	TCAAGGAAAC	CAATGCTAAG	1500
GTTGAGGAAA	TGGGCTTCAA	GCCGTTGACA	GATGCGGTGA	CAGCCAAGGA	ATTCCCTTCGC	1560
CGTCCAGAAG	TTTCTTACCA	AGATGTGGTG	GCCTTCATCG	GACCAGCTGC	AGAGGAATTA	1620
GATGACAAGA	TTATCGAATT	GATTGAAACA	GAAATCAAGT	ACGAAGGTTA	CATCTCAAAA	1680
GCCATGGATC	AGGTTGCTAA	GATGAAGCGC	ATGGAAGAAA	AACGTATTCC	AGCCAATATC	1740
GACTGGGATG	ACATTGATTC	TATCGCAACC	GAAGCCCGTC	AGAAGTTCAA	ACTCATCAAT	1800
CCAGAAACCA	TCGGCCAAAG	CAGCCGTATT	TCGGGAGTAA	ACCCAGCAGA	TATTTCTATT	1860
TTGATGGTGT	ATCTGGAAGG	TAAAAATCGT	AGTATTTCTA	AAACTCTTCA	AAAATCAAAA	1920
TGA						1923

(2) INFORMATION FOR SEQ ID NO:2100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 912 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2100:

AAGATGAACA	TTCAACAATT	ACGCTATGTT	GTTGCCATTG	CCAATAGTGG	TACTTTCCGT	60
GAAGCTGCTG	AAAAAGATGTA	TGTTAGTCAG	CCGAGTCTGT	CTATTTCTGT	TCGTGATTTG	120
GAAAAAGAGT	TGGGTTTTAA	GATTTTCCGT	CGGACCAGCT	CAGGGACTTT	CTTGACCCGT	180
CGTGGGATGG	AATTCTATGA	AAAATCGCAA	GAATTGGTTA	AAGGATTTGA	TATTTTTCAA	240
AATCAGTATG	CCAATCCTGA	AGAAGAAAAA	GATGAATTTT	CTGTTGCTAG	CCAGCACTAT	300
GACTTCTTGC	CACCAACTAT	TACGGCCTTT	TCAGAGCGCT	ATCCTGACTA	TAAGAACTTC	360
CGTATTTTTG	AATCAACTAC	TGTTCAAATA	TTAGATGAAG	TGGCGCAAGG	GCATAGTGAG	420
ATTGGGATTA	TCTACCTCAA	CAATCAAAAT	AAAAAGGGGA	TTATGCAACG	GGTTGAAAAA	480
TTAGGTCTGG	AGGTCATCGA	ATTGATTCCCT	TTCCATACCC	ATATTTATCT	CCGTGAGGGT	540
CATCCTTTAG	CCCAGAAAGA	GGAATTAGTC	ATGGAGGATT	TAGCGGATTT	ACCAACGGTT	600
CGTTTCACTC	AAGAGAAAGA	CGAGTACCTT	TATTATTTCAG	AGAACTTTGT	CGATACCAGC	660
GCTAGCTCAC	AGATGTTTAA	TGTGACAGAC	CGTGCCACCT	TGAATGGTAT	TTTGGAGCGG	720
ACGGACGCCT	ATGCGACAGG	TTCTGGATTT	TTAGATAGTG	ACAGTGTTAA	TGGTATTACA	780
GTTATTCGTC	TCAAGGATAA	CCTAGATAAC	CGCATGGTCT	ATGTTAAACG	TGAAGAAGTG	840
GAGCTTAGTC	AAGCTGGGAC	TCTCTTCGTA	GAAGTCATGC	AAGAATATTT	TGATCAAAAG	900
AGGAAATCAT	GA					912

(2) INFORMATION FOR SEQ ID NO:2101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2101:

AACAAGAACA	TGGCAAGGTG	CAGCAACTGG	TGCTGCGGGA	GGAGCTATAC	TTGGAGGTGT	60
GGCCTATGCA	GCGACATGTT	GGTGGTAATT	ATGGATTTTA	AAAGTTTTAT	TATTGGTTTA	120
GTAATTGGTA	TATTTGGTCC	TTATATGGAT	GATTTAATTA	GAAAAAAATT	TTTAAAGTCT	180
TCGGAGAAGA	AAACAGAAAA	ATCTATTAAA	AAATAA			216

(2) INFORMATION FOR SEQ ID NO:2102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1449 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2102:

CTTAATGACA	TTGCCCAAGC	AGCCACTTCT	TTTAATAGGG	GAAATGGAAG	TCAGGCAGAA	60
CAACGTGGAG	AACTCGATTT	AGAACGAGAT	AAGGCAATGA	AAGCGGTCAG	TGAATATGTA	120
GGAAAAATGG	TGAGAGATGC	CTATGTAAAA	TCAGATAGAA	AACGACATAA	AAATACTGTA	180
GCTCTAGTTA	ACCAGTTGGG	AAACATTAAG	AACAGGTATT	TGAATGAAAT	AGTTCATTCA	240
ACCTCAAAAA	GCCAACTACA	GGAAGTATG	ATGAAGAGTC	AATCAGAAAGT	AGATGAAGCT	300
GTGTCTAAAT	TTGAAAAGGA	CTCATTTTCT	TCGTCAAGTT	CAGGATCCCTC	CACTAAACCA	360
GAAACTCCGC	AGCCGGAAAA	TCCAGAGCAT	CAAAAACCAA	CAACTCCATC	TCCGGATACC	420
AAACCAAGCC	CTCAACCAGA	AGGCAAGAAA	CCAAGCGTAC	CAGACATTAA	TCAGGAAAAA	480
GAAAAAGCTA	AGCTTGCTGT	AGTAACCTAC	ATGAGCAAGA	TTTGTAGATGA	TATACAAAAA	540
CATCATCTGC	AGAAAGAAAA	ACATCGTCAG	ATTGTTGCTC	TTATTAAGGA	GCTTGATGAG	600

CTTAAAAAGC	AAGCTCTTTC	TGAAATTGAT	AATGTAAATA	CCAAAGTAGA	AATTGAAAAT	660
ACAGTCCACA	AGATATTTGC	AGACATGGAT	GCAGTTGTGA	CTAAATTCAA	AAAAGGCTTA	720
ACTCAGGACA	CACCAAAAAGA	ACCAGGTAAC	AAAAAACCAT	CTGCTCCAAA	ACCAGGTATG	780
CAACCAAGTC	CTCAACGAGA	GGTTAAACCG	CAGCTGGAAA	AACCAAAACC	AGAGGTTAAA	840
CCGCAACCAG	AAAAACCAAA	ACCAGAGGTT	AAACCGCAGC	CGGAAAAACC	AAAACCAGAG	900
GTTAAACCGC	AGCCGGAAAA	ACCAAAACCA	GAGGTTAAAC	CGCAGCCGGA	AAAACCAAAA	960
CCAGAGGTTA	AACCGCAGCC	GGAAAAACCA	AAACCAGAGG	TTAAACCGCA	GCCGGAAAAA	1020
CCAAAACCAG	AGGTTAAACC	GCAGCCGGAA	AAACCAAAAC	CAGAGGTTAA	ACCGCAGCCG	1080
GAAAAACCAA	AACCAGAGGT	TAAACCGCAG	CCGGAAAAAC	CAAAACCAGA	GGTTAAACCG	1140
CAGCCGGA	AACCAAAACC	AGAGGTTAAA	CCGCAACCAG	AAAAACCAAA	ACCAGAGGTT	1200
AAACCGCAAC	CAGAAAAACC	AAAACCAGAT	AATAGCAAGC	CACAAGCAGA	TGATAAGAAG	1260
CCATCAACTA	CAAATAATTT	AAGCAAGGAC	AAGCAACCTT	CTAACCAAGC	TTCAACAAAC	1320
GAAAAAGCAA	CAAATAAACC	GAAGAAGTCA	TTGCCATCAA	CTGGATCTAT	TTCAAATCTA	1380
GCACTTGAAA	TTGCAGGTCT	TCTTACCTTG	GCGGGGGCAA	CCATTCTTGC	TAAGAAAAGA	1440
ATGAAATAG						1449

(2) INFORMATION FOR SEQ ID NO:2103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 671 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2103:

TGCATCTGCA	TATGGGTATT	TATAAGAGGA	ATTATGACAT	ATTTAGACGC	TTTTAAATCA	60
GGTACCTTGG	TTTTACCGAG	TGCCCTGCTC	TTGCATTTTA	AGGAAC TATT	TCCTTCTAGC	120
GACGATTTTC	TGGTTTGGCA	ATTTTCTAT	TTGCAAAATA	CGACAGGCTT	AGAAGAAATG	180
TCGCCAAGCC	AGATTGCTGA	AAGGATTGGC	AAGGAAATTT	CGGATGTCAA	CCAGTCCATT	240
TCTAATCTGA	CGGAAAGGGG	ACTGCTCCAG	TATCGTACTA	TCGAATTAAA	TGGCGAAATT	300
GAATTGCTCT	TTGATGCTAG	TTTGGCCTTG	GAACGTTTGG	ATGACCTGTT	TGGAGCAGTT	360
CATTCAAGTT	CAGACCAGCT	AACACCTCAA	AACCAGCTCA	AGGATTTGGT	GGAAACCTTC	420
CAGCAGGAGT	TGGGACGATT	GTTGACGCCT	TTTGAGATTG	AGGATTTGAC	CAAGACACTA	480
AAGGAAGATG	GAACCAAGTGC	TGACTTGATT	AAGGAGGCTC	TTCGTGAAGC	TGTTTTGAAT	540
GGAAAACCAA	ACTGGAAGTA	CATTCAAGCG	ATTTTGAGAA	ACTGGCGCCA	TGAAGGAATC	600
AAGAGTGTGG	CTCAAATTGA	GGCCAAGAGA	GCAGAAAGAG	AAGCAAGCAA	CCCTCAGTCT	660
TCACCACGGG	T					671

(2) INFORMATION FOR SEQ ID NO:2104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2190 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2104:

AATAAACGCA	TGAAATTAGA	TAAATTATTT	GAGAAATTTT	TTTCTCTTTT	TAAAAAAGAA	60
ACAAGTGAAC	TAGAGGACTC	TGATTCTACT	ATCTTACGTC	GCTCTCGTAG	TGATCGAAAA	120
AAATTAGCCC	AAGTAGGTCC	GATTTCGAAA	TTCTGGCGTC	GTTATCATCT	AACAAAGATT	180
ATCCTTATAC	TAGGTTTGAG	TGCAGGATTG	CTAGTTGGAA	TCTATTTGTT	TGCTGTAGCC	240
AAGTCGACCA	ATGTCAATGA	TTTGCAAAAT	GCCTTGAAAA	CTCGGACTCT	TATTTTTGAC	300
CGTGAAGAAA	AAGAGGCTGG	TGCCTTGTCT	GGTCAAAAGG	GAACCTATGT	TGAGCTGACT	360
GACATCAGTA	AAAACCTGCA	GAATGCTGTT	ATTGCGACAG	AAGACCGTTC	TTTCTATAAA	420
AATGACGGGA	TTAACTATGG	CCGTTTCTTC	TTGGCTATTG	TCACTGCTGG	ACGTTTCAGGT	480
GGTGGCTCTA	CCATTACCCA	ACAGCTGGCT	AAAAACGCCCT	ATTTATCGCA	GGATCAAACCT	540
GTTGAGAGAA	AAGCGAAAAG	ATTTTTCCTT	GCCTTAGAAT	TAAGCAAAAA	ATATAGTAAG	600
GAGCAAATTC	TAACCATGTA	CCTTAACAAC	GCTTATTTTG	GAAATGGTGT	GTGGGGTGTA	660
GAAGATGCGA	GTAAGAAAATA	CTTTGGAGTT	TCTGCATCAG	AAGTGAGTCT	GGATCAAGCT	720
GCGACTCTGG	CAGGGATGCT	CAAGGGGCCG	GAACGTGATA	ATCCCTTGAA	TTCTGTAGAA	780
GATTCTACTA	ATCGGCGCGA	TACTGTCTTG	CAGAATATGG	TTGCAGCAGG	ATATATTGAT	840
AAAAACCAAG	AAACCGAAGC	TGCTGAAGTT	GATATGACTT	CGCAATTGCA	CGATAAGTAT	900
GAAGGAAAAA	TCTCAGATTA	CCGTTACCCC	TCTTATTTTG	ATGCGGTGGT	TAATGAAGCT	960
GTTTCCAAGT	ATAATCTAAC	AGAGGAAGAG	ATTGTCAATA	ATGGCTACCG	CATTTACACA	1020
GAGCTGGACC	AAAACCTACCA	AGCAAATATG	CAGATTGTTT	ATGAAAACAT	ATCGCTATTT	1080
CCGAGGGCAG	AGGATGGAAC	GTTTGCTCAA	TCAGGAAGTG	TAGCTCTCGA	ACCGAAAACA	1140
GGGGGAGTTC	GTGGAGTTGT	CGGTCAAGTT	GCTGACAAATG	ATAAACTGG	ATTCCGGAAT	1200
TTCAACTATG	CAACCCAATC	AAAGCGTAGT	CCTGGTTCTA	CAATTAAGCC	TTTAGTTGTT	1260
TATACGCCAG	CAGTTGAAGC	AGGCTGGGCT	TTGAATAAGC	AGTTGGATAA	CCATACCATG	1320
CAGTATGACA	GCTATAAGGT	TGATAACTAT	GCAGGGATCA	AAACGAGTCG	AGAAGTTCCT	1380
ATGTATCAAG	CCTTGGCAGA	ATCGCTTAAT	CTACCTGCTG	TTGCCACTGT	TAATGATTTG	1440
GGTGTCGACA	AGGCTTTTGA	GGCAGGCGAA	AAATTCCGAC	TCAACATGGA	AAAGGTCGAC	1500
CGTGTTCTTG	GTGTCGCCCTT	GGGAAGCGGT	GTTGAAACCA	ACCCCTCTTCA	AATGGCTCAA	1560
GCATACGCTG	CCTTTGCAAA	TGAAGGTTTA	ATGCCTGAAG	CTCATTTTAT	TAGTAGAATT	1620
GAAAAATGCTA	GTGGACAAAGT	TATTGCGAAT	CATAAAAAAT	CACAAAAACG	GGTGATTGAT	1680
AAGTCTGTAG	CTGACAAGAT	GACCAGTATG	ATGTTGGGGA	CTTTCACCAA	CGGTACCGGT	1740
ATTAGTTCAT	CGCCTGCAGA	CTATGTCATG	GCAGGGAAAA	CTGGAACAAC	TGAAGCAGTT	1800
TTCAATCCGG	AGTACACAAG	TGACCAGTGG	GTAATTGGTT	ATACTCCGGA	TGTAGTGATT	1860
AGCCACTGGC	TTGGCTTTCC	GACCACTGAT	GAAAATCACT	ATCTAGCTGG	CTCTACTTCA	1920
AACGGTGCAG	CTCATGTCTT	TAGAAACATT	GCCAATACCA	TTTTACCTTA	TACGCCAGGA	1980
AGTACCTTTA	CGGTTGAAAA	TGCTTATAAG	CAAAATGGAA	TTGCACCAGC	CAATACAAAA	2040
AGACAAGTAC	AAACCAATGA	TAATAGCCAG	ACAGATGATA	ATTTGTCTGA	TATTCGAGGG	2100
CGTGCGCAAA	GTCTAGTAGA	TGAGGCTAGC	CGGGCTATCT	CAGATGCGAA	GATTAAGGAA	2160
AAGGCTCGAA	CGCTAAAGTG	GTATTCAGTA				2190

(2) INFORMATION FOR SEQ ID NO:2105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 456 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2105:

AGAGGGCGCA TAGTCAATTT AAAAATGAAT AAAAAAGAGA GACTTGAAAA AATTAGAAGA	60
TTGGTGACAG ATTATCAAAT CGGCACGCAA GAAGAAATTG TAGAACATTT GAAAGAAGCA	120
GGTATCACTG CCACTCAGGC GACGGTATCC CGAGATATCA AAGAGTTAGG TATTGTCAAA	180
ATTCCTTTGA GAGACAACAC CTATGTCTAC GAATTGCCAA AATCAATCGT AAAAAGTCTG	240
CAACTGGCTG AAGACAATAT CGAATCGGCT GAATTGATGG ATAAGATGAT CAATCTCCAA	300
GTTATTCCAG GAAATACGGC TTTTGTAATA GCTCAGTTAA TCGATACTTT TGCAGACAAG	360
ATTTTGTAGT GTTTGACTGA TGATAGCTCG ATTTTAGTCA TTGCCAGAAG TGGAAGTCTA	420
GCAGAGGAAA TCTTTGAACA AGTAAAAAAT TGGTAG	456

(2) INFORMATION FOR SEQ ID NO:2106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1107 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2106:

GAGATTAGCA TGACCATAAC AGGTATTATC GCGGAGTTCA ATCCTTTTCA TAATGGCCAT	60
AAATACCTGC TGGATCAGGC AGAGGGACTG AAAATTGTTG CCATGTCAGG GAATTTTCATG	120
CAGCGTGGAG AGCCTGCTAT TGTGGATAAG TGGACAAGGA CCCAGATGGC GCTGGAAAAAT	180

GGCGCAGACT	TGGTAGTGGA	ATTGCCCTTT	TTAGTCAGTG	TTCAGGCAGC	TGATTTCTTT	240
GGTCAAGGAG	CTATGGATAT	CTTGGATCGC	TTGGGCATTG	ATAGTCTAGT	TTTTGGGACA	300
GAGGAAGTTC	GAGATTATCA	GAAAAATTGCT	GACTTATACA	CAGAGAAAGG	TGCTGAGATG	360
GAGAAATTTG	TGGAAAATCT	GCCTGATTCC	CTTTCCTATC	CCCAGAAAAC	CCAAGCTATG	420
TGGAAGGAAT	TTGCTGGTCT	TGATTTTTCA	GGTAATACCC	CCAATCATGT	TCTTGCTCTG	480
GCCTATGCCA	AGGCGGTTGC	AGGACGAAAT	ATCAAGCTGC	ATCCGATTCA	GCGTCAGGGG	540
GCAGGTTACC	ATTCTGTGAA	TAAAGATGTG	GACTTTGCCCT	CGGCGACAGC	CCTCCGTCAA	600
CATCAGAAGG	ACCAAGATTT	CTTAGAACGT	TTTATGCCCT	CTGTTGCCCT	ATTTGAGCAG	660
GCCAGTAAGG	TGATCTGGGA	AGACTATTTT	CCCTTGCTCC	GCTATCAAAT	CTTGTCAAAT	720
CCCAGACCTAA	CCACCATCTA	TCAGGTCAAT	CAAGAAATGG	CTGTGCGCAT	TAAAGAAGCT	780
ATTA AACACAG	CCCAGTCTGT	GGAAGAATTG	GTCGAGTTAG	TGACTACCAA	ACGTTACACC	840
AAGGCGCGTG	TCAGACGCCT	ATTGACCTAT	ATTTTGGTGC	AGGCTAGAGA	AAATGTCTTG	900
CCAGAAGCCA	TTCATGTCCT	TGGATTTACT	GAAAAAGGCA	GGCAACATCT	CAAGTCTCTG	960
AAAGGACAGG	TCAATCTAGT	CAGCCGAATT	GGCAAAGAAC	CTTGGGATGC	TATGACTCAA	1020
AAGGTTGACC	AGATTTACCA	ACTAGGAAAG	CCAAGTATAG	CAGAGCAAAA	TTTTGGCAGA	1080
GTGCCGATTA	GAATAGAAAC	AAACTAA				1107

(2) INFORMATION FOR SEQ ID NO:2107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 996 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2107:

AGGAGTAGCA	TGGAAACTGC	ATTAATTAGT	GTGATTGTGC	CAGTCTATAA	TGTGGCGCAG	60
TACCTAGAAA	AATCGATAGC	TTCCATTTCAG	AAGCAGACCT	ATCAAAATCT	GGAAATTATT	120
CTTGTTGATG	ATGGTGCAAC	AGATGAAAGT	GGTCGCTTGT	GTGATTCAAT	CGCTGAACAA	180
GATGACAGGG	TGTCAGTGCT	TCATAAAAAG	AACGAAGGAT	TGTCGCAAGC	ACGAAATGAT	240
GGGATGAAGC	AGGCTCACGG	GGATTATCTG	ATTTTTATTG	ACTCAGATGA	TTATATCCAT	300
CCAGAAATGA	TTCAGAGCTT	ATATGAGCAA	TTAGTTCAAG	AAGATGCGGA	TGTTTCGAGC	360
TGTGGTGTCA	TGAATGTCTA	TGCTAATGAT	GAAAGCCAC	AGTCAGCCAA	TCAGGATGAC	420
TATTTTGTCT	GTGATTCTCA	AACATTTCTA	AAGGAATACC	TCATAGGTGA	AAAAATACCT	480
GGGACGATTT	GCAATAAGCT	AATCAAGAGA	CAGATTGCAA	CTGACCTATC	CTTTCCTAAG	540
GGGTTGATTT	ACGAAGATGC	CTATTACCAT	TTTGATTTAA	TCAAGTTGGC	CAAGAAGTAT	600
GTGGTTAATA	CTAAACCCTA	TTATTACTAT	TTTCATAGAG	GGGATAGTAT	TACGACCAAA	660
CCCTATGCAG	AGAAGGATTT	AGCCTATATT	GATATCTACC	AAAAGTTTTA	TAATGAAGTT	720
GTGAAAAACT	ATCCTGACTT	GAAAGAGGTC	GCTTTTTTCA	GATTGGCCTA	TGCCCACTTC	780
TTTATTCTGG	ATAAGATGTT	GCTAGATGAT	CAGTATAAAC	AGTTTGAAGC	CTATTCTCAG	840
ATTCATCGTT	TTTTAAAAGG	CCATGCCCTT	GCTATTTCTA	GGAATCCAAT	TTTCCGTAAG	900
GGGAGAAGAA	TTAGTGCTTT	GGCCCTATTC	ATAAATATTT	CCTTATATCG	ATTCTTATTA	960
CTGAAAAATA	TTGAAAAATC	TAAAAAATTA	CATTAG			996

(2) INFORMATION FOR SEQ ID NO:2108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 243 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...243
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2108:

TCTACGAGCA	TAGTCTTCTT	CAGCTTGTTG	ATCATCTGTT	TTTCTGCTT	TTGGTTGTTT	60
AGCTGGCTTG	TCTGGTTTTG	GTGCGGGAGC	TGGATTCTCA	GGCTCTTCAG	TTGGTTTTTC	120
TGGTTGAGGA	GCCGGCGCTG	GTTGTGGTTG	TTCAGCTGGT	TTTTCTTTAA	CTTTATCTTC	180
TTCTGCTGCT	TTTCGTTTAG	CTTCTTCTTC	TGCTTTTTTA	CGATCTGTCT	TGATTTTTTC	240
TAA						243

(2) INFORMATION FOR SEQ ID NO:2109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1218 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1218
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2109:

AACAGGAGCA	TTGGTCAACA	AGGAGGGCCT	ATGAAATTAT	CCAACCGTGT	TTTAGAAATG	60
GAAGAAAGTG	TGACTTTGGC	TGCTGGAGCC	CGTGCCAAAG	CACTGAAGGC	TGAGGGCAGA	120
GATATTTTGT	CTCTAACCTT	GGGTGAGCCA	GATTTCACTA	CTCCCAAAAA	TATCCAAGAT	180
GCCGCCATTG	CATCGATTCG	AGATGGGCGT	GCTTCTTTTT	ATACAGTAAC	CTCAGGTCTG	240

CCAGAGCTTA	AGGCGGTGGT	CAATAGCTAC	TTTGAGCGCT	TTTACGGCTA	TTCTGTAGCG	300
CCAAATCAAG	TGACAGTCGC	TGCGGGAGCC	AAATATTCTC	TCTATACCTT	CTTTATGGCT	360
GTGGTCAATC	CAGGTGATGA	AGTCATCATC	CCAACCCCAT	ACTGGGTTAG	CTATGGAGAT	420
CAGGTCAAGA	TGGCAGAAGG	CGTTCCCGTC	TTTGTTCCTG	CTAAGGAAGA	CAATCACTTT	480
AAGGTGACCG	TAGAGCAGTT	AGAAGCAGCT	CGCACTGACA	AGACCAAGGT	TTTGGTGCTG	540
AATTTCGCCAT	CTAATCCCAC	AGGTATGATT	TACACCCGTG	AGGAACTCTT	GGCAATTGGA	600
AACTGGGCTG	TAGAAAATGA	TATTCTCATC	CTAGCAGATG	ATATCTATGG	CCGCTTG GTT	660
TATAATGGTC	ATGAGTTCAC	ACCGATTTC	AGCCTATCGG	AAGCGATTTC	CAAGCAAACA	720
GTGGTCATCA	ATGGTGTGTC	TAAAACCTAT	GCCATGACTG	GTTGGCGGAT	TGGTTATGCC	780
GTTGGAGAAG	CAGACATTAT	CGCTGCCATG	TCCAAGATTG	CAGGTCAAAC	AACTTCGAAT	840
CCGTCAGCAG	TAGCCCAATA	TGCAGCAGTT	GAGGCTCTAT	CAGGTGAGCA	AGATACTGTA	900
GAAAGCATGC	GTCAGGCCTT	TGAGAAACGT	CTTAATACCA	TCTATCCCCT	CCTTGCAGAG	960
GTGCCAGGAT	TTGAAGTGGT	CAAACCACAA	GGGGCTTTCT	ATCTATTCCC	AAATGTCAAA	1020
AAGGCCATGG	AGATGAAAGG	CTACACGGAT	GTGACAGACT	TTACAACTGC	TATATTAGAA	1080
GAAGCCGAAG	TGGCCTTGGT	AACAGGAGCT	GGATTGGAG	CACCAGAAAA	TGTCCGCCTC	1140
AGCTATGCGA	CAGACCTAGA	CACGCTTAAA	GAAGCAGTCG	AACGCTTGAA	AGCATTTATG	1200
GGTAGTGAGA	ATGATTGA					1218

(2) INFORMATION FOR SEQ ID NO:2110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2110:

TTCATTGGCA	TTCGGAGTTT	ATCTGAGATT	GGTAATCCGG	GATGGACCCC	TCACCCAAAT	60
AGTGCTCTAC	CTCCAAGAAT	CTCTAATGTC	GACGCTAGCC	CTAAAGCTAT	TTCGGAGAGA	120
ACCAGCTATC	TCCAAGTTCG	TTTGGAATTT	CTCCGCTACC	CACAAGTCAT	CCAAGCACTT	180
TTCAACGTGC	CCTGGTTCGG	TCCTCCAGTG	CGTCTTACCG	CACCTTCAAC	CTGCTCATGG	240
GTAGGTCACA	TGGTTTCGGG	TCTACGTCAT	GATACTAAGG	CGCCCTATTC	AGACTCGGTT	300
TCCCTACGGC	TCCGTCTCTT	CAACTTAACC	TCGCATCATA	ACGTAACTCG	CCGGTTCATT	360
CTACAAAAGG	CACGCTCTCA	CCCATTAAACG	GGCTCGAACT	TGTTGTAG		408

(2) INFORMATION FOR SEQ ID NO:2111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...216
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2111:

GGAGAAGGCA	TGAAACTTAA	TGAAGTAAAA	GAATTTGTTA	AAGAACTTCG	TGGTCTTTCT	60
CAAGAAGAAC	TCGCGAAGCG	CGAAAAACGAA	TTGAAAAAAG	AATTGTTTGA	ACTTCGTTTC	120
CAAGCTGCTA	CTGGTCAATT	GGAACAAACA	GCTCGCTTGA	AAGAAGTTAA	AAAACAAATC	180
GCTCGTATCA	AAACAGTTCA	ATCTGAAGCG	AAATAA			216

(2) INFORMATION FOR SEQ ID NO:2112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...234
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2112:

TTTTTTGTTT	TATACCCAAA	TATGAATAGA	GACGTAGCTA	ATAAGTTGAA	TAACATATTT	60
GGAAAAATGA	GAAATAGCAA	TATTACTAGA	ACTTTTAGAA	ACAATCAATA	TTTAAAAAGA	120
AAAAAGCTCA	AAGAATTTAT	TAAACCATGT	TATAATAGAT	ATAGCTATAA	TTTTATTTAT	180
AACAAGAGGA	TAGAAATGAC	CGAATTAGAA	AGAAAAAATC	GAAAAATTAG	CTAA	234

(2) INFORMATION FOR SEQ ID NO:2113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 183 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2113:

TTTATTTTAA TCTATTTTAA GGGGGTTCTC ATGAAACTAA GAATATTTGC GGAAGATAAG	60
CCGGCTAAGA AGGTATTTGA ATATCAATTA GAACTTGCTG ATCGTACAAT TCTTCTATCG	120
ACAGCACTCT TGTCAGGTGC TATTGCTTTA GCAGGAATCT TTTCTGCTTT GAAAGAAAAA	180
TAA	183

(2) INFORMATION FOR SEQ ID NO:2114:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 651 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2114:

AATATTTTAA TAATTTTCAT GAACTTTCAA TTAGCTAAAT ATTCTTTACT GAAGAAATTT	60
TTAGAAAATA TAGGATTTAC CACACTAGAG GAATATGGTG CCATCTTCAA ATACCTGATT	120
GAGAATGTCA AGACGGATCG TCAGATCATC TGTTCGCCTC ACTGTCATGA TGACCTCGGA	180
ATGGCAGTGG CAAATAGCCT TGCTGCTGTC AAGAATGGTG CAGGACGTGT TGAAGGGACT	240
ATCAATGGTA TTAGGGAGCG AGCTGAAAAT GCTGCTTTGG AAGAAATTGC AGTGGCTCTC	300
AATATTCGCC AAGATTACTA CCAAGTAGAA ACCAGTATTG TCCTAAATGA GACCATCAAT	360
ACGTCAGAAA TGGTTTCTCG CTTCTCTGGT ATTCCAGTTC CTAAAAACAA AGCCGTCGTT	420
GGTGGCAATA CCTTCTCCCA CGAATCTGGT ATTCACCAAG ATGGAGTCCT TAAAAATCCT	480
CTCACTTATG AGATCATCAC ACCTGAATTG GTTGGTGTTA AGATTCCGCT TGGAGAATTA	540
TCTGGTCGCC ATGCTTTTGT TGAGAACTG AGAGAATTGG CCCTAGATTT TACAGAAGAG	600
GATATCAAAC CACTCTTTCG TAAGTTCAAG GCACTGGCCG ATAAGAAGTA A	651

(2) INFORMATION FOR SEQ ID NO:2115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 222 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...222
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2115:

AAATATTTAA	TTTTAGAGAT	AAAGAGCTTA	TCTTTTTTAA	GTAAGATTGT	AAATGGGCTG	60
ATACAAAATA	TTGAGGAGAA	TTTAGAGGAT	GATATTGAAA	GGATATTGAA	ATATTTATAT	120
ATATGTTTAT	TTAACGAAAT	ATTCATTATT	AAGAATAAGG	TGAATTTTTT	TGATGATGTG	180
GAATTTAATC	AGACACTTAG	TGAATTTTTA	GATAAATTGT	AG		222

(2) INFORMATION FOR SEQ ID NO:2116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 777 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...777
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2116:

CTTGACTTAA	TTTTTTTTTT	AATGTATATT	AAGAGACAGG	AGGAATACAA	GTTTATGATA	60
CGTATCGAAA	ATCTCAGTGT	CTCCTACAAA	GAAACGTTGG	CACTTAAGGA	TATTTCACTA	120
GTGCTCCATG	GACCAACAAT	TACCGGCATC	ATTGGTCCAA	ACGGCGCTGG	GAAATCAACA	180
CTATTAAAAG	GTATGCTGGG	AATTATCCCA	CATCAAGGTC	AGGCATTTCT	CGATGACAAG	240
GAAGTTAAAA	AATCCTTACA	CCGAATTGCC	TATGTCGAAC	AAAAAATCAA	TATCGACTAC	300
AACTTTCCCA	TCAAGGTCAA	GGAATGCGTC	TCGTTAGGAC	TATTTCCCTC	TATTCCTCTC	360
TTTCGAAGTT	TAAAGGCTAA	ACATTGGAAG	AAAGTGCAAG	AGGCCCTTGA	AATCGTCGGC	420
CTAGCTGACT	ACGCTGAACG	TCAAATTAGT	CAACTGTCTG	GAGGTCAATT	CCAGCGGGTC	480

TTGATTGCCA	GATGTTTGGT	GCAGGAAGCC	GACTATATCC	TCTTGGATGA	ACCCTTTGCT	540
GGGATTGACT	CTGTCACTGA	GGAAATCATC	ATGAATACGC	TGAGAGATTT	GAAAAAAGCT	600
GGGAAGACGG	TTCTCATCGT	TCACCACGAC	CTCAGCAAGA	TTCCCCACTA	CTTCGATCAA	660
GTCTTACTTG	TCAATCGAGA	AGTGATTGCC	TTTGGTCCAA	CAAAAAGAAAC	TTTTACCGAA	720
ACCAATCTAA	AAGAAGCTTA	CGGTAATCAA	CTCTTTTTC	ATGGAGGTGA	CCTATGA	777

(2) INFORMATION FOR SEQ ID NO:2117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 408 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...408
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2117:

CCATGCTTAA	TAAAAAGGAG	AAAACAAATG	GAACCTGTAT	TACCAAATAA	TTATGTTGTG	60
ATTGATGAAG	AAGAGATGAT	GTACCTTGAT	GGGGGTGGTG	TTGGTTGTAA	CTGGTGGAAT	120
AGTAGAGGTA	GTTTTGCAAC	AGTTCTGGAT	GTAGGTTTGG	CCATCTATAG	TGGTGGTGCA	180
ACAATTTATT	CTGCTTATGC	GATAAAAAAA	GCTATCTCAG	CTAATAGAGG	GGCTATTACG	240
AGAACATTAC	GTAGTTTAAT	AATTAAACAT	GTAGGTAGTG	CAGCTGGCCA	TTTAGTCAAT	300
ACTGCACTAA	ACGTTGCACT	AACTGTTACT	GGATTTTCAC	TAGGTGGAGC	AATCGCATAT	360
GGGGCTGATT	GGGCTGACGG	TAGCTTAGAT	GGTTATATTT	TTGCTTAA		408

(2) INFORMATION FOR SEQ ID NO:2118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 678 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2118:

ATGAAATTAA	TCGTTTCAGT	AATGCCAAGA	AGTTTAGAGG	AGGCTCAGGC	TCTGGATGCC	60
ACGAGGTACC	TGGATGCCGA	CATCATTGAA	TGGCGTGCCG	ACTATCTGCC	TAAAGAAGCG	120
ATTTTGCAGG	TAGCTCCAGC	CATTTTGTAA	AAATTCGCAG	GCCGTGAGTT	GGTTTTACAG	180
CTACGAACTC	GCTCCGAAGG	TGGAGAAATC	GACCTTTCTC	CAGAAGAGTA	TATCCATCTA	240
ATCAAGGAAG	TTGCGCAATT	CTATCAACCA	GACTATATTG	ATTTTGAGTA	CTATAGCTAC	300
AAGGATGTTT	TTGAGGAAAT	GCTGTACTTC	CCAAATCTTG	TTTTGAGTTA	CCATAATTTT	360
CAAGAAACAC	CTGAGAACAT	GATGGAAATC	TTGTCAGAGT	TGACGATCCT	AAATCCAAAA	420
CTTGTTAAGG	TTGCGGTGAT	GGCTCACACG	GAGCAGGATG	TCTTAGACTT	GATGAACTAT	480
ACACGAGGCT	TTAAAACCCCT	CAATCCTGAA	CAGGAATATG	TGACCATTTC	TATGGGTAAG	540
GTGGGCAAGG	TCTCTCGTAT	CACTGCGGAT	GTGACTGGTT	CGAGTTGGTC	TTTTGCCAGT	600
CTGGATGAGG	TTAGTGCCCC	TGGGCAGATT	TCTCTAGCTA	GCATGAAAAA	AATCAGGGAG	660
ATTTTGGATG	AAGCTTGA					678

(2) INFORMATION FOR SEQ ID NO:2119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2119:

ACCCATTCCCT	TGGATTCCGT	GCTCTTCGTA	TCTCTATCTC	TGAGACTGGA	GATGCTATGT	60
TCCGCACACA	AATCCGTGCT	CCTTCTTCGT	GCGTCTGTTC	ACGGTCAATT	GCGTATCATG	120
TTCCCAATGG	TTGCGCTCTT	GAAAGAATTC	CGTGACGCGA	AAGCAGTCTT	TGATGAAGAA	180
AAAGCAAACC	TTCTTGCTGA	AGGTGTTGCA	GTTGCGGATA	ACATCCAAGT	TGGTATCATG	240
ATCGAGATTC	CTGCAGCGGC	TATGCTTGCA	GACCAATTTG	CTAAAGAAGT	TGACTTCTTC	300
TCAATTGGTA	CAAACGACTT	GATCCAATAT	ACAATGCGAG	CAGACCGTAT	GAACGAACAA	360
GTTTCATACC	TTTACCAACC	ATACAACCCA	TCAATCCTAC	GCTTGATTAA	CAATGTGATC	420
AAAGCAGCTC	ACGCTGAAGG	TAAATGGGCT	GGTATGTGTG	GTGAGATGGC	TGGTGACCAA	480
CAAGCTGTTT	CACCTCTTGT	CGGAATGGGC	TTGGATGAGT	TCTCTATGTC	AGCAACATCT	540
GTACTTCGTA	CACGCAGCTT	GATGAAGAAA	CTCGACACAG	CTAAGATGGA	AGAGTACGCA	600
AACCGTGCCC	TTACAGAATG	CTCAACAATG	GAAGAAGTTC	TTGAACTTCA	AAAAGAATAC	660
GTAAATTTTG	ATTAA					675

(2) INFORMATION FOR SEQ ID NO:2120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 858 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...858
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2120:

TGTTATCTAA	TTAGAAAATG	CTTTTTTTGT	AGGAAATATA	ATATGATAAG	GTGTAAAAAA	60
GAAATAAGGA	GTTTGTATAT	GGCTGAACAA	GACTTAGCTA	TGCAAGTATT	ACAACAAGTG	120
GTAAACTAC	CAGTTGTTAA	GGTTGATAGT	TCGAAATTTT	TAGTGGATAA	GTTTTCCAAA	180
GAATTGGGTC	CACAGGACAT	TCCTACCTTA	TTGGAACAAG	GTCCAACGTC	TCTCTTATCT	240
CAAGAAATCT	TAGATCGAGT	AGCTAATGCT	TGTATTCGGG	ACAATGTATT	ATTAGCGAGT	300
GGGACTTCTG	TTTTGGCAGG	ATTACCTGGA	GGGCTTGCTA	TGGCAATTAC	CATTCCAGCT	360
GATGTGGCTC	AATTTTATGC	TTTCTCTCTG	AAATTGGCTC	AAGAATTAGG	TTATATTTAT	420
GGTTATGAGG	ATCTTTGGGT	TTCACGAGAG	GAGTTGAGTG	AAGATGCTCA	AAATACCCTC	480
TTGCTTTTATC	TAGGCGTAAT	GTTAGGGGTG	AATGGAACTG	CTGCTTTGCT	ACGTGCTGGT	540
GGTATAACAA	TTGCCAAACA	GGTAATGAAA	ACAGTGCCTA	ATAAAGCTTT	AACAAAGACG	600
CTTTGGTACC	CTATTTTGAA	AAAAGTCTTA	AAAAATTTTG	GTGTGAATCT	TACCAAGGGA	660
GGGTTGGCCA	AAGGAATGGG	GAAATTTATT	CCTATCTTGG	GTGGTATCAT	TTCAGGTGGT	720
TTAACCTTTG	CAACTATGAA	ACCAATGGGG	GAAAGCTTGC	AGAAAGAATT	ATCCAAGCTA	780
GTCAACTATA	GTGAAGTTCA	ATATCAAGAA	GATGTTGAAA	CAATCCGAAA	AGAGGCTGAA	840
ATCATCGAAG	GAGAGTAA					858

(2) INFORMATION FOR SEQ ID NO:2121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...195
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2121:

GTAAATCTAA	TACTCAAAAT	CAAAGAACAA	ACTAGGAAGC	TAGCCGCAGG	TTGCTCAAAA	60
CACTGTTTTG	AGGTTGTAGA	TGAAACTGAC	GAAGTCAGTA	ACCATACATA	CGGTAAGGCG	120
ATGCTGACGT	GGCTTGAAGA	GATTTTCGAA	GAGTATAAAA	TCAAATTTTA	TCCAAC TGAT	180
CCCTCCATTT	CATAG					195

(2) INFORMATION FOR SEQ ID NO:2122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2122:

TTTTTTTATAA	TGAAAACGAT	TGGTAATCGC	TATGTTGTGG	TGGATTTAGA	GGCAACTAGC	60
ACAGGTAGTA	AGGCTAAAAT	TATCCAAGTG	GGAATTGTCG	TGATTGAGGA	CGGAGAAATC	120
GTCGATCACT	ATACGACGGA	TGTCAATCCA	CATGAACCCCT	TGGATGCTCA	TATCAAAGAA	180
CTGACAGGAT	TGACAGACCA	ACGTCTGGCG	CAAGCACCTG	ATTTTTCGCA	AGTTGCCAGA	240
AAAATATTTG	ACTTGGTGGA	GGATGGGATT	TTTGTAGCCC	ATAATGTTCA	GTTTGATGCT	300
AATCTCTTGG	CGGAAAATTT	ATTTTTTGAA	GGCTATGAGC	TAAGAAAACC	TCGTGTTGAT	360
ACGGTCGAAT	TGGCCCAGGT	CTTTTCCCT	GAAGTGGAAA	AATATAGCTT	GCCGATTTTG	420
TGTCGAGAAT	TAGGAATTCC	TCTTAAACAC	GCACACACAG	CCCTTTCAGA	TGCCCAAGCT	480
ACAGCAGAAT	TACTTCTTTT	TTTACGGGAA	AAGATGACCC	AGCTTCCTAA	AGGTCTCTTG	540
GAACGCTTGC	TGGAAATGGC	TGACGCTCTC	CTATATGAGT	CCTACCTGGT	TATTGAGGAA	600
ACTTATCGCA	ACCAATCTAT	CCTGAGTTCT	CCAGACTTGG	TCCAAGTTCA	AGGTCTGTAT	660
TTTAAGAAAA	CGGCAGCTTC	TCTGGAGCTA	CGAAAACCTAT	CTCAAGACTT	TTCTAAAAAT	720
ATTTCTCTGT	TGAACCTTGA	AGTGAGGGAG	GAACAAGAAA	GTTTTGCTAA	AGAGGTTGGC	780
TTGCTATTGA	AAGATGAACC	TGCTTTTCTG	ATTCAAGCGC	CGACAGGGAT	TGGGAAAACC	840
TATGGCTATC	TCTTACCCGC	TTTATCTCAA	TCCAAAGAGC	GACAAATTGT	TCTTAGTGTT	900
CCGACAAAGA	TTCTTCAAAA	TCAAATCATG	GAAGAAGAAG	GTAAACGTCT	CAAGGAAGTG	960
TTCCATACAG	ATATTCATAG	CTTAAAGGGA	CCACAAAATT	ATCTGAAGTT	GGATGCCTTT	1020
TATCATTCCT	TGCAGGAAAA	TGATGAAAAT	CGCTTATTTA	GACGCTTTAA	AATGCAAGTC	1080
TTGGTCTGGC	TTACTGAGAC	AGAGACAGGA	GATTTGATG	AAATCGGGCA	ACTCTACCGT	1140
TACCAACATT	TTCTAGCAGA	CCTTCGTCAT	GATGGGAATT	TATCATCCCA	GAGCTTATTT	1200
GTGACGGAAG	ATTTTTGGAA	ACGTAGTCAA	GAAAGGGCAG	AGACTTGCAA	GCTTTTAGTG	1260
ACTAATCATG	CCTATCTCGT	GACCAGACTT	GAAGATAATC	CTGAATTTGT	CAGTGACCGT	1320
TTACTGATTA	TTGATGAAGT	CCAAAAGATT	TTGTTAGCTC	TAGAAAATCT	GCTTCAAGAG	1380
ACCTACGATA	TACAATCTAT	TATCGATTTA	ATTGATAAGG	CTTTAGTAGG	AGAAGAAAAC	1440
AGGGTTCAAC	AACGGATACT	AGAAAATATT	CGCTTTGAGT	GTCTCTACTT	GATAGAACAA	1500
TTTCAGTCTG	GTAAATCTAG	GAAAAATATC	TTAGATTCTC	TGGACAACTC	CCATCAGTAT	1560
TTTTCAGAAAT	TAGAAGTAGA	AGGCTTTGAT	GAGCTGGTTC	GCTATTTTAC	AGCTGAAGGT	1620
GATTACTGGC	TTGAAGTAAC	TGAAACGAGT	CAAAAGAAAA	TTCAGATTTT	TTCTACAAAA	1680
TCAGGCCGTA	CTCTTCTGTC	CTCTTTACTT	CCTGAGAGTT	GCCAAGTCCT	GGGAGTATCG	1740

GCTACTCTTG	AGATTAGTCA	GAGGGTTTCT	TTGGCAGACC	TTTtaggcta	TCCTGAAGCT	1800
AAATTTGTCA	AGATTGAATC	TCGGGGAAAA	CAGGAACAAG	AAGTGGTCAT	GGTCAAAGAT	1860
TTCCCTCTGG	TAACAGAAAC	CTCCTTAGAA	GTCTATGCCA	GAGAGGTAGC	TGCTTTACTA	1920
GTGGAAATTC	AAGCTTTCCA	GCAACCGATT	TTGGTTCTCT	TTACCGCTAA	AGACATGCTT	1980
CTAGCAGTAT	CGGATTTACT	TACAGTTAGC	CACTTGGCCC	AGTATAAAAA	TGGGGATGTT	2040
CATCAGCTAA	AGAAACGCTT	TGAAAAAGGT	GAACAACAAA	TCTTGCTTGG	TGCAGCAAGT	2100
TTCTGGGAGG	GAGTTGATTT	TTCAAGCCAT	CCTTTTGTGA	TTCAAGTTGT	ACCGAGGCTT	2160
CCTTTCCAAA	ATCCTCAAGA	ACCCTTGACG	AAAAAGATTA	ATCAAGAACT	GAATCAAGAA	2220
GGGAAAAATG	CCTTTTATGA	TTATCAATTG	CCAATGGCCA	TTATTCGTTT	AAAACAGGCT	2280
TTGGGAAGAA	GTATGAGACG	TGAATACCAA	CGTTCCTTAA	CTCTTATTTT	GGATAGGAGA	2340
ATCGTCGGAA	AACGATACGG	CAAACAAATA	GTAGCATCTC	TAGCAGAAGA	AGCGACTGTT	2400
AAAACCATCT	CTCGATCCGA	AGTTGACGAG	GCTATTGATA	GATTTTTTAA	TGAACTTTGA	2460

(2) INFORMATION FOR SEQ ID NO:2123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 648 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2123:

AGAATTGTTT	TCAACGGATG	CAGAGGAAGA	GGAAGAAGAT	TTCGAATCGG	GTATTTAAAG	60
GGTAAAAGAA	TGATAAAAAA	GGTTACGATT	GAaaaaataa	AATCGCCTGA	GCGCTTCTTA	120
GAAGTACCAC	TTCTGACGAA	AGAAGAAGTC	GGCCAGGCAA	TCGATAAGGT	TATTCGGCAG	180
TTAGAACTCA	ACCTTGACTA	TTTCAAGGAA	GATTTCCCGA	CACCAGCTAC	CTTTGATAAT	240
GTCTATCCAA	TCATGGATAA	CACGGAATGG	ACCAATGGTT	TCTGGACAGG	AGAACTGTGG	300
TTGGCTTATG	AATACAGTCA	ACAGGATGCA	TTTAAAAACA	TCGCTCATAA	AAATGTTCTT	360
TCTTTCCTGG	ATCGTGTCAA	TAAGAGAGTA	GAATTGGATC	ACCATGATCT	CGGCTTCTTG	420
TACACACCGT	CTTGATGGC	TGAATATAAG	ATAAATGGAG	ATGGAGAGGC	TAGAGAAGCA	480
ACCTTGAAAAG	CTGCAGATAA	GTTGATTGAA	CGCTATCAAG	AAAAAGGTGG	TTTTATTCAA	540
GCTTGGGGAG	ACTTGGGCAA	GAAAGAGCAT	TACCGTTTGA	TTATCGACTG	CTTGCTCAAT	600
ATCCAACCTCT	TATTCTTTGC	TTATCAAGAA	ACAGGCGATC	AAAAATAG		648

(2) INFORMATION FOR SEQ ID NO:2124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 246 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2124:

AAGACTATAA	TAAAGTCAAA	TATATACGAC	ACAAATCAGA	AAGGAGACCA	GATGAATCGT	60
GTGAAAGAAT	TTCGCAAGGA	ACTGGGCATT	TCCCAGCTCG	AGCTCGCCAA	GGATATCGGT	120
GTCTCGAGAC	AGACCATCAA	TATGATTGAA	AACGACAAGT	ACAATCCAAC	TCTGGAACTC	180
TGTCTCAATC	TCGCCCCGAG	CCTCCAAACT	GACCTCAACA	GTCTCTTTTG	GAAGGAAGAT	240
TTTTAA						246

(2) INFORMATION FOR SEQ ID NO:2125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2256 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2125:

AGTGGTATAA	TACTTTTTAG	AAAGAACATT	TTAGAAAAGA	GCATGCATAT	GATTGCACTA	60
GAAGAAAAAA	TTACAAATTTT	GCCAACTCTC	TTCGTTCGAGA	AACGAGATGG	GAGACGTGTT	120
GTATTTGATG	TGGACAAGAT	TGACAAGGCT	CTCCACAAGG	CGGCTGACAA	GGTTATGGAT	180
GTGACACCCC	TGGTTGAAAA	ACGCCTCAAT	GATCTGACTG	AGCGAATTAT	TACAGAAAATT	240
CATAGTCGCT	TTCCACAGGG	AATTAAAGATT	TACGAAATTC	AAAATATCGT	AGAACATGAA	300
CTCCTTGAAG	CCAAAAGAATA	TGCGCTGGCT	GAGGAGTATA	TTACTTATCG	GACACAGAGG	360
GATTTTGAGC	GCTCAAAAGC	GACGGATATC	AACTTTAGTA	TTCATAAACT	TCTCAACAAA	420
GACCAGACAG	TTGTCAATGA	AAACGCTAAT	AAAGACAGTG	ATGTCTTTAA	CACTCAGCGT	480
GATTTGACAG	CAGGGATTGT	TGGGAAATCA	ATCGGACTGC	AAATGCTTCC	TAAGCACGTA	540
GCCAAATGCC	ACCAAAAGGG	GGATATCCAC	TATCACGATT	TGGACTACAG	TCCCTATAAC	600
CCTATGACCA	ACTGCTGTTT	GATTGATTTT	AAGGGTATGT	TGGAAAATGG	TTTTAAGATT	660
GGAAATGCAG	AGGTAGAGAG	TCCCAAGTCT	ATCCAGACTG	CGACAGCACA	GATTTCTCAA	720
ATCATTGCCA	ACGTGTGCTT	TAGCCAGTAC	GGTGGCTGTT	CAGCTGACCG	TATCGATGAA	780
ATTTTGCGC	CTTATGCAGA	GAAGAATTAT	CAAAAACATC	TCAAAGATGC	AGAAGAGTGG	840

GTATTGCCTG	AAAAACGGGA	AGATTACGCT	TGGAAGAAAA	CGCAAAAGGA	CATCTACGAT	900
GCCATGCAAT	CTCTTGAGTA	TGAAATCAAT	ACTCTCTTCA	CTTCAAATGG	ACAAACACCT	960
TTTACTTCGT	TAGGTTTTGG	TCTGGGAACC	AGTCGTTTTG	AACGAGAAAT	TCAAAAAGCT	1020
ATTTTAAACA	TTCCGATCAA	GGGTCTTGGT	TCAGAACACC	GTACGGCTAT	CTTTCCTAAA	1080
CTTATTTTCA	CTCTGAAAAG	AGGCCTTAAT	TTAGAGGAAG	GAAC TCCCAA	CTACGACATC	1140
AAGCAGTTGG	CTCTTGAGTG	TGCAACCAAA	CGGATGTATC	CAGATGTTTT	ATCTTACGAT	1200
AAGATTGTTG	ACTTGACAGG	ATCCTTCAAG	GTGCCATATG	GTTGCCGTTT	TTTCCTCCAA	1260
GGATGGAAGG	ATGAAAATGG	TGTAGAAGTC	AATTCAGGTC	GCATGAATCT	GGGTGTTGTG	1320
ACGGTTAATC	TGCCTCGTAT	TGCTCTTGAG	TCTGAAGGTG	ATATGAATAA	GTTC TGGGAA	1380
ATCTTCAACG	AGCGAATGAA	TATCGCAGAA	GATGCTCTTG	TTTACCGTGT	CGAACGCACT	1440
AAAGAGGCGA	CACCAGCAAA	TGCTCCTATT	CTTTATCAGT	ACGGTGCTTT	TGGCCATCGT	1500
CTAGGTAAAG	AAGAAAGTGT	TGACCAGCTC	TTTAAGAATC	GTCGTGCTAC	CGTTTCGCTG	1560
GGCTATATCG	GCTTGATGCA	AGTAGCGACA	GTTTTCTTTG	GTAACAGCTG	GGAAAGTAAT	1620
CCAGATGCTA	AGGAATTCAC	GCTAGACATC	ATTCACGATA	TGAAACGCCG	TGTAGAAGAG	1680
TGGTCAGACC	AATATGGGCTA	CCATTTCTCT	ATCTACTCAA	CACCATCCGA	AAGTCTGACA	1740
GACCGTTTCT	GCCGACTAGA	TATAGACAAG	TTTGGCTCTA	TTCTTGATAT	CACAGACAAG	1800
GAATACTACA	CCAAC TCTTT	CCACTACGAT	GTTCGTAAAA	ATCCAACACC	GTTTGAAAAA	1860
TTGGACTTTG	AGAAAGTCTA	TCCAGAAGCA	GGTGCCTCAG	GTGGTTTCAT	CCATTATTGT	1920
GAGTATCCAG	TCCTTCAGCA	AAATCCAAAG	GCCTTGGAAG	CTGTCTGGGA	TTATGCTTAT	1980
GACCGTGTAG	GCTATCTAGG	CACCAATACT	CCGATTGACC	GTTGCTACAA	GTGTGACTTT	2040
GAAGGGGATT	TTGAACCAAC	TGAGAGAGGG	TTTGCTTGTC	CAAAC TGTGG	CAATAGCGAC	2100
CCTAAACAG	TAGATGTGGT	GAAGCGAACT	TGTGGCTACC	TAGGTAATCC	TCAAGCAAGA	2160
CCGATGGTCA	ACGGGCCTCA	CAAGGAAATC	GCTGCGCGTG	TCAAACATAT	GAATGGTTCA	2220
ACGATTAAAA	TAGCTGGGCA	TCAAGTAACA	AATTAG			2256

(2) INFORMATION FOR SEQ ID NO:2126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2126:

GAATCCTCCT	TTTCCTCCTT	CTATTATAGC	ACATTTTTTAA	ATCTAGGTTT	GCTAGATTCT	60
ATGCTTCTAT	CTATTTATTC	GGAAAAGAAG	GCTTTTCTTC	AGAAGAAAGC	TAATAGCTTA	120
TTTGAAATTT	TCTCCTCTCT	GTTGGATAGT	CCCGTCTATC	TATGTTATAA	TGAAAGAAGG	180
ATTTAA						186

(2) INFORMATION FOR SEQ ID NO:2127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2127:

CAACAAATAA	TAAAAATGTT	ATTCTTATCA	CATAAGAAAG	CGGTTTCAAT	AAAAGAGAGA	60
GGAGGACTTA	TTTTGTTGCA	TTGTTGCTCA	AGGTGTGATT	TTTTTGAAAG	AAAAAATAAA	120
ATGAAAACGA	AAAAACATAG	ATTACTTGCT	CTAGCTCTTA	TTTCAAGTTT	TACATTATTG	180
GGAGCTGCAT	CAGCTGCTGT	ACAATATCCA	GATGGAGGAG	TATGGACGTA	TGGAGAAGGT	240
TCAGGAGGTG	GTTGGGCTTT	TTCAAATTAC	TATCATGGTA	AAAAATATCA	TTATTCTTCT	300
CTTGTAAGTA	GATGGAATAG	TCATTTCAGAT	AAAGGAGAAG	CTCCTGCTGG	AAAAACCTCC	360
TATGCATGGA	TTTGGACTAA	ATGGGGAGAA	CAAGTAGCAT	TTTACTGTGA	TTATGACTAA	420

(2) INFORMATION FOR SEQ ID NO:2128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1320 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2128:

GAAGAAATAA	TGAGTATGTT	TTTAGATACA	GCTAAGATTA	AGGTCAAGGC	TGGTAATGGT	60
GGCGATGGTA	TGGTTGCCTT	TCGTCGTGAA	AAATATGTCC	CTAATGGAGG	CCCTTGGGGT	120
GGTGATGGTG	GTCGTGGAGG	CAATGTGGTC	TTCGTTGTAG	ACGAAGGACT	ACGTACCTTG	180
ATGGATTTCC	GCTACAATCG	CCATTTCAAG	GCTGATTCTG	GTGAAAAAGG	GATGACCAAA	240
GGGATGCATG	GTCGTGGTGC	TGAGGACCTT	AGAGTTCGAG	TATCACAAGG	TACGACTGTT	300
CGTGATGCGG	AGACTGGCAA	GGTTTTAACA	GATTTGATTA	AACATGGGCA	AGAATTTATC	360
GTTGCCACG	GTGGTCGTGG	TGGACGTGGA	AATATTTCGTT	TTGCGACACC	AAAAAATCCT	420

GCACCGGAAA	TCTCTGAAAA	TGGAGAACCA	GGTCAGGAAC	GTGAGTTACA	ATTGGAAC TA	480
AAAATCTTGG	CAGATGTCGG	TTTAGTAGGA	TTCCCATCTG	TAGGGAAGTC	AACACTTTTA	540
AGTGTTATTA	CCTCAGCTAA	GCCTAAAATT	GGTGCCTACC	ACTTTACCAC	TATTGTACCA	600
AATTTAGGTA	TGGTTCGCAC	CCAATCAGGT	GAATCCTTTG	CAGTAGCCGA	CTTGCCAGGT	660
TTGATTGAAG	GGGCTAGTCA	AGGTGTTGGT	TTGGGAAC TC	AGTTCCTCCG	TCACATCGAG	720
CGTACACGTG	TTATCCTTCA	CATCATTTGAT	ATGTCAGCTA	GCGAAGGCCG	TGATCCATAT	780
GAGGATTACC	TAGCTATCAA	TAAAGAGCTG	GAGTCTTACA	ATCTTCGCCT	CATGGAGCGT	840
CCACAGATTA	TTGTAGCTAA	TAAGATGGAC	ATGCC TGAGA	GTCAGGAAAA	TCTTGAAGAA	900
TTTAAGAAAA	AATTGGCTGA	AAATTATGAT	GAATTTGAAG	AGTTACCAGC	TATCTTCCCA	960
ATTTCTGGAT	TGACCAAGCA	AGGTC TGGCA	ACACTTTTAG	ATGCTACAGC	TGAATTGTTA	1020
GACAAGACAC	CAGAAATTTT	GCTCTACGAC	GAGTCCGATA	TGGAAGAAGA	AGCTTACTAT	1080
GGATTTGACG	AAGAAGAAAA	AGCCTTTGAA	ATTAGTCGTG	ATGACGATGC	GACATGGGTA	1140
CTTTCTGGTG	AAAAACTCAT	GAAACTCTTT	AATATGACCA	ACTTTGATCG	TGATGAATCT	1200
GTCATGAAAT	TTGCCCCGTC	GCTTCGTGGT	ATGGGGGTTG	ATGAAGCCCT	TCGTGCGCGT	1260
GGAGCTAAAG	ATGGGGATT T	GGTCCGCATT	GGTAAATTTG	AGTTTGAATT	TGTAGACTAG	1320

(2) INFORMATION FOR SEQ ID NO:2129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...225
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2129:

CCAACCTCCT	TTTCGTTTCA	TACTCTTCAA	AAATCTCTTC	AAACCGCGTC	AACGTCGCCT	60
TGGCCGCTAT	ATATGTTACT	GACTTCGTCA	GTTCTATCTG	CAACCTCAAA	ACAGTGTTTT	120
GAGCTGACTT	CGTCAGTTCT	ATCTGCAACC	TCAAAGCAGT	GCTTTGAGCA	ACCTGCGGCT	180
AGTTTCCTAG	TTTGCTCTTT	GATTTTCATT	GAGTATCAGA	TTTAA		225

(2) INFORMATION FOR SEQ ID NO:2130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 516 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2130:

CACTTGATAA	TATGCGTTTT	TTCTAAGTGG	ATTAGTAGAG	TAGAGGATTT	TTCTCATATA	60
ATACTCTTCG	AAAATCTCTG	CAAACACGT	CAGCTTCCAT	CTGCAACCTC	AAAACAGTAT	120
TTTGAGCTGA	CTTCGTCAGT	CTTATCTGCA	ACTTCAAAAC	AGTATTTTGA	GCTGACTTCG	180
TCAGTCTTAT	CTGCAACCTC	AAAACAGTAT	TTTGAGCTGA	CTTCGTCAGT	CTTATCTGCA	240
ACCTCAAAAC	AGTATTTTGA	GCTGACTTCG	TCAGTCTTAT	CTGCAACCTC	AAAACAGTAT	300
TTTGAGCTGA	CTTCGTCAGT	CTTATCTGCA	ACCTCAAAAC	AGTATTTTGA	GCTGACTTCG	360
TCAGTCTTAT	CTGCAACCTC	AAAACAGTAT	TTTGAGCTGA	CTTCGTCAGT	CTTATCTACA	420
ACCTCAAAGC	AGTGCTTTGA	GCAACCTGTG	GCTAGCTTCC	TAGTTTGCGC	TTTGATTTTC	480
ATTGAGTATA	AGGGAAAGTA	TAGTGAATTG	AAATAA			516

(2) INFORMATION FOR SEQ ID NO:2131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2131:

AGTACGATAA	TGATTTTTTTT	AATTCGTATG	ATTTATAATG	CAGTGGATAT	TTACTCCCTG	60
ATTTTGATAG	CCTTCGCTGT	CATGTCCTGG	TTTCCAGGTG	CCTACGAATC	CAGTTTAGGT	120
CGTTGGATTG	TAGCGTTGGT	GAAACCAAGT	CTTGCTCCCT	TGCAACGCCT	GCCTTTACAG	180
ATAGCGGGTC	TTGATTTATC	TGTTTGGGTT	GCGATTGTTT	TGGTTTCGATT	TTTAGGAGAA	240
AACTTAGTGC	GTTTTCTGGC	GATGATAGGA	TGA			273

(2) INFORMATION FOR SEQ ID NO:2132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 282 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2132:

ATTGAGGTAA TAAGGATGAG ATTAGATAAA TATTTAAAG TATCGCGAAT TATCAAGCGT	60
CGTACAGTCG CAAAGGAAGT AGCAGATAAA GGTAGAATCA AGGTTAATGG AATCTTGGCC	120
AAAAGTTCAA CGGACTTGAA AGTTAATGAC CAAGTTGAAA TTCGCTTTGG CAATAAGTTG	180
CTGCTTGTA AAGTACTAGA GATGAAAGAT AGTACAAAAA AAGAAGATGC AGCAGGAATG	240
TATGAAATTA TCAGTGAAAC ACGGGTAGAA GAAAATGTCT AA	282

(2) INFORMATION FOR SEQ ID NO:2133:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 558 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2133:

AGATTATCCT TTACCAGCGC CCTTTTTCTT TAAAAATGA GAAAATTTTCG GTATAATAGT	60
CAAACAAGGT CAAGGTTTAA AGAGAGAGGT GGGTTTGTTA TGAGATTTAA AAATACATCG	120
GATCATATTG AGGCCTACAT CAAGGCGATT TTAGATCAAT CTGGTATCGT GGAGTTGCAA	180
CGGAGTCAGT TGGCAGATAC CTTTCAGGTT GTTCCTAGTC AGATTAACTA CGTGATCAAG	240
ACACGCTTTA CGGAAAGTAG AGGCTACTTG GTTGAAAGTA AGCGTGGTGG CGGAGGCTAC	300
ATTCGTATAG GACGGATTGA GTTTTCTAGT CATCATGAAA TGCTCCGGGA GCTGCTTTAC	360
TCGATTGGTG AGCGAGTCAG TCAAGAAATT TATGAGGATA TTCTCCAGCT TTTGGTTGAG	420
CAGGAATTGA TGACCAAGCA GGAGATGAAT TTGCTAGAAT CAGTAGCTTT GGATCGCGTT	480
TTAGGAGAAG AAGCTCCAGT TGTTCGAGCA AACATGCTAC GTCAGATCAT ACAAGAGGTA	540
GATAGAAAAG GGAAGTAA	558

(2) INFORMATION FOR SEQ ID NO:2134:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 402 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...402
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2134:

TTAAAATCCT	TTTCAAAAAA	TCACCTTTTC	TTGATTTTTA	ATCCTATTTG	CTGTATGATA	60
AGGGAAAAGA	AAGGAGACAG	AGATATGGCT	TTTACCAATA	CCCACATGCG	GTCTGCTAGT	120
TTTGGCATTG	TTACCAGCTT	GCCTGATGAC	ATCATTGACT	CTTTTTGGTA	TATTATCGAC	180
CATTTCTTAA	AAAATGTCTT	TGAATTGGAA	GAAGAACTCG	AGTTTCAATT	GCTTAATAAC	240
CAAGGAAAGA	TTACCTTCCA	CTTTTCAAGT	CAACACCTCC	CTACAGCCAT	TGATTTTGAC	300
TTTAACCATC	CTTTCGACCC	TCGTTATCCC	CCAAGAGTAC	TGGTTTTAGA	CATGGACGGT	360
AGAGAAACTA	TCCTCCTCCC	AGAAGAAAAT	GACCTATTTT	AA		402

(2) INFORMATION FOR SEQ ID NO:2135:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 435 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...435
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2135:

GTTATCTCAA	TGTTAATCGG	AATCCCAAAA	GAAATTAAAA	ATAACGAAAA	CCGTGTCGCC	60
CTCACACCTG	CAGGTGTTCA	TAGCTTAGTT	AGTCGTGGTC	ATCGTGCCT	TATCGAAACA	120
AATGCTGGTC	TCGGTTCTGG	CTTTACTGAT	GCTGACTATC	AAAAGCAAGG	AGCTGAGATT	180
GTCGCTACTG	CTGGTGAAGC	TTGGGCAGCA	GAGTTGGTTG	TGAAAGTAAA	AGAACCCTTA	240

AGTTCTGAAT	ACGGTTACTT	TCGCGACGAT	CTTCTTCTCT	TCACCTACTT	GCACATGGCC	300
GCTGCTCCAG	AATTAGCAGA	TGCTATGTTA	GCAGCAAAAA	CAACAGGAAT	TGCC'TATGAA	360
ACTGTTCTGT	ACAATCAAGG	ACAAC'TACCG	CTCCTCGTTC	CTATGAGTGA	GGTTGCAGAT	420
CGTATGGCTG	TTTAA					435

(2) INFORMATION FOR SEQ ID NO:2136:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 594 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...594
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2136:

AAGTACTCAA	TTTACAAGCT	AAAATGCGAC	AGAAACGAAA	ATAAAGGAGA	CGTTGGTAAG	60
AAGGCAGAGA	ATCTCATTCA	AGGCCAATTT	GAAGGCTCTA	AAGCAATGGA	AAAGTGCTAC	120
ACAGATGTGA	CAGAATTTGC	CATTCCAGCA	AGTACTCAA	AGCTTTACTT	ATCACCAGTT	180
TTAGATGGCT	TTAATAGCGA	AATTATCGCC	TATAATCTTT	CAACTTCGCC	CAACTTAGAA	240
CAAGTGAAGA	GTATGTTAGA	ACAGGCCTTT	ACAGAGAAGC	ACTACGAGAA	TACGATTCTC	300
CATAGTGACC	AAGGCTGGCA	ATACCGACAC	GATTCTTATC	ATCGGTTCCCT	AGAGAGTAAG	360
GGAATTCAAG	CATCCATGTC	ACGTAAGGGT	AACAGCCCAG	ACAATGGTAT	GATGGAGTCC	420
TTCTTTGGGA	TTCTGAAATC	GGAAATGTTT	TACGGTTTTG	AGAAGTCGTT	TCAGTCGCTT	480
AAGCAATTGG	AACAAGCTAT	TATAGACTAT	ATTGATTACT	ACAACAATAA	ACGAATTAAG	540
GTAAACTAA	AAGGACTTAT	CCCTGTGCAA	TACAGAACTA	AATCCTTCGG	ATAA	594

(2) INFORMATION FOR SEQ ID NO:2137:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 411 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2137:

AAGTACTCAA	TTTACAAGCT	AAAATGCGAC	AGAAACGAAA	ATAAAGGAGA	CGTTGGTAAG	60
AAGGCAGAGA	ATCTCATTCA	AGGCCAATTT	GAAGGATCTA	AAACAATGGA	AAAGTGCTAC	120
ACAGATGTGA	CAGAATTTGC	CATTCCAGCA	AGTACTCAAA	AGCTTTACTT	ATCACCAGTT	180
TTAGATGGCT	TTAACAGCGA	AATTATCGCC	TATAATCTTT	CAACTTCACC	CAACTTAGAA	240
CAAGTACAAA	CAATGTTGGA	ACAGGCATTC	ACAGAGAAGT	ACTACGAGAA	TACGATTCTC	300
CATAGTGACC	AAGGCTGGCA	ATACCGACAC	GATTCTTATC	ATCGGTTCCCT	AAGAGTAAGG	360
GAATTC AAGC	ATCTATGTCA	CGCAAGGGAA	ACAGCCAAGA	CAACGGTATG	A	411

(2) INFORMATION FOR SEQ ID NO:2138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 594 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2138:

AAGTACTCAA	TTTACAAGCT	AAAATGCGAC	AGAAACGAAA	ATAAAGGAGA	CGTTGGTAAG	60
AAGGCAGAGA	ATCTCATTCA	AGGCCAATTT	GAAGGCTCTA	AAACAATGGA	ACAGTGCTAC	120
ATAGATGTGA	CTGAATTTGC	CATTCCAGCA	AGTACTCAAA	AGCTTTACTT	ATCACCAGTT	180
TTAGATGGCT	TTAATAGCGA	AATTATCGCC	TATAATCTTT	CAACTTCACC	CAACTTAGAA	240
CAAGTACAAA	CAATGTTGGA	ACAGGCATTC	AAAGAGAAGC	ACTACGAGAA	TACGATTCTC	300
CATAGTGACC	AAGGCTGGCA	ATACCGACAC	GATTCTTATC	ATCGGTTCCCT	AGAGAGTAAG	360
GGAATTCAAG	CATCTATGTC	ACGTAAGGGT	AACAGCCCAG	ACAATGGTAT	GATGGAGTCC	420
TTCTTTGGGA	TTCTGAAATC	GGAAATGTTT	TACGGTTATG	AGAAGTCGTT	TCAGTCGCTT	480
AAGCAATTGG	AACAAGCCAT	TGTAGACTAT	ATTGATTACT	ACAACAATAA	GAGAATTAAG	540
GTAAACTAA	AAGGACTTAG	CCCTGTGCAA	TACAGAACTA	AATCCTTCGG	ATAA	594

(2) INFORMATION FOR SEQ ID NO:2139:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2139:

ACTTCATCAA	TACCTATGAT	TTGGAGCCAA	TGGCCAAACA	AGTTATTCCT	AAAGCAGCAT	60
TTGGCTATAT	CGTCTAGTGG	GGCGGAAGAT	ACTCTCACTT	TAAGAGAGAA	TATCCGCGCC	120
TTTAACCACA	AACTCATCGT	TCCTCATACA	CTTTGCGATG	TTGAAAATCC	AAGTACAGAG	180
ATTGAATTTG	CAGGTGAAAA	ACTATCTTCA	CCAATCATTA	TGGCGCCTGT	TGCGGCTCAT	240
AAATTGGCAA	ATGAACAGGG	GGAAGTGGCG	ACTGCGCGTG	GTGTGCATGA	GTTTGGTTCT	300
CTTTATACAA	CCAGCTCTTA	CTCTACTGTT	GACCTTCCAG	AGATTTCTGA	AGCCCTTCAA	360
GGGACACCCC	ATTGGTTCCA	ATTTTACTTT	AGTAAGGATG	ACGGTATCAA	CCGCCACATC	420
ATGGACCGTG	TGAAGGCTGA	AGGTTATAAA	GCGATTGTCT	TGACGGCAGA	TGCTACTGTA	480
GGGGGGAATC	GTGAAGTGGA	TAAGCGTAAT	GGTTTTGTCT	TCCCAGTTGG	CATGCCGATT	540
GTTGAAGAAT	ACCTGCCAGA	AGGTGCTGGT	AAATCAATGG	ACTTTGTTTA	CAAATCAGCT	600
AAACAACGCT	TGCTCCACG	CGATGTAGAA	TTTATCGCTG	AATACTCTGG	TCCTCCTGTG	660
TATGTCAAGG	GACCACAAATG	CCGTGAGGAC	GTTGAACGTT	CACCTGCTGC	AGGAGCTTCT	720
GGTATCTGGG	TAACCAACCA	CGGTGGTCGT	CAAATCGACG	GTGGACCAGC	TGCCTTTGAC	780
TCGCTTCAAG	AAGTGGCAGA	AGCAGTTGAT	AGACGTGTGC	CGATTGTCTT	GAACCTGGT	840
GTTTCGTCGTG	GTCAACACGT	CTTTAAAGCC	TTGGCTTCAG	GAGCAGACTT	GGTAGCTATT	900
GGTCGCCCTG	TTATTTATGG	CTTGGCTCTC	GGTGGTAGTG	TCGGTGTGCG	TCAAGTCTTT	960
GAACACTTGA	ATGCGGAATT	GAAGACAGTT	ATGCAATTGT	CTGGAGCTCA	GACCATTGAA	1020
GATGTCAAAC	ACTTTAAGCT	CCGTCACAAT	CCATACAACC	CAACCTTCCC	AGTTGACCCT	1080
CGTGACTTAA	AATTGTATTG	A				1101

(2) INFORMATION FOR SEQ ID NO:2140:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2140:

GTCTTGTCAA	TAGTCTTGGC	CATCTCGCCA	CCGAGGGCAT	CGACTTCACG	TACGACAATC	60
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CCCTTGGCAG	AACCACCGAT	AGAGGGATTA	CAAGGCATGA	AAGCCAGCAT	TTCAATATTG	120
ATGGTCGCAA	GCAGGACCTT	ACAGCCCATA	CGGCTAGCGG	CCAAGGAAGC	CTCAACCCCA	180
GCGTGTCCCG	CACCAATTAC	AATAATATCG	TATTCTTCAG	TAAAATGA		228

(2) INFORMATION FOR SEQ ID NO:2141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2141:

TATACTGTTT	TCATGACAGA	TTTATCAAAA	CAATTACTTG	AAAAAGCTCA	TGGTGGGTTA	60
AAAATAAAATC	CGGATGAGCA	AAGACGCTAT	CTTGGTACTT	TTGAGGAAAG	AGTTCCTTGA	120
TATGTAGATA	TTGACACAGC	AAATAGCCCT	CAGTTAGAAA	AAGGCTTTTT	ATTTATTTTA	180
GAAAACCTTC	AGGAAAAAGC	AGAGCCACTA	TTTGTGAAGA	TTTCACCAAC	TATCGAATTT	240
GATAAGCAAG	TTTTCTACTT	AAAAGAAGCA	AAAGAACTG	ATAGTCAAGC	CACCATAGTA	300
TCTGAAGAGC	ATATTACTTC	TCCTTTTGGC	CTGGTTATTC	ATAGCAATGC	ACCAGTTCAA	360
GTAGAAGAAA	TAAGACCTTC	GACTTGCTTT	TCCAAACTT	TGGGAAGTTA	A	411

(2) INFORMATION FOR SEQ ID NO:2142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2142:

GTGAAGTCAA	TGCCCCGATC	GCTTTGCTGG	AAGGATGAGT	ACACGGAGTA	CATGCATGAA	60
ATATGCCCTG	GTCGTTTAAAC	TCCTGAAGTA	ACCAGGTTGC	TGAATGAAAA	ATTTGGTACG	120
AATTATAACA	AGAGTCAAAT	CGGTGGCGTA	CGCAAACGTC	TAGGGTTAGC	AGTTGGAAAA	180
GTCTATCAAG	GTCGATTGCT	GACAAAGGAG	CAACATGATT	ATCTTGTTAT	GATCCAAAAA	240
AATAAGATTT	CTCGTAATGT	CGCAAATGAA	ATGAACCAAA	AATTTGGCTT	ATCGCTAACT	300
GAGAAACAGA	TTAAGAGTTA	TCGGAGAAAT	AATAATCTAC	ATAGTGGTTT	GACAGGAAGA	360
TTCGAGAAAAG	GTCAGACTCC	TCACAATAAG	GGGAAGAAGT	ACCCAATAT	GCCAAAAAAC	420
GGCGGGCAGT	TCAAAAAAGG	TAATCGACCT	CCGAATTATG	TACCTGTCGG	TACTATCAAC	480
TACACAACAA	ACGTTTATCC	AAAAGAAAAG	ATTGGAGAAC	CTAATCAATG	GGTTTTGAAA	540
CACCGCAAGG	TTTGGGAGGA	CCATCACGGG	CTGATACCAA	AAGGGTACTC	AATCGTTTTT	600
CTGGACGGTG	ATAAAACAAA	CTATGATATT	TCAAATCTGG	CATGTTTATC	TAAGAACGAA	660
ATTGCTAGAA	TGAATCAAAA	TCATTTATTC	ACGTCCAACG	CTGATTTGAC	TAAATCAGGT	720
ATTGGACTAA	CAAACTTAC	AAATAAAATC	AGAGAGGTAG	AAAAAATGG	CTAG	774

(2) INFORMATION FOR SEQ ID NO:2143:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...195
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2143:

AAATTTCCAA	TTCTTGGATC	TAAACAAACA	CCTTTTATTA	CAACTTCAGC	ATTTAAACTT	60
CTCCTCTCAG	CAAAAGAATC	TAGTTCATTA	AAAAAAGCAA	CACGGAGAGC	TAAGAATGTG	120
TTAGAAAAAA	GCTTAATTGC	TTCTGCTTCA	GTAGGAGAAA	CTAACATAAC	ATTTTTAATA	180
TTGGCAGTAC	TATGA					195

(2) INFORMATION FOR SEQ ID NO:2144:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2679 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2679

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2144:

CTCTTCCCAA	TGGTATTTTT	TGATTCTTTC	CTTTATAATG	GGTGATGGA	TAAGAAAAAA	60
TTATTATTGA	TTGATGGGTC	TTCTGTAGCT	TTTCGGGCGT	TTTTTGCGCT	GTATCAGCAG	120
TTGGACCGTT	TAAAGAATGC	GGCTGGTTTG	CATACCAATG	CGATTTATGG	TTTCCAGTTG	180
ATGTTGAGTC	ATTTGTTGGA	GCGGGTTGAG	CCGAGTCATA	TTTTGGTGGC	TTTTGATGCG	240
GGAAAGACGA	CCTTCCGGAC	AGAGATGTAT	GCGGACTATA	AGGGTGGTCG	GGCCAAGACT	300
CCTGATGAGT	TTCGTGAGCA	ATTTCTTTTC	ATTCGTGAGT	TGCTGGATCA	TATGGGGATT	360
CGTCACTATG	AGCTGGCTCA	GTATGAGGCG	GATGACATCA	TTGGGACGCT	GGATAAGCTA	420
GCAGAGCAGG	ATGGTTTTGA	TATTACCATT	GTCAGTGGGG	ACAAGGATTT	GATTCAGCTG	480
ACGGATGAGC	ATACGGTGGT	TGAAATTTCC	AAGAAAGGTG	TGGCTGAGTT	TGAGGCCTTT	540
ACGCCAGATT	ACCTCATGGA	AGAAATGGGC	CTCACACCAG	CTCAGTTTAT	CGATCTCAAG	600
GCGCTCATGG	GTGATAAGTC	GGATAATATC	CCTGGGGTGA	CCAAAGTCGG	TGAAAAGACG	660
GGTATTAAGC	TCTTGCTGGA	GCATGGTTTC	CTTGAGGGGA	TTTATGAAAA	TATTGATGGA	720
ATGAAGACTT	CTAAGATGAA	GGAAAATCTC	ATCAATGACA	AGGAACAGGC	CTTTTTGTCT	780
AAAACACTAG	CGACCATTGA	TACCAAGGCA	CCGATTGCGA	TTGGTTTAGA	GGACTTGGTC	840
TATAGTGGTC	CAGATGTTGA	AAATCTTGGG	AAATTTTACG	ATGAGATGGG	ATTCAAACAG	900
CTCAAGCAGG	CTTTAAATGT	GTCGTCAGCT	GATGTGGCTA	AGGGTTTGGA	TTTTACTATT	960
GTTGACCAAA	TCAGTCAAGA	TATGCTGAGT	GAAGAGTCTA	TCTTCCACTT	TGAGCTTTTT	1020
GGTGAGAAAT	ACCATAACGA	TAATTTGGTT	GGATTTGCCCT	GGTCTTGTGG	GGATAAGCTC	1080
TATGCCACAT	ACAAGCTTGA	GCTGTTGCAA	GACCCGATTT	TCAAGGATTT	CTTAGAAAAA	1140
ACATCTCTGA	GAGTTTATGA	CTTTAAGAAG	GTTAAAGTTC	TTTTTGCAACG	TTTTGGTGTG	1200
GATTTGCAGG	CGCCTGCTTT	TGACATCCGT	TTGGCTAAAT	ACCTCCTTTC	GACTGTGGAG	1260
GACAATGAAA	TTGCGACCAT	CGCTAGTCTT	TATGGTCAGA	CTTACTTGGT	TGATGATGAA	1320
ACTTTCTACG	GTAAGGGTGT	TAAAAAGGCC	ATTCCTGAAC	GTGAGAAAT	CTTGGAACAC	1380
TTAGCTTGTA	AACCTGCTGT	TTTGGTAGAA	ACAGAGCCTA	TTTTACTTGA	AAAACTCAGC	1440
GAAAATGGGC	AATTAGAGCT	TCTTTATGAT	ATGGAGCAAC	CTCTGGCTTT	TGTTCTTGCC	1500
AAGATGGAAG	TTGCTGGGAT	TGTGGTCAAG	AAAGAGACCT	TGCTTGAGAT	GCAGGCTGAA	1560
AATGAGCTTG	TCATTGAAAA	ACTGACTCAA	GAGATTTACG	AGCTGGCTGG	TGAGGAGTTT	1620
AATGTCAACT	CGCCTAAGCA	GTTGGGCGTG	CTTCTCTTTG	AGAAATTGGG	ACTTCCTCTA	1680
GAATACACTA	AGAAAACCAA	GACAGGTTAT	TCGACAGCAG	TGGATGTGTT	GGAGCGTCTC	1740
GCTCCTATTG	CTCCGATTGT	TAAGAAAATC	CTGGATTACC	GTCAAATTGC	TAAGATTCAA	1800
TCTACTTATG	TAATTGGCTT	GCAGGACTGG	ATTTTGGCTG	ATGGAAAGAT	TCATACTCGC	1860
TATATGCAGG	ATTTGACCCA	GACCGGGCGT	TTGTCTAGTG	TGGATCCAAA	CTTGCAAAAT	1920
ATTCCTGCCC	GATTGGAACA	AGGGCGCTTG	ATTCGGAAGG	CTTTTGTGCC	AGAGTGGGAG	1980
GATAGTGTGC	TACTCAGCTC	TGACTATTCA	CAGATTGAAT	TGCGCGTTTT	GGCGCATATT	2040
TCTAAGGATG	AGCACTTGAT	TAAGGCCTTC	CAAGAGGGGG	CAGATATCCA	TACTTCGACA	2100
GCCATGCGGG	TCTTTGGCAT	TGAGCGTCCCT	GATAATGTGA	CTGCAAATGA	CCGTCGCAAT	2160
GCCAAGGCAG	TTAACTTTGG	AGTGGTTTAT	GGGATTTTTC	ACTTTGGCTT	GTCTAATAAT	2220
TTGGGAATTA	GTCGTAAGGA	AGCCAAAAGCC	TACATTGATA	CCTACTTTGA	ACGTTTTTCCA	2280
GGTATTAATA	ACTACATGGA	TGAAGTGGTG	CGGGAGGCGC	GTGATAAGAG	CTATGTAGAG	2340
ACCTCTTTTA	AGCGTCGCCC	TGAGTTGCCA	GATATCAATT	CGCGCAACTT	CAATATTCGT	2400
GGTTTTGCGG	AGCGAACTGC	TATCAACTCA	CCTATCCAGG	GTTCGGCAGC	AGATATTCCTC	2460
AAGATTGCCA	TGATTCAAGT	GGATAAAGCC	TTGGTTGCAG	GTGGTTATCA	GACCAAGATG	2520
CTGTTACAAG	TGCACGATGA	AATCGTCCCT	GAAGTGCCTA	AATCTGAATT	GGTAGAGATG	2580
AAAAAATTGG	TGAAACAAAC	CATGGAAGAA	GCCATTCAAC	TCAGTGTTC	TCTTATCGCA	2640
GATGAGAATG	AAGGGGCAAC	CTGGTACGAG	GCTAAATAA			2679

(2) INFORMATION FOR SEQ ID NO:2145:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...276
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2145:

ATGACACCAA	TCACAAAACC	AACCCCAACA	ACTTGTATGG	CAATATCGTT	AGAAATACCG	60
AAAAGGCTAC	AAGCAACTGG	GATAAGAAGG	AGGGAACCTC	CGGCAATACC	TGAAGCACCA	120
CAGGCTGAGA	TAGCTGCTAC	CACACTGAGG	ACAAAGGCTG	TGGCAAAGTC	AACAGGAATT	180
CCAAGAGTGT	TAACTGCAGC	AAGGGTCAAA	AGGTTAATGG	TAATCGCTAC	TCCAGCCATA	240
TTGATAGTAG	AACCGAGTGG	GATAGAAACA	GAATAG			276

(2) INFORMATION FOR SEQ ID NO:2146:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1170 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1170
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2146:

ATGAAGCCAA	TTGACCGTTT	TTCTTATCTA	AAGAATAATC	GGGTGTCGCA	AGATACCTCA	60
TCTCTGGTAC	AGTGCTACCT	CCCGATTATC	GGTCAGGAGG	CACTGAGCCT	TTATCTTTAT	120
ACGATTAGTT	TTTGGGATAA	TGGTAGAAAG	GAATATCTTT	TTTCAAGTAT	CCTCAATCAT	180
CTCAACTTTG	GGATGGATAG	ACTGATAAAA	TCATTGAAAA	TCTTATCTGC	TTTTAATCTC	240
TTGACTCTCT	ATCAAAAGGG	GGATGTTTAT	CAGCTAGCCC	TCCATGCTCC	TCTATCTAGT	300
CAAGACTTCT	TGGGGCATCC	TGTTTATCGC	AGACTCTTAG	AGAAAAAGAT	TGGCGATGTA	360
GCTGTGGAGG	ATTTGAAAGT	TGAAAGTGCT	GATGGTGAAG	AAATACCTGT	CTCACTCAAT	420

CAAGTCTTTC	CAGAATTGGC	AGAACTAGGC	AGTCAAGAAT	ACCTTGGTCT	CAAGAAGAAA	480
GTGGCCAACG	ATTTTGACTT	GGACCATTTT	CGTCAGCTTA	TGGCTCGAGA	TGGACTTCGC	540
TTTGCGGATG	AGCAGTCCGA	TGTCTTAAAC	CTCTTTGCCA	TTGCCGAGGA	GAAGAAATGG	600
ACTTGGTTTG	AAACCTATCA	ATTGGCCAAG	TCAACAGCTG	TTTCTCAGGT	TATTTCAACC	660
AAACGCATGC	GTGAAAAAAT	TGCTCAAAAA	CCAGTTTCCT	CTGACTTTAG	TCTTAAGGAA	720
GCGATCATTA	TCAAAGAAGC	CAAAAGTAAA	ACTGCCCTGC	AGTTCTTGGC	AGAAATCAAG	780
CAAACACGCA	AGGGAACCAT	TACCCAAACA	GAAAGAGAAC	TCTTGCAACA	GATGGCTGGC	840
TTGGGTTTGC	TGGACGAAGT	CATCAATATC	ATTCTTTTAT	TGACCTTTAA	TAAGGTCGAT	900
TCGGCAAATA	TCAATGAGAA	ATATGCCATG	AAGGTAGCCA	ATGACTATGC	CTATCAAAAG	960
ATTCATTTCG	CAGAAGAGGC	AGTCTTGCGC	ATCCGTGAGC	GAGGACAGAA	AGCAAAAACA	1020
CAAAAACAGA	ATCAGACTGC	CCCAGCAAAA	ACCAATATTTC	CTAAATGGAG	TAATCCTGAA	1080
TATAAAAATA	CGTCATCCGC	TGAGGAATTA	GAAGAGATGG	AACGCCAAAC	CCTAGAATTA	1140
TTAGCAAAAT	TAGATAACGG	AGGTGATTAG				1170

(2) INFORMATION FOR SEQ ID NO:2147:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 252 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...252
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2147:

GAGGATACAA	TAATGAAGAA	AACTGTTTAT	AAAAAATTGG	GTATTTCAAT	TATTGCGAGT	60
ACTTTATTGG	CTAGCCAGTT	ATCGACAGTA	TCTGCTTTGA	GTGTTATTTT	TAGTACAGGT	120
GAAGAATATG	AGGTAAGTGA	GACACTAGAA	AAAGGTCCAG	GATCTAATGA	TTCTTCATTA	180
TCTGAGATTT	CACCAACATA	TGGTTCATAC	TACCAAAAGC	AATCAGAAGT	ATTATCGGTA	240
ATGATGATTT	GA					252

(2) INFORMATION FOR SEQ ID NO:2148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2148:

TTGTCCACAA	TGATGATGGC	TCTTATACGC	CCGAAATCGA	AGAGATTTAT	TATGGATCAT	60
AAGGCTTATA	TGTACGTTCT	GGAGTGTCGT	GATGGATCCT	ACTATATAGG	CTATACGACT	120
GATATGAGAA	GACGCCTCGC	TATCCACAAT	AGTGGGAAGG	GAGCCAAATA	TACACGAGCA	180
CGCTTGCCAG	TCAAAC TTAT	CTATGCTCAA	GGTTTTGCCA	GTAAGGAAGA	AGCCATGTCG	240
GCTGAAGCTC	TTCTCAAGCG	TAAGAAGAGG	CCACAGAAGG	AAGAATTTTT	ATCTGAAAAT	300
CAAGATAGAA	ATTTACTCCG	TTTATTTTGA				330

(2) INFORMATION FOR SEQ ID NO:2149:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 995 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2149:

TTAAACAAT	GACTTCAACT	AAACAACACA	AAAAAGTTAT	CCTTGTCGGT	GATGGTGCTG	60
TAGGTTTCATC	TTACGCTTTT	GCACTTGTTA	ACCAAGGAAT	TGCACAAGAG	CTTGGAATTA	120
TCGAAATTCC	ACAATTGCAT	GAAAAAGCTG	TTGGTGATGC	GCTTGACCTT	AGTCACGCCC	180
TTGCCTTCAC	TTACCTAAA	AAAATCTATG	CAGCTCAATA	CTCTGACTGT	GCAGACGCTG	240
ACCTTGTTGT	GATCACTGCA	GGTGCACCTC	AAAAACCAGG	TGAAACTCGT	CTTGACCTTG	300
TAGGTAAAAA	CCTTGCTATC	AACAAATCAA	TCGTAAC TCA	AGTTGTTGAA	TCTGGTTTCA	360
AAGGTATCTT	CCTTGTTGCT	GCTAACCCAG	TTGACGTTTT	GACTTACTCA	ACTTGGAAT	420
TCTCTGGTTT	CCCTAAAGAA	CGCGTTATCG	GTTCAGGTAC	TTCACTTGAC	TCAGCTCGTT	480
TCCGTCAAGC	ACTTGCTGAA	AAATTGGATG	TGGATGCTCG	TTCAGTGCAC	GCCTACATCA	540
TGGGTGAACA	CGGTGACTCT	GAGTTCGCTG	TTTGGTCACA	CGCTAACATC	GCTGGTGTA	600
ACCTTGAAGA	ATTCTTAAA	GACACTCAAA	ATGTTCAAGA	AGCTGAATTG	ATTGAATTGT	660
TCGAAGGTGT	TCGTGATGCA	GCCTACACAA	TCATCAACAA	AAAAGGTGCA	ACATACTACG	720
GTATCGCAGT	AGCCCTTGCT	CGTATCACTA	AAGCAATCCT	TGACGATGAA	AACGCAGTAC	780
TTCCACTTTC	AGTATTCCAA	GAAGGTCAAT	ACGGAGTTGA	GAATGTCTTT	ATCGGTCAAC	840
CAGCTGTTGT	TGGTGCACAT	GGTATCGTTC	GTCCAGTAAA	CATTCCATTG	AACGATGCAG	900
AAACTCAAAA	AATGCAAGCA	TCTGCTAAAG	AATTGCAAGC	TATTATTGAC	GAAGCATGGA	960
AAAATCCAGA	ATTCCAAGAA	GCTTCTAAAA	ACTAA			995

(2) INFORMATION FOR SEQ ID NO:2150:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...225
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2150:

TACGAAACAA	TTGCTAAAAC	ATTTATAGAA	ATTAATTTTA	CTTTCCCAAT	CGATTTGTTC	60
TCATCTTATT	TCAATCTGCT	ATATAATAGT	CCATGCTGTG	GCTGGATTCT	TTTCAGCCTA	120
CTTATACTCT	TCGAAACTCT	CTTCAAACCA	CGTCAGCTTC	ACCTTGCCGT	AGGTATGGTT	180
ACTGACTTCG	TCAGTTCTAT	CCACAACCTC	AAAACGGTGT	TTTGA		225

(2) INFORMATION FOR SEQ ID NO:2151:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...396
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2151:

TACGAAACAA	TTGCTAAAAC	ATTTATAGAA	ATTAATTTTA	CTTTCCCAAT	CGATTTGTTC	60
TCATCTTATT	TCAATCCGCT	ATATATTATG	GTATCGAATC	TTCATCAGAA	TGATAAAATT	120
AATCAATTAA	TATCTGATTA	CAAACAGAAT	ATGAAAGCTT	TTTATATCAC	TATTGAAAAA	180
TTTATACGAG	ATGATGAAAG	CCTTAAGTGT	TATTTTACAA	AGGTTATTTT	AAGTCGTTCC	240
AAGGTAACAA	GTCTAGATCA	GATTGAAGCT	GATAAAACGA	TACAAAGAAA	ATATTCAAGT	300

GAGCTAAAAA AATTTATTGG ATTTTATAAT GAGATTATTT GTGAGGAAAA TAGTTTCCTA	360
CATGTACGAA AGAGGTGGTC GAGTTGGTTT AGGTAG	396

(2) INFORMATION FOR SEQ ID NO:2152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 633 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...633
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2152:

CCTATGACAA TCGAACTATT GACTCCCTTT ACCAAGGTAG AGTTGGAGCC AGAAATCAAG	60
GAGAAAAAAC GCAAACAAGT TGGGATTTTA GGGGGGAATT TTAACCCCTGT TCACAATGCC	120
CATCTCATTG TTGCGGATCA AGTACGGCAA CAGTTGGGAC TGGATCAAGT TCTGCTCATG	180
CCTGAATACC AACCTCCTCA CGTTGATAAA AAGGAAACCA TCCCTGAACA CCATCGTCTC	240
AAGATGCTTG AGTTGGCAAT TGAGGGAAT T GACGGCCTAG TCATTGAAAC CATTGAGTTG	300
GAGCGCAAGG GTATTTCCCTA CACCTACGAC ACCATGAAGA TTTTGACAGA GAAGAATCCA	360
GATACGGATT ATTACTTTAT CATCGGTGCC GACATGGTTG ACTATCTGCC TAAGTGGTAC	420
CGAATTGATG AACTGGTTGA CATGGTTCAG TTTGTGGGGG TTCAGCGTCC ACGCTACAAG	480
GTAGGGACTT CCTATCCAGT TATCTGGGTG GACGTACCGC TCATGGATAT CTCGTCCAGC	540
ATGGTGCGTG CCTTCCTTGC CCAAGGTCGG AAACCCAAC TTTCTCCTACC TCAGCCAGTG	600
CTAGACTACA TCGAGAAGGA GGGGCTCTAC TGA	633

(2) INFORMATION FOR SEQ ID NO:2153:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 591 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2153:

CTGATGACAA	TGAAAGCGAT	GAAAACGATG	ATGCCGGATTA	CTGATAATCA	ACACAAGATT	60
ATTAAAGAAA	AATTTGTTGA	AGAATATCCT	AAACTAAGCA	ATCTTCTTTT	AGACAGAACC	120
TTGGAAAGTC	TATCCCAAGA	TGAACGTATT	TTCATTTTTTC	CAAATGATTT	GA CTCATACT	180
CCAGATTTGG	ATAAAAAACA	AAAGATTTTG	GAAACGATCA	ATCAGGAAAT	CAAGACAGGA	240
AATGTGATTG	GTTTTCTTGG	ATATGGTCAG	GAAAGATTAA	CGATTTTCCTC	ACGATTTTCT	300
GATGAGAGTA	ATGACCATT	TTTGCATTAT	CTCTTAAACA	AGGTTCTTCA	TATCAATCTC	360
ACTAGTTTAG	ATGTTGCTTT	GTCTCGTGAA	GAGAGGCTTT	ATCAACTTTT	GATGTATCTC	420
TTCCCCAAGT	ATCTACAAGC	TGCTATTTCGA	AAAGGTCTTT	ATAAGGAATA	TCATCGATTT	480
TCTCATAACG	ACAGTCATGT	TAAGGGAGTG	ATTGATGTAA	GAAACCATCC	TCAAGAAAAA	540
TCTTCCTTTC	ACGGGAAATA	TTGCCTACAC	AACGAGAGAG	TTCACCTATG	A	591

(2) INFORMATION FOR SEQ ID NO:2154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2154:

AGGATGACAA	TTAAACTAGT	AGCAACGGAT	ATGGACGGAA	CCTTCCTATA	TGGGAATGGA	60
CGCTTTGATA	TGGATCGTCT	CAAGTCTCTA	TTGGCTTCCT	ACAAGGAAAA	AGGGATTTAC	120
TTTGCGGTGG	CTTCGGGTCG	GGGATTTCTG	TCTCTGGAAA	AATTATTTGC	TGGTGTTCGT	180
GATGACATTA	TTTTTCATCGC	GGAAAATGGC	AGTTTGGTAA	AGTATCAAGG	TCAGGACTTG	240
TATGAAGCGA	CTATGTCTCG	TGACTTTTAT	CTGGCAACTT	TTGAAAAGCT	GAAAACGTCA	300
CCTTATGTAG	ATATCAATAA	ACTGCTCTTG	ACGGGTAAGA	AGGTTTCATAT	GTCTAGATAC	360
GTTTGA						366

(2) INFORMATION FOR SEQ ID NO:2155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2155:

AGACGGACAA TCTTGGCCGG AATACCGACA ACCGTCACAT CACTAGGTAC ATCTGCTACG	60
ACAACTGCTG CAGCACCGAC CTTGGCATTTC TCACCAATTT CCACAGGCCC GATAACTTGG	120
GCATGGGCTG ATATGAGGGC TCCCTTTCGT ACAGTCGGAT GGCCTTTGCC ACAGTCTTTC	180
CCTGTTCCCC CGAGAGTCAC TCCGTGA	207

(2) INFORMATION FOR SEQ ID NO:2156:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2156:

ACACGAGCAA TCCAAATCGG GTCACGCCTG CTGGTTTTTTA GGCAGCTAGA GCGTAAGAAG	60
TGTTATTTTT TGCAGTTATA TTAACTGAG CGTTTACGTC GCCACACGAG TCGCAAATA	120
TGCCTCATAA TGCCTGTCGA ATCCGTAACG ACCCCAAAAG ACAATAAAAC TATTATACCT	180
TATCTAACTC AAAAATGCAA AAAGAAATCA CATACCTAA	219

(2) INFORMATION FOR SEQ ID NO:2157:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2505 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2505

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2157:

AAATTTCCCT	TTTGTGGTAT	AATAGATAAA	GTGAGGAAAT	CCATGCAAAA	TCAATTAAAT	60
GAATTA AAAAC	GAAAAATGCT	GGAATTTTTT	CAGCAAAAAC	AAAAAATAA	AAAATCAGCT	120
AGACCTGGCA	AGAAAAGGTT	AAGTACCAAA	AAATCTAAAA	CCTTAGATAA	GTCAGTCATT	180
TTCCCAGCTA	TTTTACTGAG	TATAAAAAGCC	TTATTTAACT	TACTCTTTGT	ACTCGGTTTT	240
CTAGGAGGAA	TGTTGGGAGC	TGGGATTGCT	TTGGGATACG	GAGTGGCCTT	ATTTGACAAG	300
GTTCGGGTGC	CTCAGACAGA	AGAATTGGTG	AATCAGGTCA	AGGACATCTC	TTCTATTTCA	360
GAGATTACCT	ATTTCGACGG	GACGGTGATT	GCTTCCATAG	AGAGTGATTT	GTTGCGCACT	420
TCTATCTCAT	CTGAGCAAAT	TTCGGAAAAT	CTGAAGAAGG	CTATCATTGC	GACAGAAGAT	480
GAACACTTTA	AAGAACATAA	GGGTGTAGTA	CCCAAGGCGG	TGATTTCGTG	GACCTTGGGG	540
AAATTTGTAG	GTTTGGGTTT	CTCTAGTGGG	GGTTCAACCT	TGACCCAGCA	ACTAATTAAA	600
CAGCAGGTGG	TTGGGGATGC	GCCGACCCTG	GCTCGTAAGG	CGGCAGAGAT	TGTGGATGCT	660
CTTGCCCTTG	AACGCGCCAT	GAATAAAGAT	GAGATTTTAA	CGACCTATCT	CAATGTGGCT	720
CCCTTTGGCC	GAAATAATAA	GGGACAGAAAT	ATTGCAGGGG	CTCGGCAAGC	AGCTGAGGGA	780
ATTTTCGGTG	TAGATGCCAG	TCAGTTGACT	GTTCCTCAAG	CAGCATTTTT	AGCAGGACTT	840
CCACAGAGTC	CCATTACTTA	CTCTCCTTAT	GAAAATACTG	GGGAGTTGAA	GAGTGATGAA	900
GACCTAGAAA	TTGGCTTAAG	ACGGGCTAAG	GCAGTCTTTT	ACAGTATGTA	TCGTACAGGT	960
GCATTAAGCA	AAGACGAGTA	TTCTCAGTAC	AAGGATTATG	ACCTTAAACA	GGACTTTTTTA	1020
CCATCGGGCA	CGGTTACAGG	AATTTACACG	GACTATTTAT	ACTTTACAAC	TTTGGCAGAA	1080
GCTCAAGAAC	GTATGTATGA	CTATCTAGCT	CAGAGAGACA	ATGTCTCCGC	TAAGGAGTTG	1140
AAAAATGAGG	CAACTCAAAA	GTTTTATCGA	GATTTGGCAG	CCAAGGAAAT	TGAAAATGGT	1200
GGTTATAAGA	TTACTACTAC	CATAGATCAG	AAAATTCATT	CTGCCATGCA	AAGTGCGGTT	1260
GCTGATTATG	GCTATCTTTT	AGACGATGGA	ACAGGTCGTG	TAGAAGTAGG	GAATGTCTTG	1320
ATGGACAACC	AAACAGGTGC	TATTCTAGGC	TTTGTAGGTG	GTCGTAATTA	TCAAGAAAAT	1380
CAAAATAATC	ATGCCTTTGA	TACCAAACGT	TCGCCAGCTT	CTACTACCAA	GCCCTTGCTG	1440
GCCTACGGTA	TTGCTATTGA	CCAGGGCTTG	ATGGGAAGTG	AAACGATTCT	ATCTAACTAT	1500
CCAACAAACT	TTGCTAATGG	CAATCCGATT	ATGTATGCTA	ATAGCAAGGG	AACAGGAATG	1560
ATGACCTTGG	GAGAAGCTCT	GAAGTATTCA	TGGAATATCC	CTGCTTACTG	GACCTATCGT	1620
ATGCTCCGTG	AAAAGGGTGT	TGATGTCAAG	GGTTATATGG	AAAAGATGGG	TTACGAGATT	1680
CCTGAGTACG	GTATTGAGAG	CTTGCCAATG	GGTGGTGGTA	TTGAAGTCAC	AGTTGCCCGAG	1740
CATACCAATG	GCTATCAGAC	CTTAGCTAAT	AATGGAGTTT	ATCATCAGAA	GCATGTGATT	1800
TCAAAGATTG	AAGCAGCAGA	TGGTAGAGTG	GTGTATGAGT	ATCAGGATAA	ACCGGTTCAA	1860
GTCTATTCAA	AAGCTACTGC	GACGATTATG	CAGGGATTGC	TACGAGAAGT	TCTATCCTCT	1920
CGTGTGACAA	CAACCTTCAA	GTCTAACCTG	ACTTCTTTAA	ATCCTACTCT	GGCTAATGCA	1980
GATTGGATTG	GGAAGACTGG	TACAACCAAC	CAAGACGAAA	ATATGTGGCT	CATGCTTTTCG	2040
ACACCTAGAT	TAACCTTAGG	TGGCTGGATT	GGGCATGATG	ATAATCATT	ATTGTCACGT	2100
AGAGCAGGTT	ATTCTAATAA	CTCTAATTAC	ATGGCTCATC	TAGTAAATGC	GATTACAGCA	2160
GCTTCCCCAA	GCATTTGGGG	GAACGAGCGC	TTTGCTTTAG	ATCCTAGTGT	AGTGAAATCG	2220
GAAGTCTTGA	AATCAACAGG	TCAAAAACCA	GGGAAGGTTT	CTGTTGAAGG	AAAAGAAGTA	2280
GAGGTCACAG	GTTTCGACTGT	TACCAGCTAT	TGGGCTAATA	AGTCAGGAGC	GCCAGCGACA	2340
AGTTATCGCT	TTGCTATTGG	TGGAAGTGAT	GCGGATTATC	AGAATGCTTG	GTCTAGTATT	2400
GTGGGGAGTC	TACCAACTCC	ATCCAGCTCC	AGCAGTTCAA	GTAGTAGTTC	TAGCGATAGC	2460
AGTAACTCAA	GTACTACACG	ACCTTCTTCA	AGGGCGAGAC	GATAA		2505

(2) INFORMATION FOR SEQ ID NO:2158:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2158:

TNTNNNTNN	NNNNNNNNNN	NNNNNNNNNN	NNTNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	60
NNNNNNNNNN	NNNNNNANNN	NNNNNNNNNN	GNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	120
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNATTTTATA	180
ACAAGCCAAA	AACAGCGGAT	CATGTGGTAG				210

(2) INFORMATION FOR SEQ ID NO:2159:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 579 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2159:

ATGTCTCAAA	TCGAAAGAAT	CAAACAGGCT	ATCATGGCGG	ATTTCGCAGAA	TGCCAGCTAT	60
ACAGAGCGTG	GCATTGAGCC	TCTCTTTGCA	GCGCCAAAAA	CTGCTCGCAT	CAATATCATC	120
GGTCAGGCTC	CGGGACTTAA	AACTCAAGAA	GCAGGCCTTT	ACTGGAAAGA	TAAAAGTGGT	180
GACCGCTTGC	GGGACTGGCT	AGGTGTGGAT	GAAGATACCT	TTTACAATTC	AGGTATTTTT	240
GCTGTTTTGC	CTATGGATTT	CTACTTTCCA	GGACATGGCA	AGTCGGGTGA	TCTTCCGCCT	300
CGTACAGGTT	TTGCAGAAAA	ATGGCATCCG	CAGGTCTTAC	AGGAATTGCC	TGATATTCAG	360
TTAACCCTCT	TGATTGGGCA	ATATGCCCAA	GCCTACTATT	TACAGGAGAA	AATCAGTGGG	420
AAGGTAACGG	AGAGGGTGAA	ACACTATAAA	GACTATCTGC	CAGCCTATTT	TCCGCTAGTT	480
CACCCATCAC	CACGAAATCA	AATCTGGATG	GCCAAAAATC	CTTGGTTTGA	GGCAGAAGTA	540

(2) INFORMATION FOR SEQ ID NO:2160:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 654 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...654
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2160:

GCTTATCAAA	TAGGAGAAAC	CATGACCTCT	ATCACAGCGA	TTTTTTTCGA	TTTGGATGGA	60
ACCCTCGTTG	ATAGTTCTAT	CGGGATTAC	AATGCCTTTA	CCTATACCTT	TAAAGAGCTG	120
GGGTGCGCTA	GCCCTGATGC	CAAACTATT	CGTGGTTTTA	TGGGACCACC	TCTCGAAAGT	180
AGTTTTCGCGA	CCTGCCGTGC	CAAAGACCAA	ATTTCTGAAG	CCGTGCAGAT	ATATCGTTCT	240
TACTATAAGG	CAAAAGGCAT	CTATGAAGCT	CAACTCTTTC	CTCAGATTAT	AGACTTGCTT	300
GAGGAGTTAT	CGAGCAGTTA	TCCACTCTAC	ATCACCACGA	CAAAGGATAC	ATCTACTGCT	360
CAAGACATGG	CAAAAACTT	GGAAATCCAT	CATTTCTTTG	ATGGCATTTA	TGGTTCTAGC	420
CCTGAAGCAC	CCCATAAGGC	AGATGTCATT	CACCAAGCCT	TGCAGACACA	TCAACTAGCA	480
CCAGAACAAG	CCATCATCAT	CGGAGATACC	AAGTTTGATA	TGCTGGGAGC	TCGAGAAACA	540
GGTATTCAGA	AATTGGCCAT	CACTTGGGGA	TTTGGAGAGC	AAGCAGATCT	ACTAACTAT	600
CAACCTGATT	ATATCGCTCA	CAAACCCTTA	GAGGTTTTTG	CGTATTTTCA	ATAG	654

(2) INFORMATION FOR SEQ ID NO:2161:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 966 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2161:

AGTCATCAAA	TAAAGAAAGA	CTCTAAGGAG	AATCCTATGA	AATTCAATCC	AAATCAAAGA	60
TATACTCGTT	GGTCTATTCTG	CCGTCTCAGT	GTCGGTGTGTG	CCTCAGTTGT	TGTGGCTAGT	120
GGCTTCTTTG	TCCTAGTTGG	TCAGCCAAGT	TCTGTACGTG	CCGATGTGGT	CAATCCGACC	180
CCAGGTCAAG	TCTTACCTGA	AGAGACATCG	GGAACGAAAG	AGGGTGA CTT	ATCAGAAAAA	240
CCAGGAGACA	CCGTTCTCAC	TCAAGCGAAA	CCTGAGGGCG	TTACTGGAAA	TACGAATTCA	300
CTTCCGACAC	CTACAGAAAAG	AACTGAAGTG	AGCGAGGAAA	CAAAC TCTTC	TAGTCTGGAT	360
ACACTTTTTG	AAAAAGATGA	AGAAGCTCAA	AAAAATCCAG	AGCTAACAGA	TGTCTTAAAA	420
GAAACTGTAG	ATACAGCTGA	TGTGGATGGG	ACACAAGCAA	GTCCAGCAGA	AACTACTCCT	480
GAAACAAGTAA	AAGGTGGAGT	GAAAGAAAAT	ACAAAAGACA	GCATCGATGT	TCCTGCTGCT	540
TATCTTGAAA	AAGCTGAAGG	GAAAGGTCCT	TTCCTGCGCG	GTGTAAACCA	AGTAATTCCT	600
TATGAACTAT	TCGCTGGTGA	TGGTATGTTA	ACTCGTCTAT	TACTAAAAGC	TTCGGATAAT	660
GCTCCTTGGT	CTGACAATGG	TACTGCTAAA	AATCCTGCTT	TACCTCCTCT	TGAAGGATTA	720
ACAAAAGGGA	AATACTTCTA	TGAGGTAGAC	TTAAATGGCA	ATACTGTTGG	TAAACAAGGT	780
CAAGCTTTAA	TTGATCAACT	TCGCGCTAAT	GGTACTCAAA	CTTATAAAGC	TACTGTTAAA	840
GTATACGGAA	ATAAAGACGG	TAAAGCTGAC	TTGACTAATC	TAGTTGCTAC	TAAAAATGTA	900
GACATCAACA	TCAATGGATT	AGTTGCTAAA	GAAAAC TGT C	GAAAAAGCCG	TTGCAGACAA	960
CGTTAA						966

(2) INFORMATION FOR SEQ ID NO:2162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2162:

GGAGATCAAA	TCATGAATCT	TTTGATTATG	GGCTTACCTG	GTGCAGGTAA	GGGAACTCAA	60
GCAGCAAAAA	TCGTAGAACA	ATTCCATGTT	GCACATATCT	CAACAGGTGA	TATGTTCCGC	120
GCTGCAATGG	CAAAATCAAAC	TGAAATGGGT	GTTCTTGCTA	AGTCATATAT	TGACAAGGGT	180
GAATTGGTTC	CTGACGAAGT	TACAAATGGA	ATCGTAAAAG	AACGCCTTTC	ACAAGATGAT	240
ATTAAAGAAA	CAGGATTCTT	ATTGGATGGT	TACCCACGTA	CAATTGAACA	AGCTCATGCC	300
TTGGACAAAA	CATTGGCTGA	ACTTGGCATT	GAAGTAGAAG	GTGTTATCAA	TATTGAAGTG	360
AACCTTGACA	GCCTCTTGGA	ACGTTTGAGT	GGCCGTATCA	TCCACCGCGT	AACTGGAGAA	420
ACTTTCCACA	AGGTCTTTAA	CCCACCAGTT	GACTATAAAG	AAGAAGATTA	CTACCAACGT	480
GAAGATGATA	AGCCTGAGAC	AGTAAAACGT	CGTTTGGATG	TTAATATTGC	TCAAGGAGAA	540
CCAATCATTG	CTCACTACCG	TGCCAAAGGT	TTGGTTTCATG	ACATCGAAGG	TAATCAAGAT	600
ATCAATGATG	TCTTCTCAGA	TATTGAAAAA	GTATTGACAA	ATTTGAAATA	A	651

(2) INFORMATION FOR SEQ ID NO:2163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1992 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2163:

AATGTACAAA	TAGAACTAGA	GGTTTCTAAA	TTACGAATGC	TATTAACCAA	ACGAGAAGAA	60
CAATTATTGA	AGGCTTTCCT	ACATGTAGGG	AAGCTTTCAA	TGCAAGATAT	GA CTGAAATC	120
TTACAGGTTT	CATCTAGAAC	AATTTATCGA	ACTTTATCAG	ATTTGACAGA	TAGCATGGAG	180
CAATATGGAA	TCGAAATAAC	GAAGCATGGG	AAATACTATA	TTTTGACTGG	AGAGTTGGAT	240
GATTTGCCGA	CAGAACTTGA	AGTGTTAGTT	GAGTATAGTC	CCCAAGAAAG	ACAAGAGTTG	300
ATTACCTATC	GCCTTCTGAC	TGAGAGTGGT	TTTGTCACCA	ATGAAGCATT	GCAAGAGTGC	360
ACGAAAGTCA	GTAATGTAAC	TATTATTTCAG	GATATTTCAG	ATATTGATAA	GCGTCTTTTA	420
GACTTTGATC	TGAAAAATTGA	ACGACAAAAA	GGTTATCGGA	TTTCTGGTGA	TTCAGTTGGT	480
AAGAGAAGAT	TTTTGGCTAT	TTTACTGACA	AACTGTATCT	CAGTAGCAGA	TTTTTCAACC	540
GGTAATTTTG	GGAGCTTTGA	TATTTTAGAA	GCAGATAGAA	CTAGGCTGGC	CAGTCAGATT	600
GTTAATAAGC	AACTGTCAGG	TTTTCCAGAT	ATGGATGCTA	GGATGAAGAT	GTTTTTTGCG	660
ATCTTGTTAT	CTCTTATAGG	TCAGGAGCAA	AACATTGAAA	ATTCACCTAA	TACTAGTAAG	720
CAGGCTTTGG	AAATTTCTCA	AAAAATTTTT	CAAGCTTACT	CTAAGCAGAC	TGCACAATTT	780
TATAGTATTC	AGGAAATTAT	CTATTTTGCG	AGCATCTTGG	ATGAATTAAAT	CATTAAACGT	840
CAGGACAATC	CGCTCTTTAC	GGAGAAATTT	GATGGTGAAT	TTTTCTACAA	TATTTCAAAT	900
CTGATTGATA	CGGTTTCCAT	GTATACCAAG	ATTGACTTTT	TTAAGGACAA	GGTTTTATTC	960
AATTTTCTTT	TCCATCATAT	TCGGCTCAGT	TTAGGCGTCC	CTATCCTTTT	TCAGAGTGAA	1020
AATTTGCCAG	AATCTGTCCA	GATTTTAGTT	GAAAGGAATA	AATTTCTTTA	TACAGTCATC	1080
AGTCTTTTAG	TGAATGATAT	TTTTCCGAAA	TATCTTCATA	CAGACTATGA	GTATGGCATG	1140
ATTGCCCTAC	ATTTTATCTC	TAGCTTAGGC	CGTAGTCCAG	AGATTTATCC	AGTCCGTGTT	1200
TTGCTTTTAA	CGGATGAACG	TCGGGTCACT	AGAGATTTAT	TAGTCAGTAA	AATTAAGAGT	1260
GTGCTCCTT	TTGTAGAGTT	GATAGATATT	CAGTCTCTAG	TAGATTACCA	CAGTATTGAT	1320
CTCAGTCAGT	ATGATTATAT	TTTATCTACC	AAGCCGCTGA	CTAATCAGGA	AATCGATGTA	1380
ATTTCTAGTT	TTCCAACCGT	CAAAGAATTG	CTTGAATTAC	AGGAACGACT	TCAGTATGTA	1440
CAGGCACATC	GTACAATTGT	CGCGCGTGAT	GCTATCGCTC	CAGAGAAAAG	TTATGACTTG	1500
CAAGATTATT	TAATATCTAG	TAGTCAGCTT	TTGAGTCAAT	TCGAGTTGGT	TCAATTGGAG	1560
AATAATCAAT	CATTTGAGCA	TACGGTAGAA	CAAAATCATCC	AATATCAGAA	GAATGTGAGT	1620
GACAGAGATT	ACCTAACAAG	AAAATTGTTA	TCTCACTTCC	AGAATAGTCC	TATGGCTATT	1680
CCTAATACTG	GTCTGGTGCT	TTTACATAGT	CAGTCTAGCA	AAGTAACAAC	AAATAGTTTT	1740
ACTATGTTTG	AACTCAAAC	ACCTATCTCC	GCATTGTCAA	TGAAACGAGA	GGAAGAAGAG	1800
GTCAAAAGGT	GTCTGCTAAT	GCTAATGTCT	AAAGAAGCTA	GCGAGGAAGC	GAGAGATTTA	1860
ATGACAGCTA	TCAGTCAGTC	GATTATTGAA	AATCATCTTT	ATACAGAGAT	TTACAAGACG	1920
GGAAATCAAT	CCATTATTTA	TCAGATGCTA	AATACTATTT	TTAACGAAAA	AATTAAGAAA	1980
TTGGAGAACT	AA					1992

(2) INFORMATION FOR SEQ ID NO:2164:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...198
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2164:

AGTAGGCAAA	TCCCCTATTT	TCAAAAAGTT	TATCATTTTT	ATTTTAATTT	CTTGGATGAG	60
AAAAAAGACA	TATTTATGAA	AAAGCTCCAT	CGTGCTTTTA	ATGTGTTCTC	TTGTTTTCAA	120
ACTCGTAAAA	AGGGAGCCAC	TGAGCCTAAC	TCGCTCTCTC	ATTTCAAAGC	TTGTGAAAAA	180
AGACCGTTGG	GGTCTTAA					198

(2) INFORMATION FOR SEQ ID NO:2165:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...336
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2165:

ATTTTTAAAA	TGAAAAAAT	GATGACATTC	TTGAAAAAG	CTAAGGTAA	AGCTTTTACA	60
TTGGTGGAGA	TGTTGGTGGT	CTTGCTGATT	ATCAGCGTGC	TTTTCTTGCT	CTTTGTACCT	120
AATCTGACCA	AGCAAAAAGA	GGCAGTCAAT	GACAAAGGAA	AAGCAGCTGT	TGTTAAGGTG	180
GTGGAAAGCC	AGGCAGAACT	TTATAGCTTG	GAAAAGAATG	AAGATGCTAG	CCTAAGCAAG	240
TTACAAGCAG	ATGGGCGAAT	CACGGAAGAA	CAGGCTAAAG	CTTATAAAGA	ATACCATGAT	300

(2) INFORMATION FOR SEQ ID NO:2166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2166:

GAGTTTAAAA	TGAAACAAC	AACCGTTGAA	GATGCCAAAC	AAATTGAATT	AGAAATTTTG	60
GATTATATTG	ATACTCTCTG	TAAAAAGCAC	AATATCAACT	ATATTATTAA	CTACGGTACT	120
CTGATTGGGG	CGGTTTCGACA	TGAAGGCTTT	ATCCCTTGGG	ACGACGATAT	TGATTTATCC	180
ATGCCTAGAG	AAGACTACCA	ACGATTTATT	AACATTTTTC	AAAAGGAAAA	AAGCAAGTAT	240
AAGCTCCTAT	CCTTAGAAAC	TGATAAGAAC	TACTTTAACA	ACTTTATCAA	GATAACCGAC	300
AGTACGACTA	AAATTATTGA	TACTCGAAAT	ACAAAAACCT	ATGAGTCTGG	TATCTTTATC	360
GATATTTTCC	CTATAGATCG	CTTTGATGAT	CCTAAGGTCA	TTGATACTTG	TTATAAACTG	420
GAAAGCTTCA	AACTGCTGTC	TTTCAGTAAA	CATAAAAATA	TTGTCTATAA	GGATAGCCTT	480
TTAAAAGATT	GGATACGAAC	AGCCTTTTGG	TTGCTCCTTC	GACCGGTTTC	TCCTCGTTAT	540
TTTGCAAATA	AAATCGAGAA	AGAAATTCAA	AAATATAGTC	GTGAAAATGG	GCAGTATATG	600
GCTTTTATTC	CTTCAAAATT	TAAGGAAAAG	GAAGTCTTCC	CAAGTGGTAC	CTTTGATAAA	660
ACAATCGATT	TACCCTTTGA	GAATTTAAGC	CTTCCTGCAC	CTGAAAAATT	TGATACTATT	720
TTGACACAAT	TTTATGGAGA	TTATATGACC	CTACCACCAG	AAGAAAAACG	CTTCTACAGT	780
CATGAATTTT	ACGCTTATAA	ATTGGAGGAT	TAG			813

(2) INFORMATION FOR SEQ ID NO:2167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2167:

TTAATTAAAA	TTATGGAGAA	TATAGACATG	TTTAAATCAA	ATCATGAGCG	AAGAATGCGT	60
TATTCATTTC	GTAAATTTAG	TGTAGGAGTA	GCTAGCGTAG	CTGTTGCCAG	TCTTTTTATG	120
GGAAGTGTG	TACATGCGAC	AGAGAAAGAG	GGAAGTACCC	AAGCAGCCAA	TGTCATTAAAG	180
TTAGTGATCT	AA					192

(2) INFORMATION FOR SEQ ID NO:2168:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4590 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...4590

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2168:

GGAATTAAAA	TGAAAAAAG	TACAGTATTG	TCATTAAACCA	CAGCTGCAGT	TATTTTAGCA	60
GCCTATGCCC	CTAATGAGGT	AGTCTTAGCA	GACACATCTA	GCTCTGAAGA	TGCTTTAAGC	120
ATCTCTGATA	AAGAAAAAGT	AGTAGTAGAT	AAGGAAACAG	AAAATAAAGA	GAAACATAAA	180
GATATCCATA	GTGCTATGGA	AAC TTCACAG	GATTTTAAAG	AGAAGAAAAT	AGCAGTCATT	240
AAGGAAAAAG	AAGTTGTTAG	TAAAAC TCCT	GTGATAGACA	CTAAAAC TAG	CAATGAAGAA	300
AAT TCCAATA	AATCCCAAGG	AGATCATACG	GACTCATTTG	TGAATAAAAA	CACAGAAAAT	360
CCCAAAAAAG	AAGATAAAGT	TGTCTATATT	GCTGAATTTA	AAGATAAAGA	ATCTGGAGAA	420
AAAGCAATCA	AGGAAC TATC	CAGTCTTAAG	AATACAAAAG	TTTTATATAC	TTATGATAGA	480
ATTTTTAACG	GTAGTGCCAT	AGAAACAATT	CCAGATAACT	TGGACAAAAT	TAAACAAATA	540
GAAGGTATTT	CATCGGTTGA	AAGGGCACAA	AAAGTCCAAC	CCATGATGAA	TCATGCCAGA	600
AAGGAAATTG	GAGTTGAGGA	AGCTATTGAT	TACCTAAAGT	CTATCAATGC	TCCATTTGGG	660
AAAAATTTTG	ATGGTAGAGG	TATGGTCATT	TCAAATATCG	ATACTGGAAC	AGATTATAGG	720
CATAAGGCTA	TGAGAATCGA	TGATGATGCT	AAAGCCTCAA	TGAGATTTAA	AAAAGAAGAC	780
TTAAAAGGAA	CTGATAAAAA	TTTCTGGTTG	AGTGATAAAA	TCCCTCATGC	GTTCAATTAT	840
TATAATGGTG	GCAAAATCAC	TGTAGAAAAA	TATGATGATG	GAAGGGATTA	TTTTGACCCA	900
CATGGGATGC	ATATTGCAGG	GATTCTTGCT	GGAAATGATA	CTGAACAAGA	TATCAAAAAC	960
TTTAACGGCA	TAGATGGAAT	TGCGCCTAAT	GCACAAATTT	TCTCTTATAA	AATGTATTCT	1020
GACGCAGGAT	CTGGGTTTGC	GGGTGATGAA	ACAATGTTTC	ATGCTATTGA	AGATTCTATC	1080
AAACACAACG	TTGATGTTGT	TTCGGTATCA	TCTGGTTTTA	CAGGAACAGG	TCTTG TAGGT	1140
GAGAAATATT	GGCAAGCTAT	TAGGGCATT A	AGAAAAGCAG	GCATTCCAAT	GGTTGTCGCT	1200
ACGGGTA ACT	ATGCGACTTC	TGCTTCAAGT	TCTTCATGGG	ATTTAGTAGC	AAATAATCAT	1260
CTGAAAATGA	CCGACACTGG	AAATGTAACA	CGAACTGCAG	CACATGAAGA	TGCGATAGCG	1320
GTCGCTTCTG	CTAAAAATCA	AACAGTTGAG	TTTGATAAGG	TTAACATTGG	AGGACAAAGT	1380

TTTAAATACA	GAAATATAGG	GGCCTTTTTTC	GATAAGAATA	AAATCACAAC	AAATGAAGAT	1440
GGAACAAAAG	CTCCTAGTAA	ATTAAAATTT	GTATATATAG	GCAAGGGGCA	AGACCAAGAT	1500
TTGATAGGTT	TGGATCTTAG	GGGCAAAATT	GCAGTAATGG	ATAGAATTTA	TACAAAGGAT	1560
TTAAAAAATG	CTTTTAAAAA	AGCTATGGAT	AAGGGTGCAC	GCGCCATTAT	GGTTGTAAAT	1620
ACTGTAAATT	ACTACAATAG	AGATAATTGG	ACAGAGCTTC	CAGCTATGGG	ATATGAAGCG	1680
GATGAAGGTA	CTAAAAGTCA	AGTGTTTTCA	ATTTTCAGGAG	ATGATGGTGT	AAAGCTATGG	1740
AACATGATTA	ATCCTGATAA	AAAAACTGAA	GTCAAAAGAA	ATAATAAAGA	AGATTTTAAA	1800
GATAAATTGG	AGCAATACTA	TCCAATTGAT	ATGGAAAGTT	TTAATTCCAA	CAAACCGAAT	1860
GTAGGTGACG	AAAAAGAGAT	TGACTTTAAG	TTTGCACCTG	ACACAGACAA	AGAACTCTAT	1920
AAAGAAGATA	TCATCGTTCC	AGCAGGATCC	ACATCTTGCG	GGCCAAGAAT	AGATTTACTT	1980
TTAAAACCCG	ATGTTTCAGC	ACCTGGTAAA	AATATTAAAT	CCACGCTTAA	TGTTATTAAT	2040
GGCAAATCAA	CTTATGGCTA	TATGTCCGGA	ACTAGTATGG	CGACTCCAAT	CGTAGCAGCT	2100
TCTACTGTTT	TGATTCGACC	AAAATTGAAG	GAAATGCTTG	AAAAACCCGT	ATTAAAAAAT	2160
CTTAAAGGTG	ATGATAAAAT	AGACCTTACA	AGTCTTACAA	AAATAGCCCT	ACAAAATACT	2220
GCAAGACCTA	TGATGGATGC	AACTTCTTGG	AAAGAAAAAA	GTCAATACTT	TGCATCACCT	2280
AGACAGCAGG	GGGCGGGGCT	AATTAATGTG	GCCAACGCTT	TGAGAAATGA	AGTTGTAGCG	2340
ACTTTCAAAA	ACACGGATTTC	TAAAGGTTTG	GTAAATTTCAT	ATGGTTCCAT	TTCTCTTAAA	2400
GAAATAAAAAG	GTGATAAAAA	ATACTTTTACA	ATTAAGCTTC	ACAATACATC	CAACAGGCCT	2460
TTAACCTTTA	AAGTTTCAGC	ATCAGCGGTA	ACTACAGATT	CTCTAACTGA	CAGACTAAAA	2520
CTGGATGAAA	CATATAAAGA	TGAAAAATCT	CCAGATGGTA	AGCAAATTGT	TCCAGAAATT	2580
CATCCAGAAA	AAGTCAAAGG	GGCAAATATT	ACATTTGAGC	ATGACACTTT	CACTATAGGG	2640
GCAAATTCTA	GCTTTGATTT	AAATGCGGTT	ATAAATGTTG	GGGAGGCTAA	AAATAAAAAAT	2700
AAATTTGTAG	AATCATTTAT	TCATTTTGAG	TCAGTAGAAG	AAATGGAAGC	ATTAAGCTCC	2760
AATGGCAAGA	AAACCGACTT	CCAACCATCT	TTATCAATGC	CCCTAATGGG	ATTTGCTGGG	2820
AATTGGAACC	ACGAACCAAT	CCTTGATAAA	TGGGCTTGGG	AAGAAGGATC	AAAATCAAAA	2880
ACAATGGAAG	GTTATGATGA	TGACGGTAAA	CCAAAAATTC	CAGGAACCTT	AAATAAGGGG	2940
ATTGGTGGAG	AACATGGTAT	AGATAAAATTT	AATCCAGCAG	GAGTTATCCA	AAATAGAAAA	3000
GATAAAAAATA	GAACATCTCT	AGATAAAGAT	CCAGACTTAT	TTGCCTTTAA	CAACCAAGGT	3060
GTTTCATGCAG	AATCCACTAG	TGGTTCTAAG	ATTGCTAACA	TTTATCCTTT	AGATTCAAAT	3120
GGAAATCCTC	AAGATGCTCA	ACTAGAAAGA	GGACTAACTC	CATCTCCACT	TGTTCTAAGA	3180
AGTGCAGAAG	AAGGACTAAT	TTCAATTGTA	AACACCAACA	AAGAAGGAGA	AAACCAAAAA	3240
GACCTTAAAG	TTGTATCAAG	AGAGCACTTC	ATAAGAGGAA	TTCTAAATTC	TAAGGGAAAT	3300
GACGCTAAGG	GTATCAAATC	ATCCAAACTA	AAAGTTTGGG	GTGACTTGAA	ATGGGATGGA	3360
CTCATCTATA	ACCCAAGAGG	TAGAGAAGAA	AATGCCCCAG	AAAGTAAGGA	TAACCAAGAT	3420
CCAGCTACTA	AGATACGAGG	ACAATTTGAA	CCGATTGCGG	AAGGTCAATA	TTTCTATAAA	3480
TTTAAATATA	GATTAACATA	AGATTACCCA	TGGCAGGTTT	CCTATATTCC	TGTAAAAATT	3540
GATAACACAG	CCCCTAAGAT	TGTTTCGGTT	GATTTTTCAT	ATCCTGAAAA	AATTAAGCTA	3600
ATCACAAAGG	ATACTTATCA	CAAGGTAAAA	GATCAATACA	AGAATGAAAC	TTTATTTGCT	3660
AGAGATCAAA	AAGAACATCC	TGAAAAATTT	GATGAGATTG	CAAATGAGGT	GTGGTATGCA	3720
GGAGCTGCTC	TTGTTAATGA	AGATGGAGAG	GTTGAGAAAA	ATCTTGAAGT	AACTTATGCA	3780
GGTGAGGGTC	AAGGAAGAAA	TAGGAAGCTT	GATAAAGATG	GGAATACTAT	CTATGAAATT	3840
AGCGGAGCAG	GAGATCTAAG	AGGAAAAATC	ATCGAAGTAA	TCGCCCTAGA	TGGAGCAAGC	3900
AACTTTACCA	AAATCCATAG	GATTAAATTT	GCTAATCAAG	CTGATGAAAA	AGGGATGATT	3960
TCTTATTATC	TAGTAGATCC	TGATCAGGAT	TCATCTAAAT	ACCAAAAGCT	TGGCGAAATT	4020
CCTGAATCTA	AATTTAAGAA	TTTAAAAAAT	GTTAAAGATG	ATAGCCTAAA	CAAAGAGACA	4080
GCTGAGGTGG	AAAATAACCT	TTTAGTAGAT	AATCAGTCTA	TCGAAGGAAA	ATCTCTCTTT	4140
AATATTCCATA	AAACTATTTT	AACAATTAGA	GACTTTGAAA	ATAAAGACCT	AAAGAAACTC	4200
ATTAAAAAGA	AATATAAGCA	AGAAGACGAC	TTTGTAAATG	GTGGAACAAG	AACAGTAGAG	4260
CGTGATTATA	AATACGATGA	TAAAGGAAAT	ATAATAGCCT	ACGATGATGG	GACTGATCTA	4320
GAATATGAAA	CTGAGAAACT	TGACGAAATC	AAATCAAAAA	TTTATGGTGT	TCTAAGTCCG	4380
TCTAAAGATG	GACACTTTGA	AATTCCTTGA	AAGATAAGTA	ATGTTTCTAA	AAATGCCAAG	4440
GTATATTATG	GGAATAACTA	TAAATCTATA	GAAATCAAAG	CGACCAAGTA	TGATTTCCAC	4500
TCAAAAACGA	TGACATTTGA	TCTATACGCT	AATATTAATG	ATATTGTGGA	TGGCATTAGC	4560
TTTTGCAGGA	GATATGAGAT	TATTTGTTAA				4590

(2) INFORMATION FOR SEQ ID NO:2169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1440 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1440
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2169:

GGAATTAAAA	TGAGTATTTT	AGAAGTTAAA	AATCTGAGTC	ACGGTTTTTG	TGACCGTGCA	60
ATTTTGAAG	ATGTGTCCTT	CCGTCTCCTC	AAGGGAGAAC	ATATCGGCCCT	GGTCGGTGCC	120
AATGGTGAAG	GAAAATCAAC	CTTTATGAGT	ATCGTGACTG	GTAAAATGCT	GCCAGATGAA	180
GGAAAGGTTG	AGTGGTCCAA	ATATGTGACG	GCTGGTTACT	TGGATCAGCA	CTCTGTCCTT	240
GCTGAAAGAC	AGTCGGTGCG	TGATGTTCTC	CGTACGGCTT	TTGATGAGCT	TTTCAAAGCT	300
GAAGCTCGTA	TCAATGACCT	CTATATGGAA	ATGGCTGAAG	ACGGTGCGGA	TGTTGATGCT	360
CTCATGGAAG	AAGTAGGAGA	ACTTCAAGAC	CGTCTGGAGA	GTCGTGATTT	CTATACCTTG	420
GATGCTAAGA	TTGACGAAGT	AGCGCGTGCT	CTTGGTATTA	TGGACTTTTG	CATGGATACG	480
GATGTAACCT	CTTTGTCAGG	TGGGCAAAGA	ACCAAGGTGC	TTTTGGCAAA	ACTTCTCCTT	540
GAAAAGCCTG	ATATTTTGCT	GTTGGACGAG	CCGACCAACT	ACTTGGATGC	TGAGCATATT	600
GATTGGCTCA	AGCGCTATCT	CCAAAACAT	GAGAATGCCT	TTGTTCTCAT	TTCGCACGAT	660
ATTCCATTCC	TCAATGACGT	TATCAATATT	GTCTATCATG	TGGAAAATCA	ACAGCTGACG	720
CGTTACTCTG	GTGACTACTA	CCAGTTCCAA	GAAGTTTATG	CTATGAAGAA	ATCTCAGCTA	780
GAGGCAGCCT	ACGAACGCCA	GCAGAAAGAG	ATTGCAGACC	TCAAGGACTT	TGTGGCTCGT	840
AATAAGCCC	GTGTTGCAAC	TCGTAATATG	GCTATGTCTC	GTCAAAAGAA	ATTGGATAAG	900
ATGGATATTA	TCGAACTCCA	AAGTGAGAAA	CCAAAACCAT	CCTTTGATTT	CAAACCAGCT	960
CGTACACCAG	GGCGCTTTAT	CTTCCAAGCC	AAGAACTTGC	AAATTGGTTA	CGACCGTCCT	1020
CTTACTAAGC	CTTTAAATCT	TACCTTCGAA	CGCAATCAAA	AGGTTGCGAT	TATTGGTGCT	1080
AATGGTATTG	GAAAAACAAC	TCTCTTGAAG	AGTCTCTTGG	GCATTATCTC	GCCAATCGCT	1140
GGGGAAGTGG	AGCGTGGAGA	TTATTTAGAA	CTTGTTTATT	TTGAGCAGGA	AGTAGAAGGT	1200
GGTAATCGCC	AAACTCCTCT	TGAAGCTGTC	TGGAATGCCCT	TTCTTGCCCT	TAATCAAGCA	1260
GAAGTCCGTG	CAGCCCCTTG	CCGTTGTGGT	TTGACAACCA	AACATATTGA	AAGCCAGATT	1320
CAAGTATTAT	CAGGGGGAGA	GCAAGCCAAG	GTTTCGTTTCT	GTCTCTTGAT	GAATCGTGAA	1380
AACAACGTTT	TAGTGCTGGA	CGAGCCGCAC	CAACCATTTG	GATGTGGATG	CAAAGGATGA	1440

(2) INFORMATION FOR SEQ ID NO:2170:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1287 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2170:

GGTTCTAAAA	TGAGGGAACC	AGATTTTTTTA	AATCATTTTTC	TCAAGAAGGG	ATATTTTCAAA	60
AAGCATGCTA	AGGCGGTTCT	AGCTCTTTCT	GGTGGATTAG	ATTCTATGTT	TCTATTTAAG	120
GTATTGTCTA	CTTATCAAAA	AGAGTTAGAG	ATTGAATTGA	TTCTGGCTCA	TGTGAATCAT	180
AAGCAGAGAA	TTGAATCAGA	TTGGGAAGAA	AAGGAATTAA	GGAAGTTGGC	TGCTGAAGCA	240
GAGCTTCCTA	TTTATATCAG	CAATTTTTCA	GGAGAATTTT	CAGAAGCGCG	TGCACGAAAT	300
TTTCGTTATG	ATTTTTTTCA	AGAGGTTATG	AAAAAGACAG	GTGCGACAGC	TTTAGTCACT	360
GCCCACCATG	CTGATGATCA	GGTGGAAACG	ATTTTGATGC	GCTTGATTCT	AGGAACTCGC	420
TTGCGCTATC	TATCAGGAAT	TAAGGAGAAG	CAAGTAGTCG	GAGAGATAGA	AATCATTCGT	480
CCCTTCTTGC	ATTTTCAGAA	AAAAGACTTT	CCATCAATTT	TTCACTTTGA	AGATACATCA	540
AATCAGGAGA	ATCATTATTT	TCGAAATCGT	ATTTCGAACT	CTTACTTACC	AGAATTGGAA	600
AAAGAAAATC	CTCGATTTAG	GGATGCAATC	TTAGGCATTG	GCAATGAAAT	TTTAGATTAT	660
GATTTGGCAA	TAGCTGAATT	ATCTAACAAT	ATTAATGTGG	AAGATTTACA	GCAGTTATTT	720
TCTTACTCTG	AGTCTACACA	AAGAGTTTTA	CTTCAAACCT	ATCTGAATCG	TTTTCCAGAT	780
TTGAATCTTA	CAAAAGCTCA	GTTTGCTGAA	GTTTCAGCAGA	TTTTAAAATC	TAAAAGCCAG	840
TATCGTCATC	CGATTAAAAA	TGGCTATGAA	TTGATAAAAG	AGTACCAACA	GTTTCAGATT	900
TGTAAAATCA	GTCCGCAGGC	TGATGAAAAG	GAAGATGAAC	TTGTGTTACA	CTATCAAAAT	960
CAGGTAGCTT	ATCAAGGATA	TTTATTTTCC	TTTGGACTTC	CATTAGAAGG	TGAATCAATT	1020
CAACAAATAC	CTGTTTCACG	TGAAACATCC	ATACACATTC	GTCATCGAAA	AACAGGAGAT	1080
GTTTTGATTC	AAAAATGGGCA	TAGAAAAAAA	CTCAGACGTT	TATTTATTGA	TTTGAAAAATC	1140
CCTATGGAAA	AGAGAAACTC	TGCTCTTATT	ATTGAGCAAT	TTGGTGAAAT	TGTCTCAATT	1200
TTGGGAATTG	CGACCAATAA	TTTGAGTAAA	AAAACGAAAA	ATGATATAAT	GAACACTGTA	1260
CTTTATATAG	AAAAAATAGA	TAGGTAA				1287

(2) INFORMATION FOR SEQ ID NO:2171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 387 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2171:

TATAATAAAA	TAATAGAAAA	CGCTATTAAA	AGAAGGAGGG	GGATGTCGGT	GATGGAACAT	60
TTGTTTAAAT	TCTTACTTTT	AGCACCGTAC	TTTTATTTTG	ATAACTGGAT	TGAAAAGGCC	120
AACAGAAATA	GTAAGTTTTT	TCCAATTTTT	TATTATTTTT	ACTGGATTTA	CATCCCCTTC	180
TATTCTCTTT	TTAGCCTTGC	TTGGACAGTT	GTTTCAGTTC	TGTTTTTCAA	TACCGTCTTG	240
AGAAATGTGA	CAGATATCAA	GTTATGGGGC	ATTTGGTTTC	TTTTTATTCT	GCTAGCTATT	300
GGTATGAATT	GGTAACTTA	TTCCTGTTTC	AAAGAAATGT	TTCGCTTGAG	ACAGGAACTA	360
GGGAAGTCTA	AGGGTGGAAG	GCATTGA				387

(2) INFORMATION FOR SEQ ID NO:2172:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...327
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2172:

ACTGGTAAAA	TACACAAAAT	CGGTGAACTC	ACGAGGTGCG	TCACAAATGG	ACTGGATGGA	60
GCAAGAGCAA	GAACGTGGTA	TCACGATCAC	ATCTGCTGGC	GGACAACAGC	TCAATGGAAC	120
AACCACCGCG	TAAACATCAT	CGACACACCA	GGACACGTGG	ACTTCACAAT	CGAAGTACAA	180
CGTTCTCTTC	GTGTATTGGA	TGGTGCGGTT	ACCGTTCTTG	ACTCACAATC	AGGTGTTGAG	240
CCTCAAACCTG	AAACAGTTTG	GCGTCAACAA	CTGAGTACGG	AGTCCACGTA	TCGTATTTGC	300
CAACAAAATG	GACAAAATCG	GTGCTGA				327

(2) INFORMATION FOR SEQ ID NO:2173:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 666 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2173:

GGAGGTAAAA	TCGTGGGTCA	AAAAGTACAT	CCAATTGGTA	TGCGTGTCGG	CATCATCCGT	60
GATTGGGATG	CCAAATGGTA	TGCTGAAAAA	GAATACGCGG	ATTACCTTCA	TGAAGATCTT	120
GCAATCCGTA	AATTCGTTCA	AAAAGAACTT	GCTGACGCAG	CAGTTTCAAC	TATTGAAATC	180
GAACGCGCAG	TAAACAAAGT	TAACGTTTCA	CTTCACACTG	CTAAACCAGG	TATGGTTATC	240
GGTAAAGGTG	GTGCTAACGT	TGATGCACTC	CGTGCAAAAC	TTAACAAATT	GACTGGAAAA	300
CAAGTACACA	TCAACATCAT	CGAAATCAAA	CAACCTGATT	TGGATGCTCA	CCTTGTAGGT	360
GAAGGAATTG	CTCGTCAATT	GGAGCAACGT	GTTGCTTTCC	GTCGTGCACA	AAAACAAGCA	420
ATCCAACGTG	CAATGCGTGC	TGGAGCTAAA	GGAATCAAAA	CTCAAGTATC	AGGTCGTTTG	480
AACGGTGCAG	ATATCGCCCC	TGCTGAAGGA	TACTCTGAAG	GAAGTGTTC	GCTTCACACA	540
CTTCGTGCAG	ATATCGATTA	CGCTTGGGAA	GAAGCAGATA	CTACATACGG	TAAACTTGGT	600
GTAAAGTAT	GGATCTACCG	TGGTGAAGTT	CTTCCAGCTC	GTAAAAACAC	TAAAGGAGGT	660
AAATAA						666

(2) INFORMATION FOR SEQ ID NO:2174:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 282 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2174:

GAGATCAAAA	TTAAGCTCGT	GTTTGGAAAA	TTTTCTCTAA	TAGCTTTCAA	GAGCTTGGAC	60
TCTGTAATGG	TATCCAGTGC	CGAGGTTGCA	TCATCTAGGA	TGAGAAACGG	AGCTTGGCGC	120
AAGACTGCTC	GGGCGATAGA	CAATCTTTGT	TTTTGTCCAC	CTGAGAAATT	TCGCCCCCCT	180
GCCTCAACTA	GAGCATCCAA	GAGTCCTTCC	TTTTCACTGA	CAAAATCCTT	AGCTTGCGCA	240
ATCTCCAAGG	CCTGCCAGAG	TTCTTGGTCA	GATACTTCTT	GA		282

(2) INFORMATION FOR SEQ ID NO:2175:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2175:

TCCTCCAAAA	TAGTTTATAC	GGGAACAAGC	CCGTGTCCTC	TTAGTGAACA	GATAATATTC	60
CAATCCCCTA	GTAATGGACT	AAACACTATG	GGCACGAGTG	GACTCGAACC	ACCGACCTCA	120
CGCTTATCAG	GCGTGCGCTC	TAACCACCTG	AGCTACGCGC	CCAAGTCAAA	AACTTGGTAC	180
AAAGAACAAA	GTTCAAAGCG	GGTGACGAGA	ATCGAACTCG	CGACAACAGC	TTGGAAGGCT	240
GTAGTTTTAC	CACTAAACTA	CACCCGCTAA				270

(2) INFORMATION FOR SEQ ID NO:2176:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1128 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2176:

TTTAACAAAA	TAAAGGAGAA	AAACATGGTT	AAATACGGTG	TTGTTGGAGC	AGGGTATTTT	60
GGAGCTGAAT	TGGCTCGCTA	TATGCAAAAG	AATGATGGAG	CAGAGATTAC	TCTTCTCTAT	120
GATCCAGATA	ATGCAGAGGC	GATTGCAGAA	GAATTGGGAG	CAAAAGTAGC	AAGTTCCTTA	180
GATGAGTTGG	TTTCTAGCGA	TGAAGTAGAT	TGTGTTATCG	TCGCCACTCC	AAATAATCTT	240
CATAAGGCAC	CGGTTATTAA	GGCTGCACAG	CATGGTAAAA	ATGTTTTCTG	TGAAAAACCA	300
ATTGCGCTTT	CTTATCAAGA	TTGTCGCGAG	ATGGTAGATG	CGTGTAAGA	AAACAATGTA	360
ACCTTTATGG	CAGGACATAT	TATGAATTTT	TTTAATGGTG	TTCATCATGC	AAAAGAACTC	420
ATTAATCAAG	GAGTTATCGG	AGACGTTCTA	TATTGTCATA	CAGCTCGTAA	TGGTTGGGAA	480
GAACAACAAC	CGTCAGTATC	ATGGAAAAAA	ATTCGTGAAA	AATCAGGTGG	TCACTTGTAT	540
CACCACATCC	ATGAATTGGA	TTGCGTTCAA	TTCTTTATGG	GGGGCATGCC	TGAAACTGTA	600
ACCATGACAG	GTGGAAATGT	GGCCCATGAA	GGTGAACATT	TCGGTGATGA	AGATGATATG	660
ATTTTTGTCA	ATATGGAATT	TTCTAATAAG	CGTTTTGCCT	TGTTAGAATG	GGGTTCAGCT	720
TATCGTTGGG	GTGAACATTA	TGTCCTTAATC	CAAGGAAGCA	AAGGTGCCAT	CCGCTTAGAC	780
TTATTCAACT	GTAAAGGAAC	TCTTAAGCTA	GATGGGCAAG	AAAGCTATTT	CTTGATTCCAC	840

GAATCGCAAG	AAGAAGATGA	TGATCGGACT	CGTATCTATC	ATAGTACAGA	GATGGATGGA	900
GCAATTGCTT	ATGGTAAACC	AGGTAAACGT	ACTCCATTAT	GGCTATCATC	TGTCATTGAT	960
AAAGAAAATGC	GCTATCTGCA	TGAGATTATG	GAAGGAGCTC	CAGTATCAGA	AGAATTTGCA	1020
AAACTTTTGA	CAGGTGAAAGC	TGCCCTAGAA	GCAATTGCTA	CTGCAGATGC	TTGTACCCAG	1080
TCTATGTTTG	AAGATCGCAA	AGTAAATTTG	TCAGAAATTG	TAAATAA		1128

(2) INFORMATION FOR SEQ ID NO:2177:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1326 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1326
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2177:

GACAACAAAA	TCAAGCTCTT	GCAAGAATTG	AAAGAGCAGG	TTGAGGTTGG	GACTGCCATT	60
AATGCTAGTA	ACATTGAACA	TTCCAAAGCA	CGTGGCGACT	TAGGCATTTT	TTATGACCAA	120
GAGTTCTTTC	GTTTGATTGA	CAAATTCAAT	GAATTAGGGA	TTTTTGTGG	TTCCGTTGTC	180
ATTACACAAT	ACACTGGCCA	ACCCGCTGCA	GATGCCTTCC	GCAACCAACT	TGAGAAAAAC	240
GGAATTGATT	CTTATCTTCA	TTATCCAATC	AAAGGATATC	CGACGGATAT	GGATCACATC	300
ATTTCTCTCA	AAGGCATGGG	CAAAAACGAC	TACATCAAAA	CCAGTCGCAA	CTTGATTGTC	360
GTAACCGCTC	CTGGACCCGG	TTCTGGAAAA	TTGGCAACGT	GTATGTCCAA	TATGTACCAC	420
GACCAAATCA	ATGGCATCAA	GTCTGGCTAC	GCTAAATTTG	AAACCTTCCC	TGTTTGGAAT	480
CTTCCCCCTC	ATCATCCAAGT	TAACTTGGCT	TATGAAGCTG	CCACAGCTGA	CCTTGATGAT	540
GTCAACATGA	TTGACCCCTT	CCATCTTCAA	ACCTATGGAG	AAACCACTGT	CAACTACAAC	600
CGTGATATCG	AAATCTTCCC	AGTGCTCAAG	CGCATGTTGG	AACGTATTCT	CGGAAATCA	660
CCATACGCTT	CACCGACAGA	TATGGGTGTC	AACATGGTTG	GTTTCGCTAT	TACAGATGAC	720
GAGGCTGCTG	TCGAAGCTTC	TAAACAAGAA	ATCATCCGCC	GTTACTATCA	AACAGTTCTT	780
GACTTCAAAG	CTGAAAAAGT	TGGCGAAGCT	GCCGTCAAGA	AAATTGAGTT	GCTCATGAAC	840
GACCTCGGTA	TCACACCTGC	AGACCGTAAG	GTTGCTGTCT	TTGCGCGCCA	AAAAGCAGAA	900
GAAACTGGTG	GACCAGCCCT	AGCCTTTGAA	TTGCCAAATG	GGGAAATCGT	CACTGGTAAG	960
AACTCAGAAC	TCTTTGGGCC	TACAGCCGCT	GCCTTGATCA	ACGCCATCAA	AAAATCAGCT	1020
GACATCGCTA	AAGAAGTAAA	ACTAATCGAG	CCTGAAGTTG	TTAAGCCAAT	CCAAGTCTT	1080
AAAATCGATC	ATCTCGGTAG	CCGCAATCCA	CGCCTTCATT	CAAATGAAAT	TCTGATTGCA	1140
CTTGCTATCA	CAGCTACAGA	AAATCCTGAT	GCTGCCCGCG	CTATGGAAGA	ACTCGGCAAC	1200
CTCAAAGGAA	GCGAAGCCCA	CTCAACCATC	ATCTTGACTG	ATGAAGACAA	GAATGTCCTT	1260
CGTAAACTGG	GTATCAACGT	AACCTTTGAC	CCATACTACC	AATACGACCG	CTTATATCGT	1320
AAGTAA						1326

(2) INFORMATION FOR SEQ ID NO:2178:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 900 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...900
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2178:

ATATTAAAAA	TAATTCCTTT	AGATATTTCC	ATAAGAGTTC	CTCCTCTTCA	TAAGTCTATC	60
CTATCACAAA	AACGAAAGAA	AAACAATTAC	GAACGAAAGT	TTAATTTGTT	GTTTTTTTGCT	120
TTTTATTTTG	GTAGAAATAA	ACGGAGGTGT	AAAATGAAAA	GATTGGAACA	AAATTATTAAA	180
TTAGTATCAG	AACATGAAAA	GATCGACGTT	AATACATTAT	CGGAAAAATT	AAATGTATCG	240
AAAGTAACGA	TTAGAAAAGA	TTTAGATAAA	TTAGAGTCAA	AAGGTTTATT	ACACAGAGAG	300
CATGGATATG	CTGTATTAAA	TAGTGGAGAT	GACTTAAATG	TACGTTTGTC	AATTAACTAT	360
GAAATTAAGA	GAATAATTGT	TCAGGAAGCA	GTAAAAATTG	TGTCAGATAA	TGAAACAATA	420
ATGATAGAA	CTGGATCGAC	CTGTGCTTTA	CTTGCTGAGG	AAATTTGCAA	GCAAAAAAGA	480
AATGTTACGA	TTGTAACAAA	TTCAATTTTT	ATAGCAAATT	TTGTGAGAGC	TTATGATTCA	540
TGTCGTATTA	TTGTTCTTGG	TGGAGAGTTT	CAGAAGGATT	CACAGGTTAC	TGTGGGACCT	600
TTATTAAAA	AAATGATACA	GACTTTTTCAT	GTGCGTCAAG	CTTTTGTGTT	GACAGATGGC	660
TACGATAAAG	AGATGGGCTT	TACAGGAAAA	GATTTAATGC	GCAGTGAGGT	AGTTCAATAT	720
ATTTTCAGCAG	CGTCGGATAA	AGTCATTGTA	CTAACTGACT	CAAGTAAATT	TGATAAAAGG	780
GGTACAGTAA	GAAGATTTGC	TTTAAGTCAA	GTCTATGAAG	TAATAACAGA	CGAAAAACTT	840
TCTAAACAAA	ATATAGCTAC	ATTAGAAAAT	GCTGGGATAA	TGGTTAAGGT	AGTTTCGTAA	900

(2) INFORMATION FOR SEQ ID NO:2179:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...240
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2179:

CCATTAAAAA	TCAAACAAAT	TTTCAGAATA	TTTAGGCTTG	TTGGCACAAA	TTTTTCATTT	60
TTTTTTGAAT	ATATGATTCA	AATTGTCTGT	CGAAGTGTCA	AAGACTACAG	TGAAAAATAGG	120
AAATTTGACG	CAGAACTTT	GGAGTTTAGG	AAGACATACA	GTAAAAATGAA	ATACGGACGG	180
AACAATGTGA	TTTTGGAAAT	CAAATTAAAT	TATAACAATA	TTGTAGAAGT	ATCATTCTAG	240

(2) INFORMATION FOR SEQ ID NO:2180:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 912 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...912
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2180:

CCCATAAAAA	TATACAGGAG	GCCTGATAAA	ATGGCAATCG	TTTCAGCAGA	AAAATTTGTC	60
CAAGCAGCCC	GTGACAACGG	TTATGCAGTT	GGTGGATTTA	ACACAAACAA	TCTTGAGTGG	120
ACTCAAGCTA	TCTTGCGCGC	AGCAGAAGCT	AAAAAAGCTC	CAGTTTTGAT	CCAAACTTCA	180
ATGGGTGCTG	CTAAATACAT	GGGTGGTTAC	AAAGTTGCTC	GCAACTTGAT	CGCTAACCTT	240
GTTGAATCAA	TGGGTATCAC	TGTACCAGTA	GCTATCCACC	TTGACCACGG	TCACTACGAA	300
GATGCACTTG	AGTGTATCGA	AGTTGGTTAT	ACTTCAATCA	TGTTTGACGG	TTCACACCTT	360
CCAGTTGAAG	AAAACTTTAA	ATTGGCTAAA	GAAGTTGTTG	AAAAAGCACA	CGCTAAAGGT	420
ATCTCAGTAG	AAGCTGAAGT	TGGTACTATC	GGTGGTGAAG	AAGACGGAAT	CATCGGTAAA	480
GGTGAATTGG	CTCCAATCGA	AGACGCTAAA	GCAATGGTTG	AAACTGGTAT	CGACTTCTTG	540
GCAGCTGGTA	TCGGTAACAT	CCACGGTCCT	TACCCAGTAA	ACTGGGAAGG	TCTTGACCTT	600
GACCACTTGC	AAAAATTGAC	AGAAGCTCTT	CCAGGATTCC	CAATCGTATT	GCACGGTGGA	660
TCAGGTATTC	CTGATGAGCA	AATCCAAGCA	GCTATCAAAC	TTGGTGTTCG	CAAAGTTAAC	720
GTTAACACAG	AATGCCAAAT	CGCATTCGCT	AACGCAACTC	GTAAATTTGC	TCGTGACTAC	780
GAAGCAAACG	AAGCAGAATA	CGACAAGAAA	AACTCTTCG	ACCCACGTAA	ATTCTTGGCT	840
GACGGTGTA	AAGCTATCCA	AGCATCGGTT	GAAGAACGTA	TCGACGTATT	CGGTTAGAA	900
GGTAAAGCAT	AA					912

(2) INFORMATION FOR SEQ ID NO:2181:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2181:

NNNNNAANNNN	NNNNNAAAAA	AAAAAAAANN	NANNNNNNNN	AAAAGGGAAA	NNAAAAA	60
GAGGGAAANN	NGAAGGGGGG	GGAGAAAANG	GGGAGGGAGG	GAAAGGAGGA	AGAAGGNGGG	120
GTGANGGNNG	GGGGGGGGAA	AAGAAGGAAA	AAAAGGGTGT	TGNGGGAGGT	NTGGGGAAAA	180
AGGGGGAAGG	AAAAGGNGGG	GNNGGGGGGA	GGTTGGGAGG	GGGAAAGAAA	GGAAGAAANG	240
GGAATGGGGG	TGGGTGTGGG	GGAAAGTGAA	AAAAAA			276

(2) INFORMATION FOR SEQ ID NO:2182:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 888 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2182:

AAAGCAAAAA	TGAACGGTAT	TATCAACTTA	AAAAAAGAAG	CAGGAATGAC	CTCGCATGAT	60
GCGGTTTTTA	AACTGCGTAA	GATTTTGGGA	ACCAAGAAAA	TTGGTCATGG	CGGAACCTTG	120
GATCCGGATG	TGGTGGGTGT	TTTGCCGATT	GCGGTTGGCA	AGGCGACACG	CATGGTCGAG	180
TTTATGCAGG	ACGAGGGTAA	GATCTATGAG	GGGGAAATCA	CTCTGGGTTA	TTCCACGACG	240
ACTGAGGATG	CTAGTGGGGA	AGTGGTCGCA	GAAACCCCTG	TTTTGTCTCC	CTTGGATGAA	300
AAGCTTGTTG	ATGAAGCGAT	TGCTAGCTTG	ACTGGGCCTA	TTACCCAGAT	TCCCCCTATG	360
TATTCGGCAG	TTAAGGTTAA	TGGTCGCAAG	CTCTATGAGT	ATGCGCGTGC	TGGTCAGGAA	420
GTGGAGCGTC	CAGAACGTCA	GGTGACCAT	TATCAATTTG	AGCGAACAAG	TCCGATTTCT	480
TATGATGGCC	AACTTGCCCC	ATTCACTTTT	CGTGTAATA	GCAGTAAAGG	GACTTACATC	540
CGTACTTTGT	CAGTTGATTT	GGGTGAAAAG	CTTGGTTATG	CGGCTCATAT	GTCCCATTTG	600
ACTCGTACTA	GTGCTGCTGG	CTTACAATTA	GAAGACGCTC	TTTCCTTGGA	GGAAATTGCT	660
GAAAAAGTAG	AGGCTGGGCA	ATTAGATTTT	CTCCATCCTT	TAGAGATTGG	GACAGGTGAC	720
CTTGTCAAAG	TTTTCCTAAC	TCCAGAAGAG	GCTACAGAAG	TTCGCTTTGG	TCGTTTTATT	780
GAGCTAGACC	AAACGGACAA	AGAACTGGCT	GCCTTTGAAG	ATGATAAATT	GTTAGCCATT	840
CTAGAAAAAC	GGGGCAATCT	CTATAAGCCA	AGGAAGGTTT	TTAGCTAG		888

(2) INFORMATION FOR SEQ ID NO:2183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2183:

TATAAAAAAA TTCAAACTAG AATTCTTCTT AGAAAAGGCC GTTTTAAGTG CTATCATTGC	60
TCAAAAATGG AGGTCGCTGA GACTTCTATC GTCAAGAAGA ATCATCAAAT TCCTTGTATC	120
ATCAACCAAA AGATTGATCA GAAGCTAATT GAAAAGACTT CTATGACCGA CATTGATCAT	180
CAGTTGTCTA TTTCAACTTC AACTGTCAAT CGCAAGATCA ATGATTTTCA CTTTGAGCAT	240
GATTTTTCGC GTCTTCCTGA GATTATGTCC TAG	273

(2) INFORMATION FOR SEQ ID NO:2184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2184:

GTNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNCA AAAAAANNNN NNNNNNNNGN	60
NNNNNNNNNN NGNGGGNNNN NGGGGNGNGG GGNGNNGGGG GGGGGGGGGG GGGGGGGGNG	120
GGGGGGGGGG GGGGGGGGGG GGGGGGNGGG NNGGGGGGGG GGGGGGGGNG GGGGGGGGGG	180
NGGGGNGGGN GGGGGGGGGG GGGG	204

(2) INFORMATION FOR SEQ ID NO:2185:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...327
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2185:

ATANNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NTGGGGGNAA	NNNAATANNN	60
NNAANNNNNN	NNNAAAAAAA	AAAAAANNNA	NNNNNNNNNA	AAGGGAAANN	AAAAAAAAGA	120
GGGAAANNNG	AAGGGGGGGG	AGAAAANGGG	GAGGGAGGGA	AAGGAGGAAG	AAGNGGGGGT	180
GANGGNNGGG	GGGGGGAAAA	GAAGGAAAAA	AAGGGTGTTG	NGGGAGGTNT	GGGGAAAAAG	240
GGGGAAGGAA	AAGNGGGGN	NGGGGGGAGG	TTGGGAGGGG	GAAAGAAAGG	AAGAAANGGG	300
AATGGGGGTG	GGTGTGGGGG	AAAGTGA				327

(2) INFORMATION FOR SEQ ID NO:2186:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1002 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1002
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2186:

TTNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNA	CAGTAATTTT	CTTTGGTTTG	60
CTAGCTACGA	ATACAGTATT	TGCAGATAAC	TCTGAAGTAT	GGCAGTTTGT	CCAAGAAAAC	120
GGTAGAACCT	ATTACAAAAA	GGGGGACCTC	AAAGAAACCT	ACTGGCGAGT	GATTGATGGT	180

AAGTACTATT	ATTTTGATTC	TCTATCTGGA	GAGATGGTTG	TCGGCTGGCA	ATATATCCCCG	240
TTTCCATCTA	AAGGTAGTAC	AATTGGTCCT	TACCCAAATG	GTATCAGATT	AGAAGGTTTTT	300
CCAAAGTCAG	AGTGGTACTA	CTTCGATAAA	AATGGAGTGC	TACAAGAGTT	TGT'TGGTTGG	360
AAAACATTAG	AGATTAAAAAC	TAAAGACAGT	GTTGGAAGAA	AGTACGGGGA	AAAACGTGAA	420
GATTCAGAAAG	ATAAAGAAGA	GAAACGTTAT	TATACGAACT	ATTACTTTAA	TCAAAATCAT	480
TCTTTAGAGA	CAGGTTGGCT	TTATGATCAG	TCTAACTGGT	ATTATCTAGC	TAAGACGGAA	540
ATTAATGGAG	AAAACACCT	TGGTGGTGAA	AGACGTGCGG	GGTGGATAAA	CGATGATTCCG	600
ACTTGGTACT	ATTTAGATCC	AACAACGGT	ATTATGCAAA	CAGGTTGGCA	ATATCTACGT	660
AATAAGTGGT	ACTACCTCCG	TTCCTCAGGA	GCAATGGCCA	CTGGCTGGTA	TCAGGAAGGT	720
ACCACTTGGT	ATTATTTAGA	CCAGCCAAAT	GGCGATATGA	AAACAGGATG	GCAAAACCTT	780
GGGAACAAAT	GGTACTATCT	CCGTTCGTCA	GGCGCCATGG	TGACTGGCTG	GGTGAAAGAT	840
GACTCAACTT	GGTATTACCT	AAATGCAGGT	AATGGAGACA	TGAAGACAGG	TTGGTTCCAG	900
GTCAATGGCA	GATGGTACTA	CGCTTATAGC	TCAGGTGCCT	TGGCAGTGAA	TACGACCGTA	960
GATGGCTATT	CTGTCAACTA	TAATGGCGAA	TGGGTTCCGT	AA		1002

(2) INFORMATION FOR SEQ ID NO:2187:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 204 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...204
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2187:

NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NANNNNNNNNN	NNNNNGNNNN	60
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	120
NNNNNNNNNN	NNNNNNNATT	TTATAACAAG	CCAAAAACAG	CGGATCATGT	GGTAGAGGAG	180
GAAGCACACG	ATGACTGGAT	CTAA				204

(2) INFORMATION FOR SEQ ID NO:2188:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1416 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2188:

GTGAAAAAAA	TGACAAAAAC	ACTTCCAAAA	GACTTTATTT	TCGGTGGCGC	AACAGCTGCT	60
TATCAAGCAG	AAGGTGCTAC	ACATACTGAT	GGAAAAGGAC	CAGTTGCTTG	GGATAAATAT	120
CTTGAGGATA	ACTACTGGTA	CAC TGCCGAA	CCAGCTAGTG	ATTTTTACAA	TCGATATCCA	180
GTTGACCTCA	AGCTAGCAGA	AGAGTATGGT	GTCAATGGTA	TTCGAATTTT	TATTGCTTGG	240
TCACGTATTT	TCCCGACTGG	TTACGGCCAA	GTAAATGCTA	AAGGTGTTGA	GTTTTATCAT	300
AATTTATTTG	CAGAGTGTC	CAAACGTCAT	GTTGAGCCTT	TTGTAACCT	TCATCACTTT	360
GACACTCCAG	AAGCTCTCCA	CTCAAATGGA	GACTTCTTAA	ACCGTGAAAA	TATCGAACAT	420
TTTGTAGACT	ACGCTGCCTT	CTGTTTTGAA	GAATTTCCAG	AAGTAAACTA	TTGGACAACC	480
TTTAATGAAA	TTGGACCAAT	CGGTGATGGT	CAATATTTGG	TTGGGAAATT	CCCTCCAGGT	540
ATCCAGTACG	ACCTTGCCAA	AGTCTTTCAA	TCACACCACA	ATATGATGGT	GTCTCATGCA	600
CGCGCGGTAA	AATTGTACAA	AGAGAAAGGC	TATAAAGGGG	AAATTGGTGT	TGTTCCAGCC	660
CTGCCTACTA	AATATCCTCT	AGATCCTGAA	AATCCAGCAG	ATGTTTCGTG	AGCTGAGTTG	720
GAAGATATCA	TCCACAATAA	ATTCATCTTA	GACGCAACTT	ATCTAGGTCG	CTATTCAGCT	780
GAAACCATGG	AAGGTGTCAA	CCATATCTTA	TTAGTCAATG	GTGGTAGTTT	GGATCTTCGT	840
GAAGAAGATT	TTACAGCATT	AGAAGCTGCA	AAAGACTTGA	ATGATTTTCT	AGGAATCAAC	900
TACTATATGA	GTGACTGGAT	GGAAGCCTTT	GATGGAGAAA	CTGAAATTAT	CCATAATGGT	960
AAAGGTGAAA	AAGGAAGCTC	TAAGTATCAA	ATCAAAGGTG	TTGGTCGTCG	TGTAGCTCCT	1020
GACTATGTAC	CACGCACGGA	TTGGGATTGG	ATTATCTACC	CTCAAGGTTT	GTATGACCAA	1080
ATCATGCGCG	TGAAGAAAGA	TTATCCTAAC	TATAAGAAAA	TCTACATCAC	TGAAAATGGT	1140
CTTGGATATA	AAGATGAGTT	CGTTGATAAC	ACTGTTTACG	ATGATGGTCG	TATTGATTAC	1200
GTGAAACAAC	ACTTGAGAT	CTTGTC TGAT	GCGATTGCAG	ATGGAGCTAA	TGTAAAAGGT	1260
TACTTCATTT	GGTCATTAAT	GGATGTCTTC	TCATGGTCAA	ACGGTTATGA	GAAACGTTAT	1320
GGTCTCTTCT	ACGTAGATTT	TGAAACTCAA	GAACGTTATC	CTAAGAAATC	AGCTCACTGG	1380
TACAAGAAAG	TAGCGGAAAC	TCAGATTATA	GACTAG			1416

(2) INFORMATION FOR SEQ ID NO:2189:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2189:

AAAGAAAAAA	TCGAAAAATT	AGCTAAGAAA	TATTCTGATA	ACTTAAACAT	CAAAGTTCAA	60
GAGAGAGTTC	GTGAAATGGC	AAATGATAAT	AAGAGCCATT	ATTTGATATA	CAGAGTTTTA	120
GGTATTTTCAT	TTGAAGAAGG	AGAAAATATC	GATTTGTATC	AAAATAAAGG	TCGTTTTTTA	180
TACAAATATG	CTGGTTCATT	TTTAGAAGAA	GCTGCAGTAC	TATCCTTTAA	CGAAAAATTT	240
GGTACAGAAA	ATACTTAA					258

(2) INFORMATION FOR SEQ ID NO:2190:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...237
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2190:

GGAGAAAAAA	TGAGTTACGA	ACAAGAATTT	ATGAAGGAAT	TTGAAGCTTG	GGTCAATACC	60
CAAATCATGA	TTAACGACAT	GGCGCACAAG	GAAAGCCAAA	AAGTTTACGA	AGAAGACCAG	120
GACGAGCGTG	CCAAAGATGC	CATGATTTCG	TACGAGAGTC	GCTTGGATGC	TTATCAGTTC	180
TTGCTTGGTA	AGTTTGAAAA	CTTCAAAGTA	GGCAAGGGAT	TCCATGATTT	GCCAGAA	237

(2) INFORMATION FOR SEQ ID NO:2191:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 888 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...888
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2191:

AAGGAAAAAA	TGACAAAAAA	AGTTGGTGTC	GGTCAGGCAC	ATAGTAAGAT	AATTTTAATA	60
GGGGAACATG	CGGTCGTTTA	CGGTTATCCT	GCCATTTCCC	TGCCCTCTTTT	GGAGGTGGAG	120
GTGACCTGTA	AGGTAGTTCC	TGCAGAGAGT	CCTTGGCGCC	TTTATGAGGA	GGATACCTTG	180
TCCATGGCGG	TTTATGCCCTC	ACTGGAGTAT	TTGGATATCA	CAGAAGCCTG	CATTCGTTGT	240
GAGATTGACT	CGGCTATCCC	TGAAAAACGG	GGGATGGGTT	CGTCAGCGGC	TATCAGCATA	300
GCGGCCATTG	GTGCGGTATT	TGACTACTAT	CAGGCTGATC	TGCCCTCATGA	TGTATTAGAA	360
ATCTTGGTCA	ATCGAGCTGA	AATGATTGCC	CATATGAATC	CTAGTGGTTT	GGATGCTAAG	420
ACCTGTCTCA	GTGACCAACC	TATTCGCTTT	ATCAAGAACG	TAGGATTTAC	AGAACTTGAG	480
ATGGATTTAT	CCGCTATTTT	GGTGATTGCC	GATACGGGTG	TTTATGGTCA	TACTCGTGAA	540
GCCATCCAAG	TGGTTCAAAA	TAAGGGCAAG	GATGCCCTAC	CGTTTTTTGCA	TGCCTTGGGA	600
GAATTAACCC	AGCAAGCAGA	AGTTGCGATT	TCACAAAAAG	ATGCTGAAGG	ACTGGGACAA	660
ATCCTCAGTC	AAGCGCATTT	ACATTTAAAA	GAAATTGGAG	TCAGTAGCCC	TGAGGCAGAC	720
TTTTTTGGTTG	AAACGACTCT	TAGCCATGGT	GCTCTGGGTG	CCAAGATGAG	CGGTGGTGGG	780
CTAGGAGGTT	GTATCATAGC	CTTGGTAACC	AATTTGACAC	ACGCACAAGA	ACTAGCAGAA	840
AGATTAGAAG	AGAAAGGAGC	TGTTTCAGACA	TGGATAGAGA	GCCTGTAA		888

(2) INFORMATION FOR SEQ ID NO:2192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2192:

GGCAGAAAAA	TGAAAACCAA	ACTACCGACT	GAATGGCAAG	AACTGAGTGA	CCAACTCGGT	60
TTCCAAGAAT	TCACCCCAT	TCAAACTCAA	CTATTTGATC	CCCTTCTTAC	TGGAGAAAAC	120
CTCCTAGGAG	TGAGCCAAAC	CGGAACTGGT	AAGACCCTAG	CGTATCTCCT	ACCAAGTCTT	180
CTCAGACTAC	AAAAGAAAAA	AGCCCAACAA	CTCTTGATTG	TAGCACCAA	CACGGAACCT	240
GCTGGACAGA	TTTTTGATGT	ATGTAAAACG	TGGGCAGAAG	CTATCGGATT	GACTGCTCAA	300
CTCTTCCTTT	CAGGTTCAAG	TCAGAAACGA	CAAATTGAAC	GCCTTAAAAA	GGGGCCAGAA	360
ATTCTGATTG	GAACCTCTGG	CCGTATCTTT	GAACTCATTA	AACTTAAAAA	AATCAAGATG	420
ATGAATGTGG	AAACCATCAT	CCTGGATGAA	TTTGACCAAT	TACTAGATGA	TTCTCAGATT	480
CACTTTGTAG	AAAAATCAC	TCACTACGCA	CCTCGTGACC	ACCAACTGGT	CTACATGAGT	540
GCCACGACCA	AGTTTGATCA	AGAAAAGATT	GTGCCGAATA	CACGCACTAT	TGATCTCTCT	600
AATCAAAAAT	TGGACAATAT	CCAGCATTTT	TACATGCAGG	TAGACCAACG	TCATCGAGTG	660
GATATACTAC	GAAAACGGC	TCATGTAGAG	GATTTCCGTG	GTCTAGTCTT	CTTCAATAGC	720
CTGTCTAGAC	TTGGGAATGC	CGAGGAAAAA	CTACAGTATC	GTGATATATT	GGCTGTTTCC	780
CTCGCTAGTG	ATGTTAATGT	TAAATTTAGA	AAAGTCATCT	TAGAAAAGTT	TAAAGATAAC	840
CAACTAACCC	TGCTTCTTGC	AACTGACCTT	TTGGCTCGTG	GAATTGATAT	CGATAGCCTA	900
GAATGTGTCTG	TAAACTTTGA	TATTCCTAGA	GATAGCGAAA	CCTACACACA	CCGTGCTGGC	960
CGTACTGGCC	GTATGGGCAA	GGAAGGATAT	GTTATTACTC	TCGTCACTCA	TCCAGAAGAA	1020
ATCAAAAAAC	TTAAAAAGTT	TGCAAGTATC	CGAGAAATTG	TCCTAAAAAA	CCAAGAACCT	1080

(2) INFORMATION FOR SEQ ID NO:2193:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 660 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...660
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2193:

AGTATGAAAA	TTTAAATTGT	AGAAGATGAA	GAGATGATCC	GTGAGGGGGT	CAGTGATTAT	60
TTGACGGATT	GTGGCTATGA	AACTATTGAG	GCAGCGGACG	GTCAGGAAGC	TCTGGAGCAA	120
TTTTCTAGCT	ATGAGGTGGC	CCTGGTTTTA	CTGGATATCC	AGATGCCCAA	GCTTAACGGC	180
TTAGAAGTTC	TAGCTGAGAT	TCGTAAAACC	AGTCAGGTTT	CTGTCTTGAT	GTTGACAGCT	240
TTTCAGGATG	AGGAATACAA	GATGAGTGCC	TTTGCCTCTT	TGGCAGATGG	CTATCTGGAA	300
AAACCTTTCT	CCCTCTCCCT	CTTAAAAGTG	AGGGTGGACG	CGATTTTCAA	GCGCTACTAC	360
GATACAGGAC	GAATCTTTTC	TTACAAGGAT	ACCAAGGTGG	ACTTTGAAAG	CTACAGTGCA	420
AGCCTCGCAG	GTCAAGAAAGT	GCCTATCAAT	GCCAAAGAGT	TGGAAATTCT	GGACTATCTA	480
GTGAAAAATG	AAGGCCGGGC	CTTGACTCGG	TCTCAGATTA	TCGATGCCGT	CTGGAAAGCG	540
ACAGATGAGG	TTCCCTTTGA	CCGTGTTATT	GATGTTTATA	TCAAGGAATT	GCGGAAAAAG	600
CTAGACTTGG	ATTGTATCCT	CACTGTGCGC	AATGTTGGTT	ATAAATTGGA	GCGAAAATGA	660

(2) INFORMATION FOR SEQ ID NO:2194:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 528 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2194:

AAAATGAAAA	TCGCAATTAT	CGGATATTCT	GGTTCTGGTA	AGTCAACTCT	AGCAGAAAAG	60
TTATCTAACT	ACTACTCCAT	TCCAAAACCTG	CACATGGACA	CACTCCAATT	TCAACCTGGT	120
TGGCAAGACA	GTGACCACGA	ATGGATGTTA	ACCGAGATAA	AAAACTTTCT	CACCAAGCAT	180
AAAGCTTGGG	TCATCGATGG	TAATTATTCT	TGGTGCTACT	ACCAAGAACG	AATGCAAGAA	240
GCTGACCAAA	TCATCTTTCT	CAATTTTTTG	CCATTGACCT	GTCTCTTTAG	AGCCTTTAAG	300
CGTTATCTTA	AATACCGTGG	AAAAGTCAGA	GAAAGTATGG	CGGCAGATTG	CCCTGAACGC	360
TTTGACTGGG	AGTTTATCAG	ATGGATTCTT	TGGGATGGAC	GTAGCAAAAC	TCAAAAAGAA	420
AATTACCAAA	AACTTTGCCA	AGAATATTCA	CATAAAGTCA	CTATTCTTCG	AAATCAGAGA	480
GAGCTAGATC	AATTTCTGGA	TAAGAAAAGG	AAGTCCTACA	ATTCATAA		528

(2) INFORMATION FOR SEQ ID NO:2195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2195:

ATAAAGAAAA	TCCCGTTGCA	AGACGGGGTT	TTGTGTTATA	ATAGAGACAT	GAAAACAAAT	60
GATATTGTCT	ATGGTGTCCA	CGCCGTTACC	GAAGCCCTCC	TTGCAAATAC	AGGAAACAAA	120
CTCTACCTCC	AAGAAGATCT	CCGAGGTAAG	AATGTTGAGA	AAGTCAAGGA	ACTAGCTACA	180
GAAAAGAAGG	TGTCCATTTC	TTGGACATCA	AAAAAATCTC	TCTCTGAGAT	GACTGAAGGT	240
GCTGTTTCATC	AAGGTTTTGT	TCTACGAGTG	TCTGAATTTG	CCTATAGCGA	GCTAGATTAC	300
ATCCTTGCAA	AAACACGCCA	AGAAGAAAAT	CCACTTCTAT	TGATTCTAGA	TGGTCTAACC	360
GATCCCCATA	ATCTGGGTTT	TATCTTGCGA	ACAGCCGATG	CGACCAATGT	TTCAGGTGTC	420
ATCATTTCCA	AGCACCGTGC	TGTCGGAGTA	ACTCCTGTCT	TTGCCAAAAC	AGCCACAGGT	480
GCTATTGAAC	ACGTTCCAAT	TGCCCGAGTG	ACAAACCTCA	ATCAAACCTT	ATATAAACTC	540
AAGGATGAAG	GCTTCTGGAC	CTTTGGAACG	GATATGAACG	GTACTCCTTG	CTACAAGTGG	600
AATACAAAAG	GGAAAATCGC	CCTCATCATT	GGAAATGAAG	GAAAAGGTAT	CTCTAGCAAC	660
ATCAAAAAAC	AAGTCGATGA	GATGATTACC	ATTCCGATGA	ATGGACATGT	TCAAAGCCTT	720
AATGCCAGTG	TTGCTGCGGC	CATTCTCATG	TACGAAGTTT	TCCGAAATAG	ACTATAA	777

(2) INFORMATION FOR SEQ ID NO:2196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2196:

TCCGAGAAAA	TCTTGCAACG	CTTAGAAGTC	TATAAAAACT	ATCAACATTT	ATATGACTTG	60
CGAATGACAA	TTCTATTAAA	CCTTTCCACA	CTCTATCTAT	ACAATCAAGA	TAAAAACATG	120
TGTAAGCAAA	TCTGCTACAC	TTTACTGGAG	GACGCCAAGA	ATAAGAAAAG	CTACGATAGG	180
CTGGCTATCT	GCTATGTCGG	CATTGGGATT	TGTAGGGATA	ATGCGAAACT	TATCCAAAAA	240
GGGTTCTCAC	TCCTAGAGCT	GACCGAGGAA	ACTTCTATGC	TGTCTCATCT	CAAAAAAGAA	300
GTAGAGATCT	ATTACCAAGC	GAAGGAAAGA	TAA			333

(2) INFORMATION FOR SEQ ID NO:2197:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 621 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2197:

GGAGAGAAAA	TGTCTGCAAT	AGAACGTATT	ACAAAAAGCTG	CTCACTTAAT	TGATATGAAC	60
GATATTATCC	GTGAAGGGAA	TCCTACTCTA	CGCGCGATTG	CTGAGGAAGT	CACTTTCCCC	120
CTATCTGACC	AGGAAATCAT	CCTAGGCGAA	AAGATGATGC	AATTCCCTTAA	ACATTCCCCAA	180
GATCCTGTCA	TGGCTGAAAA	AATGGGACTC	CGCGGTGGTG	TTGGACTGGC	TGCTCCCCAG	240
TTAGATATCT	CAAAACGCAT	TATCGCTGTT	TTGGTACCTA	ATATTGTTGA	AGAAGGCGAA	300
ACTCCACAGG	AAGCCTACGA	TTTGGAAGCC	ATTATGTACA	ATCCAAAAAT	CGTCTCTCAC	360
TCTGTTCAAG	ATGCTGCTCT	TGGCGAAGGA	GAAGGTTGCC	TGTCTGTTGA	CCGTAACGTG	420
CCTGGCTATG	TTGTTTCGCCA	TGCCC GCGTT	ACTGTTGACT	ACTTTGACAA	AGATGGAGAA	480
AAACACCGTA	TCAAAC TCAA	AGGCTACAAC	TCCATTGTTG	TTCAGCATGA	AATTGACCAC	540
ATTAACGGTA	TCATGTTTTA	CGATCGCATC	AATGAAAAAG	ACCCATTTCG	AGTTAAAGAT	600
GGTTTACTGA	TTCTTGAATA	A				621

(2) INFORMATION FOR SEQ ID NO:2198:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 552 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...552
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2198:

CAGGAGAAAA	TAAACATGTC	ACGTATTGGT	AATAAAGTTA	TCGTGTTGCC	TGCTGGTGTT	60
GAAGTCGCTA	ACAATGACAA	CGTTGTAAC	GTAAAAGGAC	CTAAAGGAGA	ACTTACTCGT	120
GAGTTCTCAA	AAGATATTGA	AATCCGTGTG	GAAGGTACTG	AAGTAACTCT	TCACCGTCCA	180
AACGATTCAA	AAGAAATGAA	AACTATCCAC	GGAAGTACTC	GTGCCCTTTT	GAACAACATG	240
GTGTTGGTG	TATCAGAAGG	ATTCAAGAAA	GAAGTTGAAA	TGCGTGGGGT	TGGTTACCGT	300
GCACAGCTTC	AAGGATCTAA	ACTTGTTTTG	GCTGTTGGTA	AATCTCATCC	AGACGAAGTT	360
GAAGCTCCAG	AAGGAATTAC	TTTTGAACTT	CCAAACCCAA	CAACAATCGT	TGTTAGCGGA	420
ATTTCAAAAAG	AAGTAGTTGG	TCAAACAGCT	GCTTACGTAC	GTAGCCTTCG	TTCACCAGAA	480
CCATATAAAG	GTAAAGGTAT	CCGTTACGTT	GGTGAATTTCG	TTCGCCGTAA	AGAAGGTAAA	540
ACAGGTAAAT	AA					552

(2) INFORMATION FOR SEQ ID NO:2199:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 792 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...792
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2199:

AAGGAGAAAA	TCATGCCAGT	AATGAAAATC	GAGTATTACT	CACAAGTATT	GGATATGGAG	60
TGGGGGATGA	ATGTCCTCTA	CCCTGATGCC	AATCGAGTGA	GAGAACCCAGA	GTGTGAAGAT	120
ATCCCCGTCT	TGTACCTTTT	GCACGGGATG	TCTGGAAAATC	ATAATAGTTG	GCTTAAGCGG	180
ACCAATGTAG	AACGCTTGCT	TCGAGGAACT	AATCTCATCG	TTGTTATGCC	CAATACCAGC	240
AATGGTTGGT	ACACCGATAC	CCAGTATGGT	TTTGACTACT	ACACGGCTCT	AGCAGAGGAA	300
TTGCCACAGG	TTCTGAAACG	CTTCTTCCCT	AATATGACTA	GCAAGCGTGA	AAAGACCTTT	360
ATAGCTGGTC	TTTCTATGGG	AGGCTACGGC	TGTTTCAAAC	TGGCTCTTGC	GACAAATCGT	420
TTTTCTCATG	CAGCTAGTTT	TTCAGGTGCC	CTCAGCTTTC	AAAACCTTTC	TCCTGAAAGT	480
CAAAATCTGG	GAAGTCCAGC	CTACTGGAGA	GGTGTTTTTG	GAGAGATTAG	AGACTGGACA	540
ACTAGTCCCT	ATTCTCTTGA	AAGTCTGGCT	AAAAAATCGG	ATAAAAAGAC	CAAACCTTGG	600
GCGTGTGTG	GCGAACAGGA	TTTCTTGTA	GAAGCCAATA	ATCTCGCAGT	GAAAAATCTC	660
AAAAAACTAG	GTTTTGATGT	GACCTATAGC	CATAGCGCTG	GAACTCACGA	GTGGTACTAC	720
TGGGAAAAAC	AATTGGAAGT	TTTTTTAACA	ACTCTACCAA	TTGATTTCAA	ATTAGAAGAG	780
AGACTGACTT	AG					792

(2) INFORMATION FOR SEQ ID NO:2200:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...366
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2200:

AGGGTTGAAA	TAAGGAGGAG	AAACATGACT	CAAGCTGAAC	GAATTAGGGA	ATATTATAGA	60
GAGCACCTTG	CTGCCTCATA	TGATGAAGTG	GCTGAGGTCG	TTGGTACAAC	AAATAGTAAT	120
GTGAGAGCGA	ACCTGGCCAA	AGACATCAAG	GCAGGCAGAT	GCGTTCGCTT	GGAAGATAAG	180
TCATACGATT	ACTCGCCTTA	CTATAACCAT	ACACAGGCAC	TCACTGAGTT	GGTTGACTGG	240
AAGAATGACA	ACAGACGTGA	GTGGGTGGAT	ATGCTGACAA	GAGCAGCAGA	GAAAGAAACG	300
GATAGCAACG	TTATGCGTTT	GTTAATCAAA	GAAGCAAATA	AATTGATGAA	AGAGGTGACT	360
AAGTAG						366

(2) INFORMATION FOR SEQ ID NO:2201:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2201:

ATGAACGAAA	TTTGTCAATTT	ATTTATTTTAT	TCGGTTCTTA	AAGGTTACTC	TCTTGAAGGA	60
TGGAAGAAAA	TAAATGGTAG	TTGGTACTAT	TATAGACAAC	ATGATAAACA	AACGGGTTGG	120
CAGGAGATAA	ATGATACTTG	GTATTATTTA	GACAGTTCCG	GTAAGATGCT	TACAGATTGG	180
CAAAAAGTAA	ATGGAAAATG	GTATTATCTC	AATTCAAATA	GAGCAATGGT	TACAGGTAGC	240
CAAACTATCG	ATGGTAAAGT	TTATAACTTC	GCTTCATCTG	GTGAGTGGAT	TTGA	294

(2) INFORMATION FOR SEQ ID NO:2202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 837 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2202:

GAAATAGAAA	TGAAATTAAG	AAGAAGTGAT	CGGATGGTTG	TCATTTCCAA	CTATTTGATT	60
AATAATCCTT	ATAAACTAAC	TAGTCTCAAT	ACTTTTGCTG	AAAAGTATGA	GTCTGCTAAA	120
TCATCCATCT	CAGAAGATAT	CGTCATTATC	AAACGCGCCT	TTGAGGAAAT	TGAAATCGGT	180
CATATCCAGA	CAGTGACTGG	GGCTGGCGGA	GGTGTCATCT	TCACACCGTC	TATTTTCGAGT	240
CAGGATGCTA	AGGAAATGGT	TGAAGACTTG	CGTACCAAGT	TGTCAGAAAG	TGACCGTATC	300
TTGCCAGGTG	GTTATATCTA	TCTGTCTGAT	TTGCTTAGCA	CACCAGCCAT	CTTGAAAAAT	360
ATTGGTCGTA	TTATTGCCAA	AAGCTTTATG	GACCAAAAAA	TTGACGCGGT	TATGACCGTA	420
GCAACTAAGG	GTGTGCCACT	TGCAAATGCA	GTTGCCAATG	TCCTCAATGT	CTCTTTTGTC	480
ATTGTGCGCC	GTGACCTGAA	AATTACCGAA	GGTTCAACTG	TTAGCGTCAA	CTATGTTTCA	540
GGTTCAAGTG	GTGACCGTAT	CGAGAAAATG	TTCTTTTCAA	AACGTAGTCT	TAAGGCAGGC	600
AGCCGTGTCT	TGATTGTGGA	TGACTTCCTG	AAAGGTGGCG	GAACGGTCAA	CGGTATGATT	660
AGTCTCTTGC	GCGAGTTCGA	CTCAGAACTG	GCAGGTGTAG	CGGTCTTTGC	GGACAATGCC	720
CAAGAAGAAC	GTGAAAAGCA	GTTTGACTAC	AAGTCACTCT	TGAAGGTAAC	TAATATTGAT	780
GTCAAGAACC	AAGCCATCGA	TGTTGAGGTT	GGCAATATCT	TTGACGAAGA	TAAATAA	837

(2) INFORMATION FOR SEQ ID NO:2203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2203:

GGAGAAGAAA	TGAAACCCTC	AATTCATAGT	TTGGCACATC	AAACCATGCA	GGAATGGGTA	60
TTGGAGCAGG	GAGAAAAGAA	ATTCCGTGCA	GATCAAATCT	GGGAATGGCT	CTACCGTAAA	120
CGTGTGCAGT	CATTGAAGA	AATGACCAAC	CTTTCCAAGG	ATTTGATTGC	TAAGCTCAAT	180
GACCAGTTTG	TGGTCAATCC	CTTGAAACAA	GGTATTGTGC	AAGAGTCTGC	TGATGGTACA	240
GTCAAATATC	TCTTTGAAAT	GCCCGACGGT	ATGTTAATTG	AGACTGTACT	CATGCGTCAA	300
CACTATGGTT	TATCTGTCTG	TGTGACCACT	CAGGTCGGCT	GTAATATCGG	TTGTACCTTC	360
TGTGCCTCTG	GTTTGATTAA	GAAGCAACGT	GACCTCAATA	ACGGTGAAAT	CGTAGCGCAA	420
ATCATGCTGG	TTCAGAAATA	CTTTGCTGAG	CGTGGTCAGG	ATGAACGCGT	CAGCCATATC	480
GTTGTCATGG	GAATCGGTGA	GCCCTTTGAT	AATTACAACA	ATGTCTTGAA	TTTCTTTCTG	540
ACTATCAATG	ATGATAAAGG	AATGGCTATC	GGTGCTCGTC	ACATCACGGT	TTCAACCTCA	600
GGTTTGGCTC	ATAAAATTCG	TGACTTTGCT	GATGAAGGGG	TTCAGGTCAA	TCCTGCCGTG	660
TCTCTTCACG	CACCTAACAA	TGAACCTCGT	TCAAGTATCA	TGAAGATTAA	CCGTGCCTTT	720
CCGATTGAAA	AACTCTTTGC	TGCTATTGAA	TACTACATTG	AGACAACAAA	CCGTGGTGTA	780
ACCTTTGAAT	ATATCATGCT	TAATGAAGTC	AACGACGGTG	TAGAACAAGC	CTTGGAATTG	840
ACTGAATTGC	TCAAGAACAT	CAAGAAATTG	TCTTATGTAA	ACTTGATTCC	TTATAACCCA	900
GTTAGTGAGC	ATGACCAATA	TAGCCGTAGT	CCCAAAGAGC	GCGTGTTGGC	TTTCTATGAT	960
ACGCTTAAGA	AAAAAGGGGT	CAACTGTGTG	GTTCGTCAAG	AGCATGGTAC	AGATATTGAC	1020
GCAGCTTGTG	GACAATTGCG	CTCTAACACA	ATGAAACGTG	ACCGCCAGAA	GGCAGTCGCA	1080
GCGGTAAATC	CTTAA					1095

(2) INFORMATION FOR SEQ ID NO:2204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2204:

GACAGAGAAA	TATCTTTTTT	CTTATTGATT	TCTCCACTAG	TTGGCTCCTC	TTCTCCTACT	60
AAAATCTTCA	AAAGAGTAGA	CTTACCTGCA	CCATTTTTC	CAACAAGGGC	AATCCGATCT	120
CGTTCATCAA	CCTGCAGGTT	GATATTATCG	AAAAGAACCT	CTCCTGCAAA	AGAACGTTCA	180
ATTTTATTAG	CTTGTAATAA	AATCATACAA	G TAGTATAG			219

(2) INFORMATION FOR SEQ ID NO:2205:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 714 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2205:

GCAGGAGAAA	TTGGAAGAAT	GAATAAGCAG	GAACTGATTA	AACGTATCGA	GGATTTGCCT	60
TATACAGAGG	GGCCTATCGC	AGATACAATC	GAAATTAATA	GAAATTGGAT	ATTGAAATCA	120
ATTGAACAGC	TAGCCGAATC	CGAAATAGGT	CACGCAGATG	AAGCTCCACG	CTACGTAAAG	180
AACATACTAG	CACGATTGCG	AGAATTGCCA	TTGCATGATA	GAGAGTTTTG	GTTAAAGGCT	240
ATCATGAGCG	AATTTGAACA	GGATTTTAGC	CATGCAAAAT	GGCGAGAGGG	CTACGAGCAA	300
GGTAAAATTG	AGGGTATGGT	TGAACGTGAA	AAAGTCATAG	TTCCGCAGTG	TGTGGCGGAA	360
TATATAGAAT	TTAAAAAGAA	AAACAATTTT	CATGTTTACG	GTGCAATGAG	AGTAATTGAA	420
GATCATTATG	ATAAGAAAGT	TCCTGATTGG	TTTTACGAAA	ATAACATCGA	AAAATTCGTG	480
CTTGCTTGGC	TTGACGGCTA	CGAGGTTGAA	AAAGAGAAGC	GGTATTTTGT	TAAGATTAAA	540
GGGAATATTA	AAGAAAATAT	GTTGGTTTAT	GGAGAACTTT	TGAAAAGGTA	TTTCTTTACA	600
AAAAGCTTTA	GTTTAGACGA	TGTTATATAT	TCCCACACCC	GTAAAGAACT	AGAAAATGCA	660
AAAATCGGCT	GGGTGTTTGA	TTGTGAAGGG	TTTGAGATTG	AGGAGGTGGA	GTGA	714

(2) INFORMATION FOR SEQ ID NO:2206:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 978 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2206:

AAAGGAGAAA	TTATGAAAAC	ATCTCTTAAA	CTTTATTTCA	CTGCCCTAGT	GGCCAGCTTC	60
TTGCTCCTAC	TTGGTGCATG	TAGTACAAAC	TCAAGCACTA	GTCAGACAGA	GACCAGTAGC	120
TCTGCTCCAA	CAGAGGTAAC	CATTAAAAGT	TCAC TGGACG	AGGTCAAAC T	TTCCAAAGTT	180
CCTGAAAAGA	TTGTGACCTT	TGACCTCGGC	GCTGCGGATA	CTATTTCGCGC	TTTAGGATTT	240
GAAAAAATA	TCGTCGGAAT	GCCTACAAAA	ACTGTTCCGA	CTTATCTAAA	AGACCTAGTG	300
GGAACGTCA	AAAATGTTGG	TTTTATGAAA	GAACCTGATT	TAGAAGCTAT	CGCCGCCCTT	360
GAGCCTGATT	TGATTATCGC	TTCAACACGT	ACACAAAAAT	TCGTAGACAA	ATTCAAAGAA	420
ATCGCCCCAA	CCGTTCTCTT	CCAAGCAAGC	AAGGACGACT	ACTGGACTTC	TACCAAGGCT	480
AATATCGAAT	CCTTAGCAAG	TGCC TTCGGC	GAAACTGGTA	CACAGAAAGC	CAAGGAAGAA	540
TTGGCCAAGC	TAGACAAGAG	CATCCAAGAA	GTCGCTACTA	AAAATGAAAG	CTCTGACAAA	600
AAGGCCCTTG	CGATCCCTCT	TAATGAAGGA	AAAATGGCAG	CCTTTGGTGC	CAAATCTCGT	660
TTCTCTTTCT	TGTACCAAAC	CTTGAAATTC	AAACCAACTG	ATACAACATT	TGAAGACTCA	720
CGCCACGGAC	AAGAAGTCAG	CTTTGAAAGT	GTCAAAGAAA	TCAACCCTGA	CATCCTCTTT	780
GTCATCAACC	GTACCTTTGC	CATCGGTGGG	GACAACTCTA	GCAACAACGG	TGTCCTAGAA	840
AATGCCCTTA	TCGCTGAAAC	ACCTGCTGCT	AAAAATGGTA	AGATTATCCA	ACTAACACCA	900
GACCTCTGGT	ATCTAAGCGG	AGGCGGACTT	GAATCAACAA	AACTCATGAT	TGAAGACATA	960
CAAAAAGCTT	TGAAATAA					978

(2) INFORMATION FOR SEQ ID NO:2207:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 660 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...660
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2207:

GAAGGAGAAA	TCATGACTTT	ATTACAATTA	CAAGATGTTA	CCTACCGTTA	TAAGAATACT	60
GCTGAAGCAG	TCCTATATCA	GATCGATTAT	AATTTTGAAC	CCGGAAAATT	TTACAGTATT	120
ATTGGGGAAT	CAGGAGCAGG	AAAATCCACA	CTCTTGTCCT	TACTTGCTGG	TCTAGATAGT	180
CCTGTTGAAG	GTTCTATCCT	TTTTCAAGGA	GAGGATATTC	GTAAGAAGGG	CTATTCTTAC	240
CATCGCATGC	ACCATATTTT	CCTGGTCTTT	CAAAATTATA	ACTTGATAGA	TTATCTTTCT	300
CCGCTGGAAA	ATATCCGCTT	GGTCAACAAA	AAGGCAAGCA	AGAATACACT	TCTTGAGCTT	360
GGTTTGGATG	AAAGCCAGAT	CAAGCGGAAT	GTTCTCCAGT	TATCAGGTGG	TCAACAGCAA	420
CGTGTGCCA	TTGCTCGCAG	TTTGGTCTCA	GAAGCTCCAG	TTATTCTAGC	TGATGAGCCA	480
ACAGGAAATC	TGGATCCTAA	AACTGCTGGA	GATATTGTCT	AACTACTCAA	ATCACTTGCC	540
CAGAAAACAG	GTAAATGTGT	GATTGTCTGA	ACTCACAGTA	AAGAAAGTGC	ACAAGCGTCA	600
GATATTACAC	TTGAATTAAA	GGATAAGAAA	CTGACTGAAA	CGCGCAATAC	TAGTAAATAA	660

(2) INFORMATION FOR SEQ ID NO:2208:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 453 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...453
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2208:

TATATGGAAA	TCAAAGATAT	TCTTAATGTG	AGTCTGATCC	AGACGGATTT	ACAGATGCAG	60
AGCAAAGAAG	AGGTTTTTTGA	GGCATTAGCT	CAACTATTGG	TTGAGACGGG	TTATGTGTCT	120
GATAGAGACC	AATTTATCGA	AGTTCTTTAT	CAGAGAGAGG	CAGAAGGACA	GACCGGTATT	180
GGGAATTATA	TTGCTATTCC	CCATAGCAAG	AGTTCTGCTG	TGGAGAAGGC	GGGGGTAGTC	240
ATAGCTATAA	ATCACAATGA	GATTCCTTGG	GAGACCATTG	ATGGGAAAGG	GGTCAAAGTA	300
ATTGTACTCT	TTGCAGTTGG	TGATGATACA	GAAGCTGCTA	GGGAGCATTT	GAAGACCTTA	360
TCACTCTTTG	CTCGAAAAC	TGGTAATGAC	GAAGTTGTTG	CCAAATTAGT	TCGGGCTCAG	420
ACATCTGATG	ATGTGATTGC	AGCTTTTTGT	TAA			453

(2) INFORMATION FOR SEQ ID NO:2209:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2209:

AATATGGAAA	TTAATGTGAG	TAAATTAAGA	ACAGATTTGC	CTCAAGTCGG	CGTGCAACCA	60
TATAGGCAAG	TACACGCACA	CTCAACTGGG	AATCCGCATT	CAACCGTACA	GAATGAAGCG	120
GATTATCACT	GGCGGAAAGA	CCCAGAATTA	GGTTTTTTCT	CGCACATTGT	TGGGAACGGT	180
TGCATCATGC	TAGGGTAG					198

(2) INFORMATION FOR SEQ ID NO:2210:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 516 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2210:

CACATGGAAA	TTTCATTATT	AACAGATGTT	GGTCAGAAAC	GAACAAATAA	CCAAGACTAT	60
GTCAACCACT	ATGTCAATAG	AGCTGGACGT	ACCATGATTA	TTTTAGCTGA	TGGGATGGGA	120
GGTCATCGTG	CAGGGAATAT	CGCTAGTGAA	ATGGCGGTCA	CAGACCTGGG	TGTAGCTTGG	180
GTTGATACCC	AGATCGATAC	AGTCAATGAA	GTGCGTGAAT	GGTTCGCCCC	TTACCTAGAA	240
ATTGAAAATC	AAAAGATTCA	CCAGCTTGGT	CAGGATGAAG	CTTACAGAGG	CATGGGAACT	300
ACTTTGGAAG	TCCTTGCTAT	TATTGATAAT	CAGGCTATCT	ATGCTCATAT	TGGTGATTCTG	360
CGTATCGGCT	TGATTCTGGG	AGAAGAATAC	CATCAGTTGA	CGAGCGATCA	TTCTTGTT	420
AATGAAATTGC	TCAAGGCTGG	TCAATTGACA	ACCAGAAGAG	GCAGAAGCTC	ATCCGCAAAA	480
AAATATTATC	ACCCAGTCTA	TTGGGCAAAA	AGATGA			516

(2) INFORMATION FOR SEQ ID NO:2211:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2211:

GCAATGGAAA	TGATGGAACT	ACCAAGTCAG	GATATTTTGA	TTTTTACAAA	ACAAATTCGT	60
CATTGGATTC	TTAGTGAACA	AGTTATTTCA	GGAGAAAGAA	AACTTTTCTT	CCGGGAAGAT	120
ACTCCAAAAG	AGATTTTAGA	TATGTACGAA	AACATTAAAT	CTAAACTTGA	TTGTGCTTAC	180
CAAGAAGTTT	AG					192

(2) INFORMATION FOR SEQ ID NO:2212:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 726 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2212:

AGTAAGGAAA	TAATCATGAC	AGCCACTAGT	CTTGGGTTAT	CAAATATTGA	AATAGTTGTC	60
AGGATTGTTT	TATCAGTAGT	CATTGGTAGT	ATAATTGGTT	TAGAGAGAGG	GAGCAAATCC	120
CAGCCTGCAG	GCATCCGAAC	TTATAGTATT	GTTTGTCTAG	CTGCATGTTT	GATTATGATG	180
ACGAATGAAT	ACGTATCTTA	TAAATTTGGG	ACAGGAGATC	CTACACGATT	AGGAGCTCAA	240
GTTATATCAG	GTGTGGGTTT	TCTAGGCGCT	GGAACGATTC	TTATTACAGA	TAAAAAGAAA	300
ATTACAGGTC	TGACAACTGC	AGCAGGCATT	TGGGCTTCGG	CAGGAATTGG	ATTAGCTATT	360
GGAGTAGGTT	TTTATGAGGG	AGCTCTTTTA	GTAGCCATTT	CTGTTTGGGG	TGTGATATCC	420
ATGTTCCAAC	CACTAAAAAA	ATATCTGCAA	AATCGTTCTA	AAATGATTGA	ATTGTATATA	480
GTAGTTAAAT	CTACAGAAGC	CTATAATCGT	GTATTGGTTT	ATTGTGCAGA	AAATGGTATC	540
AGAATGACCG	ATTCAAGAAC	AGCGTTTGGA	GATGTTAATT	CTGACAGAAT	TGAATACTTT	600
GATGTTCCGG	ACAAAAAAAT	AGCGTCATTT	ATTACTCTGG	AATTATCAGG	TAGATTTGAA	660
CATCTTCGAC	TGATGGAAGA	AATTGCTAAT	ATTGTAGGTG	TTATTTATGT	CGAAGAAATT	720
AGCTGA						726

(2) INFORMATION FOR SEQ ID NO:2213:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1332
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2213:

GAGAAGGAAA	TGTTAGAATT	GCTTAAATCA	ATCGATGATT	TTGCTTGGGG	ACCGCCCCTC	60
TTGATTTTAT	TGGTCGGAAC	AGGGATTTAC	CTAACCATGC	GGCTAGGACT	CTTGCAGGTT	120
TTGCGTCTGC	CCAAGGCCCT	TCAGCTTATT	TTTATCCAGG	ATAAGGGACA	TGGTGATGTA	180
TCCAGTTTTG	CAGCTCTGTG	TACAGCCTTG	GCATCAACTG	TTGGAACAGG	AAATATCATA	240
GGAGTTGCGA	CGGCTATCAA	GGTTGGTGGA	CCAGGAGCTC	TATTTTGGAT	GTGGATGGCG	300
GCTTTCCTTG	GAATGGCTAC	CAAGTATGCG	GAAGGACTCT	TGGCCATCAA	ATACCGCACC	360
AAGGACGACC	ATGGTGCAGT	AGCGGGAGGT	CCCATGCATT	ATATCCTTCT	AGGGATGGGA	420
GAAAAGTGGC	GACCACTTGC	TGTTTTGT'TT	GCAGTANCAG	GAGTATTGGT	TGCTCTCTTG	480
GGAATCGGAA	CCTTCACCCA	AGTCAACTCG	ATTACAGAAT	CTATCCAAAA	TACAACGACG	540
ATTTTCGCCAG	CCATCACAGC	TCTCGTCTTG	TCTGTCTTTG	TAGCGATTGC	AGTCTTTGGT	600
GGACTCAAGT	CTATTTCTAA	GGTTTCAACT	ACTGTTGTTC	CTTTTATGGC	CATCATTTAT	660
ATCTTAGGAA	CTCTTACAGT	TATTTTCTTT	AATATCGGAA	AAATCCCTGG	CACAATCGCT	720
TTAGTCTTTA	CCTCAGCTTT	TAGTCCCTTT	GCTGCGGTAG	GTGGATTTGC	TGGTGCTAGC	780
GTTCGGATGG	CTATTCAAAA	TGGTGTGGCG	CGTGGTGTGT	TCTCAAACGA	ATCTGGTCTG	840
GGTTCGTGCTC	ATATTGCAGC	TGCAGCTGCC	AAGACAAATG	AACCAGTAGA	GCAAGGTTTG	900
ATTTCCATGA	CAGGAACCTT	TATTGATACC	CTCATCATTT	GTA CTCTAAC	TGGTTTGACC	960
ATCTTGGTAA	CTGGAGTTTG	GAGTGGTGAC	TTGAATGGGG	TTGCCTTGAC	TCAGTCAGCT	1020
TTCTCAACAG	TCTTTTCACA	CTTTGGCCCT	GCCCTCTTGA	CCATCTTCCT	TGTGCTTTTTT	1080
GCCTTTACAA	CGATTCTAGG	TTGGAACAT	TACGGAGAAC	GCTGTTTTGA	GTTCTCTTTT	1140
GGGGTTCGCT	TTATCTGGCT	CTACCGTGTG	GTTTTTGTGC	TCATGGTCTT	GTTAGGAGGA	1200
TTTATCGAGT	TGGATATGGT	CTGGATTATC	GCAGATATCG	TTAACGCCTT	GATGGCTCTG	1260
CCAAACTTGA	TTGCCCTCTT	GGTCTTGTCTG	CCAGTCGTTA	TTGCTGAAAC	TAAAAAGTAT	1320
TTTGACAAAT	AA					1332

(2) INFORMATION FOR SEQ ID NO:2214:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 948 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2214:

AGAGGTGTTT	TCATGTCTTA	TCAAGATTTA	AAAGAGTGTA	AAATCATCAC	AGCCTTTATT	60
ACTCCCTTCC	ACGAGGATGG	TTCCATCAAC	TTTGATGCTA	TTCCAGCCTT	GATTGAGCAT	120
TTATTGGACC	ATCATACGGA	TGGAATTCTT	CTCGCAGGGA	CCACTGCTGA	GAGTCCAAC	180
TTGACCCACG	ATGAGGAGTT	GGAGTTATTT	GCGGCTGTAC	AAAAGATTGT	CAATGGACGA	240
GTTCCCTTGA	TTGCGGGTGT	AGGTACTAAT	GATACGCGTG	ACTCTATCGA	GTTTGTCAAA	300
GAAGTAGCGG	AATTCGGCGG	TTTTGCTGCT	GGTCTTGCTA	TTGTTCCCTT	CTACAACAAA	360
CCTTCTCAAG	AAGGAATGTA	TCAGCATTTT	AAAGCCATTG	CAGATGCTTC	TGACCTACCA	420
ATTATTATCT	ATAACATTCC	AGGGCGTGTG	GTGTGTGAAT	TAACCTCCAGA	AACCATGCTT	480
CGCTTGGCTG	ATCATCCAAA	TATTATCGGT	GTCAAAGAAT	GTACTAGCTT	GGCTAATATG	540
GCTTACTTGA	TTGAGCACAA	ACCAGAAGAG	TTCTTGGTCT	ATACTGGTGA	GGATGGAGAT	600
GCTTTCCATG	CCATGAACCT	TGGGGCGGAT	GGGGTTATTT	CTGTTGCCCT	TCATACAAAT	660
GGGGATGAAA	TGCACGAGAT	GTTTATTGCC	ATTGCAGAAA	GTGATATGAA	GAAAGCCGCA	720
GCTATTCAAC	GTAAATTCAT	TCCTAAGGTT	AATGCTCTCT	TCTCTTATCC	AAGTCCTGCT	780
CCAGTTAAGG	CAGTTTGTAA	CTACATGGGA	TTTGAAGCTG	GACCAACTCG	TCTACCTCTT	840
GTTCCAGCAC	CAGAAGAAGA	TGCTAAACGC	ATTATCAAGG	TTGTCGTAGA	TGGCGACTAC	900
GAAGCGACCA	AGGCAACTGT	AACAGGTGTC	TTAAGACCAG	ATTACTAA		948

(2) INFORMATION FOR SEQ ID NO:2215:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 774 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2215:

CGGGAACCCT	TATCCTTGGG	ATGGATTTCAT	ATCTGCGACA	GTAAGATGAG	TAATGTAGAT	60
AAGATTTCGAA	AAATACATAT	TATCGTATGT	TGGATGTATA	TATTTTTTATC	ATTTCAGGGCG	120
ATTATAAATG	ACACGGAGTA	TTTTTTTGCTT	ATTTTTTTTAG	CTTTTATCTA	CTCAATAGTA	180
TCACTACCTC	TATATTCTGT	GAAAAATAAA	ATAGTATCTA	TCTGTCTAGC	CATAAATTCC	240

ATTCTGTTAA	TGAGTTTCCC	CATTTTAATC	AATAAGTTTT	TCCCAGAAAAG	TTTTTTGACT	300
TATACCGTAT	TAATAAGTGT	TTTTATCCTA	GAGTTAGCAA	TCTTTCATTT	AATTGGGGAA	360
GATTTTGCTA	CTAAATTGAC	TAACGAATAT	AAGAAAATTA	GTCAGTTTAG	AAGCAAGGTG	420
TCTCAATCTC	CTTGGATAAA	ATATTTAGAG	ATTTCTAGTT	TTATATTAAC	TATATTTCCA	480
TCTATTCTTT	ATGGTACAGT	TGATAATCAT	GTA CTGACTC	TTATCTTTTT	GATAAAAATT	540
TGTGCAGATA	CCACGATAAA	ATTTTTATTTC	ATCAGATTAT	TTGACACAAG	TACTTTAATG	600
AAGAGGAGAA	TATTTTTTCT	TTTCGCATTG	GATGTTATAG	TTTACTTATT	TTTAGGATAT	660
CTTTTAGTGA	TTCAAAAAGC	AGGCTATTTG	TTTTCGGTTT	TACTTCTTTT	TTCTAATTTT	720
TCAGTTCCAT	TTATCAAAGA	AAAGGAATAC	GAATTATTTA	AAAATAGCAA	GTAA	774

(2) INFORMATION FOR SEQ ID NO:2216:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...225
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2216:

TCTTTTCGAA	TTCCTTTTAC	TGTCCCAATA	AGTTCTCTAC	GCCCCTCAGG	ATCCAACATA	60
CTCGTTGCTT	CATCTAAGAT	TAAAATAGCT	GGTCTTAGGG	CTACAACACC	TGCAATGGCC	120
ACACGTTGCT	TTTGGCCACC	TGATAGACGC	GCTGGCTCTC	TCTTTTAA	GTCCAACATG	180
CCAACTAAAG	CCAGAGCTTC	TTCCACTCTC	TTTTTCATTT	CTTGA		225

(2) INFORMATION FOR SEQ ID NO:2217:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1329 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...1329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2217:

TCTATGCGAA	TTGGTTTATT	TACAGATACC	TATTTTCCTC	AGGTTTCTGG	TGTTGCGACC	60
AGTATTCGAA	CCTTGAAAAC	AGAACTTGAA	AAGCAGGGAC	ATGCTGTTTT	TATCTTTACG	120
ACGACAGATA	AGGATGTCAA	TCGCTACGAA	GATTGGCAAA	TTATCCGCAT	TCCAAGTGTT	180
CCTTTCTTTG	CTTTTAAGGA	TCGTCGCTTT	GCCTACCGAG	GTTTTAGCAA	GGCACTTGAA	240
ATTGCTAAAC	AGTATCAGCT	AGATATTATC	CATACTCAGA	CAGAATTTTC	TC TTGGCCTG	300
TTGGGGATTT	GGATTGCGCG	TGAATTGAAA	ATTCCAGTCA	TCCATACCTA	TCACACCCAG	360
TATGAAGACT	ATGTCCATTA	TATTGCTAAG	GGGATGTTGA	TCCGGCCGAG	TATGGTCAAG	420
TATCTGGTTA	GAGGTTTCCT	GCATGATGTG	GATGGGGTTA	TTTGCCCTAG	TGAGATTGTC	480
CGTGACTTGC	TATCTGATTA	TAAGGTCAAG	GTTGAAAAAC	GGGTCATTCC	TACTGGGATT	540
GAATTAGCCA	AGTTTGAGCG	TCCGGAATC	AAGCAGGAAA	ATTTGAAAGA	ACTGCGTAGT	600
AAACTAGGGA	TTCAAGATGG	TGAAAAGACG	TTGCTTAGTC	TTTCGAGAAT	CTCCTATGAA	660
AAAAATATTC	AAGCAGTTTT	AGTAGCCTTT	GCTGATGTTT	TGAAAGAGGA	AGACAAGGTT	720
AAACTGGTAG	TAGCTGGGGA	TGGCCCTTAT	CTGAATGACC	TCAAAGAGCA	AGCCCAGAAC	780
CTAGAGATTC	AAGACTCAGT	TATCTTTACA	GGGATGATTG	CTCCTAGTGA	GACGGCTCTT	840
TACTATAAAG	CGGCGGATTT	CTTCATTTTCG	GCATCGACAA	GCGAAACGCA	AGGTTTGACC	900
TACTTGGAAA	GCTTAGCCAG	TGGAACACCT	GTCATTGCTC	ACGGAATCC	TTATTTGAAC	960
AACCTCATCA	GTGATAAAAT	GTTTGGAACC	TTGTACTATG	GAGAACATGA	TTTGGCTGGT	1020
GCTATTTTGG	AAGCCCTGAT	TGCAACACCA	GACATGAACG	AGCATACCTT	ATCAGAGAAA	1080
TTGTATGAGA	TTTCAGCTGA	GAACTTTGGG	AAACGAGTGC	ATGAGTTTTA	TCTGGATGCC	1140
ATTATTTCAA	ATAACTTCCA	GAAAGATTTG	GCTAAAGATG	ATACGGTCAG	TCAGCGTATC	1200
TTTAAGACAG	TTTTGTATCT	TCCGCAACAG	GTGGTTGCTG	TACCCGTAAA	AGGCTCTAGA	1260
CGCATGTTGA	AGGCTTCAAA	AACACAGTTG	ATCAGTATGA	GAGACTATTG	GAAAGACCAT	1320
GAAGAATAG						1329

(2) INFORMATION FOR SEQ ID NO:2218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2218:

CTCAAGCCCT	TACTTCATGC	AGATGAAACT	TCTTATAGGG	TGCTAGAGAG	TGATAGTCAG	60
CTGACCTACT	ATTGGACCTT	TTTGTCTGGG	AAAGCTGAGA	ATCAAGCAAT	CACGCTGTAC	120
CACCATGATC	AGCGTCGGAG	TGGTTTAGTA	GTACAAGAAT	TCCTAGGAGA	TTATTCTGGC	180
TATGTGCATT	GTGATATGTT	GCGGCAGTAA				210

(2) INFORMATION FOR SEQ ID NO:2219:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1137 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2219:

CTGTTTAGAA	TGAGGGAAAA	TATGAAGATT	GTAATTGCAC	CGGATTCGTT	TAAGGAAAGC	60
TTGACAGCTC	AACAGGTAGC	TGAAGCAATA	AAAAGAGGCT	TCCAACAATC	GATAGCAGAT	120
GTAGAATGTC	TCCTCTGCCC	TGTTGGTGAT	GGGGGAGAAG	GTACTGTAGA	TGCTATCCGA	180
CATTCTCTTG	ACCTAAAAGA	AAAAATGGATC	CAAGTGACAG	ACCCTTCTGG	ACAAAAAGAA	240
GCCATGCGCT	ATTTTCAAAA	AGGGGAACCTG	GCACTATTTG	AAGTAGCTGA	CTTGGTTGGT	300
CTTGGAAGAAA	TTCCGCTAGA	GAAACGAAAT	CCACTTCAAA	TCCAAACTTG	TGGTATTGGA	360
GAGTTGATTC	TCCATCTCAT	TTCTAAAGGG	ATTAAAGATA	TTTATATCGG	TGTTGGTGGC	420
ACGGCCAGTA	ATGATGGAGG	ACTGGGGATT	GCTGCTGGTT	TAGGTTATCA	ATTTTATGAT	480
AGGGATGGAA	ATGTCTTGCC	TGCTTCCGGT	CAATCCTTAT	TAAACTTAGC	TTCTGTTTCA	540
ACAGAAAATC	GCTATAAAAT	TCCTGAAGGT	GTTCAAATTC	ATATTTTAGC	AGATGTCGTG	600
AGTCCCTTAT	GTGGTCATCA	AGGTGCGACT	TACACTTTTG	GCAATCAAAA	AGGTCTACAT	660
CCGACTATGT	TTGCAGTCGT	AGATCAGGCG	ATCCAAGATT	TTTATGAAAA	ATTCTCACCT	720
GCAACATTAG	AAATTTAAAG	AGCAGGAGCA	GGTGGAGGCC	TTGCTGGTGG	TTTGTGTGCC	780
TTTGCTCAGG	CAAGTATCGT	GTCTGGAATT	GATACCTGCT	TGGACTTAAT	CAACTTTGAT	840
AAGAAAGTTT	CAGATGCTGA	CTTGGTTGTT	GTTGGAGAAG	GAAGACTTGA	TAGTCAAAGC	900
TTTGCTGGGA	AAGCGCCTAT	AGGTGTTGCA	ATAAGAACCC	CTGTTGGAGT	TCCTGTTATT	960
GCTATTTGCG	GTAGTCTTGC	TGAAGATTTA	CCTCCCCTAC	CATTTGAAAA	TATCCAAGCT	1020
GTCTTTTCTA	TTTTGGAGAA	AAGTGAACCT	TTAGAAGATA	GTTTGAAAAA	TGCCAGTCTC	1080
TATCTGGAGC	GCACGGCTGC	CAATATTGGG	CAC TTATTAA	ATATGTGCAA	GATTTAG	1137

(2) INFORMATION FOR SEQ ID NO:2220:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1269 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2220:

AAACTTAGAA	TGAGAAAAAT	TGTTATCAAT	GGTGGATTAC	CACTGCAAGG	TGAAATTACT	60
ATTAGTGGTG	CTAAAAATAG	TGTTGTGGCC	TTAATTCCAG	CTATTATATT	GGCTGATGAT	120
GTGGTGACTT	TGGATTGTGT	TCCAGATATT	TCGGATGTAG	CCAGTCTTGT	CGAAATCATG	180
GAATTGATGG	GAGCTACTGT	TAAGCGTTAT	GACGATGTCT	TGGAGATTGA	TCCAAGAGGT	240
GTTCAAAATA	TTCCAATGCC	TTATGGTAAA	ATTAACAGTC	TTCGTGCATC	TTACTATTTT	300
TATGGGAGCC	TCTTAGGCCG	TTTTGGTGAA	GCGACAGTTG	GTCTACCGGG	AGGATGTGAT	360
CTTGGTCCTC	GTCCGATTGA	CTTACACCTT	AAGGCGTTTG	AAGCTATGGG	TGCCACTGCT	420
AGCTACGAGG	GAGATAACAT	GAAGTTATCT	GCTAAAGATA	CAGGACTTCA	TGGTGCAAGT	480
ATTTACATGG	ATACGTTAG	TGTGGGAGCA	ACGATTAATA	CGATGATTGC	TGCAGTTAAA	540
GCAAATGGTC	GTACTATTAT	TGAAAATGCA	GCCCCGTGAAC	CTGAGATTAT	TGATGTAGCT	600
ACTCTCTTGA	ATAATATGGG	TGCCCATATC	CGTGGGGCAG	GAACTAATAT	CATCATTATT	660
GATGGTGTTG	AAAGATTACA	TGGGACACGT	CATCAGGTGA	TTCCAGACCG	CATTGAAGCT	720
GGAACATATA	TATCTTTAGC	TGCTGCAGTT	GGTAAAGGAA	TTCGTATAAA	TAATGTTCTT	780
TACGAACACC	TGGAAGGGTT	TATTGCTAAG	TTGGAAGAAA	TGGGAGTGAG	AATGACTGTA	840
TCTGAAGACA	GCATTTTTGT	CGAGGAACAG	TCTAATTTGA	AAGCAATCAA	TATTAAGACA	900
GCTCCTTACC	CAGGCTTTGC	AACTGATTTG	CAACAACCGC	TTACCCCTCT	TTTACTAAGA	960
GCGAATGGTC	GTGGTACAA	TGTCGATACG	ATTTACGAAA	AACGTGTAAA	TCATGTTTTT	1020
GAAGTAGCAA	AGATGGATGC	GGATATTTTC	ACAACAAATG	GTCATATTTT	GTACACGGGT	1080
GGACGTGATT	TACGTGGGGC	CAGTGTTAAA	GCGACTGACT	TAAGAGCTGG	GGCTGCACTA	1140
GTCATTGTTG	GGCTTATGGC	TGAAGGTAAA	ACTGAAATTA	CCAATATCGA	GTTTATCTTA	1200
CGTGGTTATT	CTGATATTAT	CGAAAAATTA	CGTAATTTAG	GAGCGGATAT	TAGACTTGTT	1260
GAGGATTAA						1269

(2) INFORMATION FOR SEQ ID NO:2221:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 819 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2221:

AAGACTAGAA	TGAGTGAAAT	AGGCTTTAAA	TACAGTATTT	TAGCGTCGGG	TTCCAGTGGA	60
AATTCTTTTT	ATCTGGAAAC	CTCAAAAAAG	AAGCTTTTAG	TAGATGCAGG	CTTGCTGGC	120

AAGAAAATTA	CCAGTCTGCT	AGCTGAAATT	AACCGTAAGC	CAGAAGACCT	GGATGCCATC	180
TTGATTACCC	ATGAGCATTC	AGATCATATC	CATGGAGTAG	GCGTTTTGGC	TCGCAAGTAT	240
GGTATGGATC	TTTATGCCAA	TGAAAAGACC	TGGCAAGCTA	TGGAAAATAG	TAAATATCTT	300
GGCAAGGTGG	ATTCTTCGCA	AAAGCATATT	TTTGAAATGG	GTAAAACCAA	AACCTTTGGA	360
GATATCGACA	TCGAGAGTTT	TGGTGTAAAG	CATGATGCAG	TCGCACCGCA	GTTCTATCGC	420
TTTATGAAGG	ATGATAAGAG	TTTTGTCTTT	TTGACAGATA	CAGGTTATGT	CAGTGACCGT	480
ATGGCGGGCA	TTGTCGAAAA	TGCGGATGGC	TATCTTATCG	AGGCCAACCA	TGATGTAGAG	540
ATTTTGGCAT	CAGGTTCTTA	CGCTTGGCGA	CTCAAACAAC	GAATCCTATC	TGACCTTGGT	600
CACCTTTCTA	ACGAGGACGG	TGCTGAAGCT	ATGATTTCGA	CGCTAGGAAA	TCGTACTAAG	660
AAGATTTACC	TTGGGCATTT	ATCTAAGGAA	AACAATATCA	AGGAACTGGC	TCATATGACC	720
ATGGTCAATC	AGCTGGCTCA	AGCTGATCTG	GGAGTCGGAG	TAGACTTTAA	GGTTTATGAT	780
ACCTCACCAG	ATACCGCAAC	ACCATTGACA	GAGATATAG			819

(2) INFORMATION FOR SEQ ID NO:2222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2222:

GAGAATAGAA	TGGCGAAAAA	ACCAAAAAAA	TTAGAAGAAA	TTTCAAAAAA	ATTTGGGGCA	60
GAACGTGAAA	AGGCCTTGAA	TGATGCTCTT	AAATTGATTG	AGAAAGACTT	TGGTAAAGGA	120
TCAATCATGC	GTTTGGGTGA	ACGTGCGGAG	CAAAGGTGC	AAGTGATGAG	CTCAGGTTCT	180
TTAGCTCTTG	ACATTGCCCT	TGGCTCAGGT	GGTTATCCTA	AGGGACGTAT	CATCGAAATC	240
TATGGCCCAG	AGTCATCTGG	TAAGACAACG	GTTGCCCTTC	ATGCAGTTGC	ACAAGCGCAA	300
AAAGAAGGTG	GGATTGCTGC	CTTTATCGAT	GCGGAACATG	CCCTTGATCC	AGCTTATGCT	360
GCGGCCCTTG	GTGTCAATAT	TGACGAATTG	CTCTTGCTCT	AACCAGACTC	AGGAGAGCAA	420
GGTCTTGAGA	TTGCGGGAAA	ATTGATTGAC	TCAGGTGCAG	TTGATCTTGT	CGTAGTCGAC	480
TCAGTTGCTG	CCCTTGTTCC	TCGTGCGGAA	ATTGATGGAG	ATATCGGAGA	TAGCCATGTT	540
GGTTTGCAAG	CTCGTATGAT	GAGCCAGGCC	ATGCGTAAAC	TTGGCGCCTC	TATCAATAAA	600
ACCAAAACAA	TTGCCATTTT	TATCAACCAA	TTGCGTGAAA	AAGTTGGAGT	GATGTTTGGA	660
AATCCAGAAA	CAACACCGGG	CGGACGTGCT	TTGAAATTCT	ATGCTTCAGT	CCGCTTGGAT	720
GTTCGTGGTA	ATACACAAAT	TAAGGGAAC	GGTGACCAA	AAGAAACCAA	TGTCGGTAAA	780
GAACTAAGA	TAAAGTTGT	AAAAAATAAG	GTAGCTCCAC	CGTTTAAGGA	AGCCGTAGTT	840
GAAATTATGT	ACGGAGAAGG	AATTTCTAAG	ACTGGTGAGC	TTTTGAAGAT	TGCAAGCGAT	900
TTGGATATTA	TCAAAAAAGC	AGGGGCTTGG	TATTCTTACA	AAGATGAAAA	AATTGGGCAA	960
GGTTCGTAGA	ATGCTAAGAA	ATACTTGGCA	GAGCACCCAG	AAATCTTTGA	TGAAATTGAT	1020
AAGCAAGTCC	GTTCTAAATT	TGGCTTGATT	GATGGAGAAG	AAGTTTCAGA	ACAAGATACT	1080
GAAAACAAAA	AAGATGAGCC	AAAGAAAGAA	GAAGCAGTGA	ATGAAGAAGT	TACGCTTGAC	1140
TTAGGCGATG	AACCTTGAAAT	CGAAATTGAA	GAATAA			1176

(2) INFORMATION FOR SEQ ID NO:2223:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 816 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2223:

AAGGATAGAA	TGATGCAGGC	ATTGACAAAT	CCTTTTCCTA	TAGGCTCTAG	TTCCCTCATT	60
CACTGTATGA	CCAATGAGAT	TTCTTGTGAG	ATGCTGGCAA	ATGGGATTTT	GGCTCTGGGA	120
TGCAAACCTG	TCATGGCAGA	TGATCCCCGT	GAAGTTCTTG	ATTTTACTAA	GCAAAGCCAG	180
GCTCTCTTCA	TCAATTTGGG	GCATTTGTCA	GCTGAGAAGG	AAAAAGCAAT	CCGCATGGCA	240
GCTTTGTATG	CAAACCAATC	TTCTCTCCCG	ATGGTAGTAG	ATGCGGTTGG	CGTAACGACT	300
TCATCCATTTC	GTAAGAGCTT	AGTTAAAGAC	CTTTTAGACT	ATAGACCTAC	GGTCCTTAAA	360
GGAAACATGT	CAGAAATTCG	AAGTCTTGTT	GGATTAAAGC	ATCACGGCGT	TGGGGTCGAT	420
GCGAGTGCTA	AAGATCAAGA	AACGGAGGAT	TTGCTTCAAG	TCTTGAAAGA	CTGGTGTCAG	480
ACCTATCCTG	GTATGCCATT	CTTAGTCACA	GGTCCCAAGG	ACCTTATTGT	TTCGGAGAAT	540
CAAGTTGCTG	TACTTGAGAA	TGGCTGTACT	GAATTAGACT	GGATAACAGG	GACAGGAGAC	600
TTGGTTGGAG	CCTTAACAGC	TGTTTTTCTC	AGCCAAGGAA	AGACTGGTTT	TGAAGCTTCT	660
TGCTTAGCAG	TCTCTTATCT	CAATATCGCT	GCTGAGAAAA	TAGTTGTTCA	AGGAATGGGA	720
TTGGAAGAAT	TCGTTACCA	AGTACTCAAT	CAGCTTTCGC	TCCTAAGAAG	AGATGAAAAT	780
TGGCTAGATA	CCATCAAAGG	AGAGGTTTAT	GAATAG			816

(2) INFORMATION FOR SEQ ID NO:2224:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 738 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2224:

GGACAAAGAA	TGATTGAATA	CAAAAATGTA	GCACTGCGCT	ACACAGAAAA	GGATGTCTTG	60
AGAGATGTCA	ACTTACAGAT	TGAGGATGGG	GAATTTATGG	TTTTAGTAGG	GCCTTCTGGG	120
TCAGGTAAGA	CGACCATGCT	CAAGATGATT	AACCGTCTTT	TGGAACCAAC	TGATGGAAAT	180
ATTTATATGG	ATGGGAAGCG	CATCAAAGAC	TATGATGAGC	GTGAACTTCG	TCTTTC TACT	240
GGTTATGTTT	TACAGGCTAT	TGCTCTTTTT	CCAAATCTAA	CAGTTGCGGA	AAATATTGCT	300
CTCATTCCTG	AAATGAAGGG	GTGGAGCAAG	GAAGAAATTA	CGAAGAAAAC	AGAAGAGCTT	360
TTGGCTAAGG	TTGGTTTACC	AGTAGCCGAG	TATGGGCATC	GCTTACCTAG	TGAATTATCT	420
GGTGGAGAAC	AGCAACGGGT	CGGTATTGTC	CGAGCTATGA	TTGGTCAGCC	CAAGATTCTC	480
CTCATGGATG	AACCCTTTTT	AGCCTTGGAT	GCTATTTCTC	GCAAGCAGTT	GCAGGTTCTG	540
ACAAAAGAAT	TACATAAAGA	GTTTGGGATG	ACAACGATTT	TTGTGACTCA	TGATACGGAT	600
GAAGCCTTAA	AGTTGGCAGA	TCGTATTGCT	GTTTTGCAGG	ATGGAGAGAT	TCGTCAGGTG	660
TCGAATCCTG	AGACTATTTT	AAAAGCTCCT	GCAACAGACT	TTGTTGCAGA	CTTGTTTGGG	720
GGTAGTATTC	ATGACTAA					738

(2) INFORMATION FOR SEQ ID NO:2225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2225:

AATAAAAGAA	TATNTAACGA	CTTCCAAGCT	TCAAAAATGA	ATTTAAACAT	TTACACAAGC	60
CCCTTGTTAG	CCTTTGTTTT	TGTCTTCATA	GGAGAGTTTG	TGGCTTATAC	TTTATATGGT	120
ATTAGTTTGT	TAGCTCTCAT	CGGACTTGCT	AGAAATTTTG	GAGAGGCTGG	TCAAAATCTT	180
GCAAGCTACT	TGCAGACCTT	GCATCAGAGC	TTGACGGATA	AAACAAGTGA	CTTTCGTTTA	240
ATTTTAGGAT	TACTGGCCTT	TGGTTTTATT	CTTAACACTG	TGTTCAAGATG	GACAAGAAAA	300
GTTGAGAAAA	GACCTATTCG	AACCTTGGGA	TTTTATAGAG	AGATTTTCCTC	AGCAATCTTC	360
TGA						363

(2) INFORMATION FOR SEQ ID NO:2226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2226:

GTGGGAAGAA TTATCAGATC AGGTGTAAAG ATGGAACATC TTGGAAAAGT ATTTTCGTGAA	60
TTTCGAACAA GTGGAAATTA TTCTTTAAAG GAAGCAGCAG GCGAATCCTG CTCTACCTCT	120
CAGTTATCTC GCTTTGAGCT TGGGGAGTCT GACCTGGCAG TCTCCCGTTT CTTTGAGATT	180
TTGGATAACA TTCATGTAAC AATCGAAAAT TTCATGGATA AGGCAAGGAA TTTTCATAAT	240
CATGAACATG TGTCATATGAT GGCACAGATT ATCCCAC'TTT ACTATTCAAA CGATATTGCA	300
GGTTTTTCAAA AGCTTCAAAG AGAACAACTT GAAAAGTCTA AGAGTTCGAC GACTCCCCCTT	360
TATTTTGAGC TGAAGTGGAT TTTGCTACAA GGTCTGATTT GTCAAAGAGA TGCGAGTTAT	420
GATATGAAGC AGGATGATTT GGATAAGGTA GCAGATTATC TCTTCAAAAC AGAAGAATGG	480
ACCATGTATG AGTTGATTCT TTTCGGTAAC CTCTATAGTT TCTACGATGT AGACTATGTC	540
ACTCGGATTG GTAGAGAAAGT TATGGAGAGG GAGGAATTTT ACCAAGAGAT TAGTCGCCAT	600
AAGAGATTAG TTTTGATTTT GGCCCTCAAT TGTTACCAGC ATTGTTTAGA GCATTCTTCT	660
TTTTATAATG CCAACTATTT TGAGGCTTAT ACAGAGAAGA TTATTGACAA AGGTATTAAG	720
CTTTATGAGC GTAATGTTTT CCATTATTTA AAAGGTTTTG CTTTATATCA AAAAGGACAG	780
TGTAAAGAAG GCTGTAAAGCA GATGCAAGAG GCCATACATA TTTTGTATGT GTTAGGTCTT	840
CCAGAGCAAG TAGCCTATTA TCAGGAACAC TACGAAAAAT TTGTCAAAAG TTAA	894

(2) INFORMATION FOR SEQ ID NO:2227:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2227:

CCTATGAGAA TTATGGGATT GGACGTCGGT TCAAAAACGG TAGGGGTGGC GATTAGCGAT	60
CCGCTTGTTT TTACAGCTCA AGGGCTTGAA ATCATCCAGA TAAATGAAGA ACAAGGCCAA	120
TTTGGTTCTG ACCGCGTTAA GGAATTGGTT GATACTTACA AGGTGGAACG ATTTGTAGTG	180

GGCTTGCCTA AAAACATGAA CAATACAAGT GGACCGCGCG TAGAAGCTAG TCAAGCATAC	240
GGAGCAAAGC TAGAAGAGTT TTTTGGTTTA CCAGTAGACT ATCAGGAGTG A	291

(2) INFORMATION FOR SEQ ID NO:2228:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...201
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2228:

AATGCGAGAA TGAAAGCACT TTGTATTTTT TTATTGAATA TGTTAGCTTG GACAGTGCTT	60
GCAATGATAA TCCGTGGAGG GCTAGATGGA TTTGATAGGC ATACTTGGAG TACTATTTTA	120
ATTGCTTCGC TGTTCGGGGT ATATGATTAT AAGCCCATAG ATAAAAATAG AAAAAAGTCC	180
AAAAGAAAAA AGAAAAATA G	201

(2) INFORMATION FOR SEQ ID NO:2229:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 573 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...573
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2229:

GAGCAGAGAA TGACAAAACG TTGTTCGTGG GTCAAGATGA CCAACCCGCT CTACATCGCC	60
TATCATGATG AGGAGTGGGG CCAGCCCCCTC CATGATGACC AAGCATTGTT TGAGTTGTTG	120
TGTATGGAAA CCTATCAGGC AGGCCTGTCT TGGGAAACGG TACTCAACAA ACGCCAAGCT	180

TTCCGAGAAG	CATTTTCATAG	CTATCAAATT	CACTCAGTCG	CAGAGATGAC	TGACACTGAA	240
TTGGAAGCCA	TGCTGGAGAA	TCCAGCTATC	ATTTCGAAATA	GAGCCAAGAT	TTTTTGCTACA	300
CGCGCTAACG	CCCAAGCTTT	TCTACAGTTA	CAGGCAGAGT	ACGGCTCTTT	TGATGCCTAT	360
CTTTGGTCTT	TTGTTGAGGG	GAAAAATTGTC	GTTAACGATG	TTCCTGATTA	TCGCCAAGCG	420
CCAGCTAAAA	CACCCTTATC	TGAGAAATTA	GCCAAAGATC	TCAAAAAACG	AGGCTTCAAG	480
TTCACAGGCC	CAGTCGCCGT	ATTGTCTTTT	CTACAGGCTG	CAGGGCTAGT	TGATGACCAC	540
GAGAATGATT	GTGAGTGGAA	AGGTCTTAAA	TGA			573

(2) INFORMATION FOR SEQ ID NO:2230:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 873 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...873
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2230:

GAGGAGAGAA	TAAAGAAATT	AGCCAAAAGA	ATTAGTAGAA	AAGAATGGGG	GATGATTTTA	60
CTAGCCATTC	TCTTTACTTG	CTTTTCGGTC	TATCTAGAGT	TGGAAGTGCC	GACCTATATC	120
TCGAAAATTA	CGGATTGCT	AGGTAGTCAA	GAAACTAATT	TAGATGAGTT	GTGGCAGCCG	180
GCAAGCATGA	TGATGGGAAT	GTCCTTCTT	GCCTTCTTGT	CCGTAGTTGC	AGTTGGATTT	240
TTTGCATCCC	GAGTGGCGGC	TTCTTATACT	AGTAGGCTGA	GAAGTGATAT	TTTTAACCGA	300
GTTTTGGATT	ACTCGCAGAC	AGAGATTAAG	AAATTTTCAA	TTCCTAGCCT	CTTGACGCGT	360
ACTACCAATG	ACATTACTCA	AGTTCAAATG	TTGATTACTA	TGGGCTTGCA	AGTGGTAACG	420
CGTGGTTCAA	TTATGGCTAT	CTGGGCTATT	GGGAAGATTT	TAGGTCATTC	AGAATACTGG	480
CTCTGGGCCG	TACTTGTGGT	AGTGATTGTC	AACGTCCTGA	TGACGACCGT	TTTGATGACG	540
CTAGCCTTTC	CAAAACAGTC	CTTGATTGAG	GGGTTGACAG	ATAAACTGAA	CAGTATCACT	600
CGTGAGAGTT	TAACAGGTAT	TCGTGTCGTT	CGTGCCCTACA	ATGCAGAGGA	TTATCAAAAT	660
GAAAAATTTG	CAGCAGTAAA	TGATGAATTG	ACCCGTTTGA	ATTTGTTTGT	CAACCGTCTT	720
ATGGCTATTT	TGAATCCTAT	CATGATGGGG	ATTTCAAGTG	GTTTGAGTGT	AGCGATTTAC	780
TGGATTGGGG	CCTATGTGAT	TAACGACGCT	GCTCCGATAG	CGCGTCTGCC	TCTCTTTAGT	840
GACATGATTG	TTTTCATGTC	TTATGCCATG	TAG			873

(2) INFORMATION FOR SEQ ID NO:2231:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 285 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2231:

AAACGGAGAA	TGAGAAATAT	GGCTTTGACA	GCAGGTATCG	TTGGTTTGCC	AAACGTTGGT	60
AAATCAACAC	TATTTAATGC	AATTACAAAA	GCAGGAGCAG	AGGCAGCAAA	CTACCCATTT	120
GCGACTATTG	ATCCAAATGT	TGGAATGGTG	GAAGATCCAG	ATGAACGCCCT	ACAAAAACTA	180
ACTGAAATGA	TAACCTCCTAA	AAAGACAGTT	CCCACAACAT	TTGAATTTAC	GGATATTGCA	240
GGGATTGTAA	AAGGAGCTTT	CAAAAGGAGA	AGGGCTAGGG	AATAA		285

(2) INFORMATION FOR SEQ ID NO:2232:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1065 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2232:

ACAAGGAGAA	TCACAATGGT	AGAATTGGGA	ATTTCAACAT	TTGGGGAAAT	AACGGAGCTT	60
GAAGGGACTG	GACAAACTTA	CAGTCATGCT	GAACGCATTC	GCCAGTTGGT	GGCAGAGATT	120
GAGCTGGCTG	ACAAGGTTGG	TTTGGACGTA	TATGGGATTG	GCGAGCACCA	TCGGGCGGAT	180
TTTGCAGTAT	CAGCCCCAGA	GATTGTCCCTG	GCCGCTGGGG	CAGTCAATAC	CAAGAAAATC	240
CGTTTGACCA	GTGCAGTCAG	CATTCTGTCA	AGCATGGACC	CGATTCTGTTT	GTTCCAACAG	300
TATGCCACTA	TCGATGCTTT	GTCAAATGGA	CGATCGGAGA	TTATGGCTGG	AAGGGGCTCT	360
TTCACGGAAT	CTTTCCCTCT	GTTTGGTTAT	GACTTGAAAG	ACTACGACTC	TCTTTTTGAT	420
GAGAAATTAG	ACTTGCTTCA	GTTAGTCAAT	GAAAAGACCA	AGTTAGACTG	GCAAGGTCGA	480
TTGACTCAAA	CGATTGCTGG	TAAAGAAGTT	TATCCTCGTC	CAGTTCAGGA	CAAATTGCCC	540
ATGTGGATAG	CTACAGGTGG	TCATGTCGAA	TCAACAGTGA	AGATTGCTCA	GGCTGGTCTA	600
CCGATTGTAT	ATGCTATTAT	TGGTGGTAAT	CCACGTTATT	TTAAAAAGTT	GATTTCAGGCT	660
TATCGTGAGA	TTGGAAGCGA	AGCGGGTCAT	GCTGACAAAG	ACTTGAAAGT	GGGAGCCCAT	720
TCTTGGGGGT	GGATTGCGGA	AGATGGTGAG	CAGGCGGTGA	AAGATTATTT	CCATCCGACT	780
AAGCAAGTGG	TGGATGCTAT	TTCCAAAGAC	CGTCCGCACT	GGCAGGAATT	GCGTTATGAG	840

CAATATTTGG	AGCAGGTAGG	GCCAAATGGC	GCCATGTTTG	TTGGCAATCC	AGATCAGGTG	900
GCCGAAAAAT	TGATTCGCAT	GATAGAGGAT	TTAGGATTGG	ACCGCTTCAT	GCTTCATCTA	960
CCGCTTGGTT	CTATGCCCTCA	TGACCAGGTT	CTGAGAGCTA	TTGAACTCTT	CGGAACACAA	1020
GTTGCACCCA	AAGTACGAGC	TTATTTTGCT	ATGAAAGAGG	CTTAA		1065

(2) INFORMATION FOR SEQ ID NO:2233:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 750 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...750
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2233:

AAAAGGAGAA	TGAATATGAA	AAAGAAACGT	AGATTGTTAT	TTTTGATGTC	TATTGTCTTG	60
GGGGGGTTCT	TGGGCATGTT	TGTAGGGATG	TTTAAGGCAC	GTGTCGAATC	CCACGAAATT	120
ATTTTAGATG	TAAAAGCCTT	GATGCCATGG	ATATCAGCTA	TTTGTTTACT	GATAGGTTTC	180
ATTAGTATGT	TTTTGACTTT	CAATTTCTTA	AAGAAAAGCA	GAAAATTTCA	TTCCTTGTAT	240
CAAGAGGAAA	TGGATGACGA	TCTGAATGAA	ACCTATTATG	TGCAAATGTA	TCGGAATCCT	300
GAGTTTGGA	CCATTGCTTT	TAATATTACA	GGTGTAGCGA	TTCCATTGGC	TATTTTTATT	360
TCATTAAGTG	AGGTGATTAT	ATTGCATACA	AACCCTCAAA	CATTTTTTCCT	TTCTTTCTTA	420
CTCTTTGTGG	TATTCTTAGT	CGCTCAAAAA	TCTCTTTTTA	AAACCATTGC	GATTGTTCGT	480
CAGTTTGATT	TGGAATTTTT	CGCTACACCA	AAGGATGTCT	TGAACTATAT	AAATTCTTAT	540
GATGAAGGGG	AGCGTCAGGC	TAATTTGGAA	CAGAGTTTTC	GAATTTTATT	CCAATTACAC	600
CAATATGTCT	TACCAGCCTT	ATATATTTTT	CTTATTATCA	TTTCTTTCTT	GACAGGAGAG	660
ATTCAGTTAC	TAGCTTCTTT	GCTTGTAGGA	GCCATCCATG	TTTATATCAA	TGTGATGCAG	720
TTACCTATGG	TAAAACGTTA	TTTCAAATAA				750

(2) INFORMATION FOR SEQ ID NO:2234:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 405 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2234:

AAAAGGAGAA	TCCTTATGGG	TAAATTATCC	TCAATCCTTT	TAGGAACCGT	TTCAGGTGCA	60
GCTCTTGCCT	TGTTTTTAAC	AAGTGATAAG	GGCAAACAAG	TTTGCAGTCA	GGCTCAAGAT	120
TTTCTAGATG	ATTTGAGAGA	AGATCCGGAG	TATGCCAAGG	AGCAAGTCTG	TGAAAACTG	180
ACAGAAGTTA	AGGAGCAGGC	TACAGATTTT	GTTCTGAAAA	CAAAAGAACA	GGTTGAGTCA	240
GGTGAATCA	CTGTGGACAG	TACTATTGCT	CAAGCTAAAT	CCTATGCTTT	TCAAGCGACA	300
GAAGCATCAA	AAAATCAATT	AAATAATCTC	AAGGAACAAT	GGCAAGAAAA	AGCCGAAGCT	360
CTTGATGACT	CAGAAGAGAT	TGTGATTGAT	ATAACAGAAG	AATAA		405

(2) INFORMATION FOR SEQ ID NO:2235:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 843 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2235:

GCTATGGGAA	TTGCTCTAGA	AAATGTGAAT	TTTACATATC	AAGAAGGTAC	TCCCTTAGCT	60
TCAGCAGCTT	TGTCGGATGT	TTCTTTGACG	ATTGAAGATG	GCTCTTATAC	AGCTTTAATT	120
GGGCACACAG	GTAGTGGTAA	ATCAACTATT	TTACAACTCT	TAAATGGTTT	ATTGGTGCCA	180
AGTCAAGGGA	GTGTGAGGGT	TTTTGATACC	TTAATCACCT	CGACTTCTAA	AAATAAAGAT	240
ATTCGTCAAA	TTAGAAAAACA	GGTTGGCTTG	GTATTTTCAGT	TTGCTGAAAA	TCAGATTTTTT	300
GAAGAAACGG	TTTTGAAGGA	CGTTGCTTTT	GGACCGCAAA	ATTTTGGAGT	TTCTGAAGAA	360
GATGCTGTGA	AGACTGCGCG	TGAGAACTG	GCTCTGGTTG	GAATTGATGA	ATCACTTTTTT	420
GATCGTAGTC	CGTTTGAGCT	GTCAGGGGGA	CAAATGAGAC	GTGTTGCCAT	TGCAGGCATA	480
CTTGCCATGG	AGCCAGCTAT	ATTAGTCTTA	GATGAGCCAA	CAGCTGGTCT	AGATCCTCTA	540
GGGAGAAAAG	AGTTGATGAC	CCTGTTCAAA	AAACTCCACC	AGTCAGGGAT	GACCATCGTC	600
TTGGTAACGC	ATTTGATGGA	TGATGTTGCT	GAATATGCGA	ATCAAGTCTA	TGTAATGGAA	660
AAGGGACGTT	TAGTAAAGGG	GGGCAAACCA	AGTGATGTCT	TTCAAGACGT	TGTTTTTATG	720
GAAGAAGTTC	AGTTGGGAGT	ACCTAAAATT	ACGGCCTTTT	GTAAACGATT	GGCTGATAGA	780
GGCGTGTCAT	TTAAACGATT	ACCGGTTAAG	ATAGAGGAGT	TCAAGGAGTC	GCTAAATGGA	840
TAG						843

(2) INFORMATION FOR SEQ ID NO:2236:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...306
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2236:

GTTTCAACCT	TGCGGTCGTA	CTCCCCAGGC	GGAGTGCTTA	ATGCGTTAGC	TACGGCACTA	60
AACCCCGGAA	AGGGTCTAAC	ACCTAGCACT	CATCGTTTAC	AGCGTGGACT	ACCAGGGTAT	120
CTAATCCTGT	TTGCTCCCCA	CGCTTTCGAG	CCTCAGCGTC	AGTTACAAGC	CAGAGAGCCG	180
CTTTCGCCAC	CGGTGTTCCCT	CCATATATCT	ACGCATTTCA	CCGCTACACA	TGGAATTCCA	240
CTCTCCCCTC	TTGCACTCAA	GTAAACAGT	TTCCAAAGCC	TACTATGGTT	AAGCCACAGC	300
CTTTAA						306

(2) INFORMATION FOR SEQ ID NO:2237:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...495
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2237:

TACACTTTGA	TTTCTAAGAC	ATTGTTAGAA	ATTAGATTAA	ATTCCTTAAT	CGATTTGCGC	60
ATGTTTTTATT	TCATTTCACT	ATACTTTAGA	TTGGAAAATA	AGGAATCACA	TAAATCGCAA	120
GAAATAGGGA	ATCTGATTCT	TGTTTATAAC	CGTTCAAAAA	GAGAAGAGGC	TGAAAGTGAG	180

CCACTTAATC	TTTATGTCGA	AGATGAAAAG	GGCAATCTCC	TGGCAGGTTT	GATAGCAGAG	240
ACTTTTGGAA	ATTGGCTAGA	ACTAGAAATC	GAGTATTTGT	TTGTAAAAGA	GGAAC TGCGA	300
GGACAAGGAA	TCGGTTCAAA	ACTATTGCAA	CAGGCAGAAA	GTGAAGCTAA	GAATCGAAAT	360
TGTTGTTTTG	CCTTTGTCAA	TACTTACCAG	TTCCAGGCAC	CGGACTTTTA	TCAGAAACAT	420
GGCTACAAGG	AAGTTTTTTC	TTTGCAAGAC	TATCTCTACA	TTAGGCAAAG	ATATTATTAC	480
CAAAAGAATC	TGTAA					495

(2) INFORMATION FOR SEQ ID NO:2238:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...303
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2238:

TTCTTCTTGA	TCATAAATAT	CTTCTTGCCA	CGGTTCTTTT	GCCATACCTT	ACTCCTTGTT	60
TTTTTTTACT	TTTCTTATTA	CAATATAAAT	ATGAACATGA	AAATCACACT	TATACCTGAA	120
CGATGTATCG	CCTGTGGACT	TTGCCAAACT	TATTCTGATT	TATTTGATTA	CCACGATAAT	180
GGAATCGTGC	GTTTTTACGA	TGACCCTGAC	CAACTGGAAA	AAGAAATTTT	TCCTAGTCAG	240
GATGTCTTAG	AGGCTGTAA	AAATTGCCCA	ACTCGCGCCC	TGATTGGAAA	CCAGGAAGCC	300
TAA						303

(2) INFORMATION FOR SEQ ID NO:2239:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 252 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2239:

CAGGGCTTGA	TGGAAGTTCA	GGCTAGCTCC	AATCTAAAAG	AATTTTAAAG	CAAGCAGAAT	60
CATCAGGCCA	AGATTTCTTC	AACTGATGAG	GTTTCAGGTTT	TGTTCCCTTAA	AAAGACACCC	120
AAAATCATAT	CCCTAGTCAA	GGAATGGAAT	CCTACTATTG	ATCTGATTGG	TTTCAAACCTG	180
CTGGTTGATG	TTACCGAAGA	TCATCTGGTT	GACATTGCAC	GAAAAATCTT	ATCAAGAATC	240
AAGCAGATTT	AA					252

(2) INFORMATION FOR SEQ ID NO:2240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...3243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2240:

TTCTTATTGA	TTTTACAATA	TGTTTATTGG	AGTGTATACA	TGCAAACAAA	AACAAAGAAG	60
CTCATTGTGA	GTTTGTCTTC	ACTTGTTTTA	TCAGGATTTT	TATTAAACCA	TTATATGACA	120
GTTGGAGCGG	AAGAAACGAC	TACGAATACT	ATTTCAGCAA	GCCAGAAGGA	AGTTCAGTAT	180
CAGCAAAGGG	ATACAAAAAA	TTTAGTTGAA	AATGGTGATT	TTGGTCAGAC	GGAGGACGGA	240
AGCAGTCCGT	GGACAGGAAG	CAAAGCTCAG	GGGTGGTCAA	CTTGGGTTAG	CCAGAAGAAT	300
AGTTCCTGCAG	ATGCCCTCAAC	TCGAGTCATT	GAGGCTAAGG	ATGGGGCTAT	CAC'TATCTCA	360
AGCCCTGAGA	AATTAAGGGC	AGCGGTTCCAC	CGTATGGTTC	CTATTGAAGC	TAAGAAAAAG	420
TATAAACTGC	GTTTCAAGAT	TAAAACAGAT	AATAAAGTCG	GGATTGCCAA	AGTTCGTATC	480
ATTGAGGAAA	GTGGTAAGGA	CAAGCGATTG	TGGAATTCTG	CAACGACGTC	AGGAACAAAG	540
GACTGGCAGA	CCATTGAAGC	AGACTATAGC	CCGACTTTAG	ATGTTGATAA	AATCAAGCTG	600
GAGTTATTCT	ATGAAACAGG	AACTGGGACT	GTTTCCTTTA	AGGATATTGA	GCTGGTAGAG	660
GTAGCAGACC	AGCTTCTCTGA	GGATTCTCAA	ACAGATAAAC	AGCTTGAGGA	AAAGATTGAT	720
TTACCAATTG	GAAAAAAACA	TGTTTTTTCT	CTTGCGGACT	ATACTTATAA	GGTAGAAAAAT	780
CCTGACGTTG	CTTCAGTCAA	AAATGGAATT	TTAGAACCCT	TTAAGGAAGG	GACAACCAAT	840
GTCATTGTCA	GTAAAGATGG	CAAGGAAGTG	AAAAAGATTC	CTTTGAAGAT	TCTAGCCTCT	900
GTTAAGGATG	CATACACAGC	CCGTTTGGAT	GACTGGAATG	GCATCATCGC	TGGGAATCAA	960
TACTATGATT	CTAAAAATGA	ACAGATGGCC	AAATTAAACC	AGGAATTGGA	AGGAAAGGTA	1020
GCTGATAGCC	TATCTAGTAT	TTCAAGTCAG	GCGGACCGCA	CCTATTTGTG	GGAAAAATTT	1080
TCAAATTATA	AAATGTCTGC	AAATCTGACT	GCCACTTATC	GGAAATTGGA	GGAGATGGCC	1140
AAGCAAGTGA	CCAATCCTTC	TTCTCGTTAT	TATCAAGATG	AAACTGTCGT	TCGAACAGTC	1200
AGGGATTCCA	TGGAATGGAT	GCATAAACAT	GTCTACAATA	GTGAAAAGAG	CATTGTTGGG	1260
AACTGGTGGG	ATTATGAAAT	CGGTACACCT	CGTGCCATCA	ACAATACCTT	GTCTCTGATG	1320
AAAGAATACT	TCTCTGATGA	GGAAATTAAA	AAATATACAG	ATGTAATTGA	AAAATTTGTA	1380
CCAGACCCCG	AACATTTCCG	AAAGACGACT	GATAACCCAT	TTAAGGCTCT	AGGTGGAAAC	1440

TTAGTTGATA	TGGGAAGAGT	AAAAGTAATA	GCTGGTTTAC	TGCGTAAAGA	TGATCAAGAA	1500
ATTTCTTCTA	CCATTCGCTC	GATTGAGCAA	GTGTTCAAGT	TGGTAGACCA	AGGTGAAGGT	1560
TTTTATCAAG	ATGGATCCTA	TATCGACCAC	ACCAATGTTG	CCTATACGGG	TGCTTATGGG	1620
AATGTTTTGA	TTGATGGCCT	GTCTCAACTG	TTGCCAGTCA	TTCAAAAGAC	CAAGAATCCA	1680
ATCGATAAAG	ATAAAATGCA	AACCATGTAC	CACTGGATTG	ATAAATCGTT	TGCTCCTTTG	1740
CTGGTGAATG	GAGAGCTGAT	GGATATGAGT	CGTGGACGCT	CGATCAGTCG	TGCAAATAGC	1800
GAGGGGCACG	TGGCCGCAGT	AGAAGTACTA	AGAGGGATTG	ACCGAATAGC	GGATATGTCT	1860
GAAGGAGAAA	CCAAACAACG	TTTGCAGAGT	CTTGTGAAGA	CCATTGTTCA	ATCGGATAGT	1920
TATTATGATG	TCTTTAAGAA	TTTGAAGACT	TATAAGGATA	TCAGTTTGAT	GCAATCCTTG	1980
TTAAGTGATG	CAGGAGTCGC	AAGTGTTCCA	AGAACAAGTT	ACCTATCTGC	CTTTAACAAG	2040
ATGGATAAAA	CAGCCATGTA	CAATGCAGAG	AAAGGGTTTG	GATTTGGCTT	GTCAC'TCTTT	2100
TCCAGTCGTA	CCTTGAATTA	CGAACACATG	AACAAGGAAA	ATAAACGTGG	TTGGTATACG	2160
AGTGATGGGA	TGTTCTATCT	TTACAATGGC	GATTTGAGTC	ACTATAGCGA	TGGCTACTGG	2220
CCAACAGTTA	ATCCATATAA	GATGCC'TGGT	ACAACAGAGA	CGGATGCTAA	GAGAGCGGAT	2280
AGCGATACAG	GTAAAGTTTT	ACCGTCTGCT	TTCGTTGGAA	CGAGCAAAC'T	AGATGATGCC	2340
AATGCGACAG	CAACCATGGA	TTTCACCAAC	TGGAATCAAA	CATTGACTGC	TCATAAGAGC	2400
TGGTTTATGC	TGAAGGATAA	GATCGCCTTT	TTAGGAAGCA	ATATCCAAAA	CACTTCAACA	2460
GATACTGCTG	CAACTACAAT	TGACCAGAGA	AAACTGGAAT	CAAGTAATCC	ATATAAAGTC	2520
TATGTCAATG	ATAAAGAAGC	CTCCC'TTACA	GAACAAGAAA	AGGATTATCC	TGAAACCCAA	2580
AGTGTCTTTT	TAGAATCGTC	CGATTGCAAA	AAGAATATTG	GTTACTTTTT	CTTTAAGAAG	2640
AGTTCAATCA	GTATGAGTAA	GGCTTTGCAA	AAGGGAGCCT	GGAAGGATAT	CAATGAAGGA	2700
CAGTCAGACA	AGGAAGTTGA	AAATGAATTT	CTTACGATTA	GTCAGGCTCA	TAAGCAAAAT	2760
GGAGATTCTT	ATGGCTATAT	GCTCATCCCT	AACGTGGATC	GTGCCACCTT	CAATCAAATG	2820
ATAAAAGAGT	TAGAAAGTAG	CCTCATCGAA	AATAACGAAA	CCCTTCAGTC	TGTTTATGAT	2880
GCTAAACAAG	GAGTTTGGGG	CATTGTGAAA	TATGATGATT	CTGTCTCTAC	TATTTCCAAC	2940
CAATTCCAAG	TTTTGAAACG	TGGAGTCTAT	ACCATTGCAA	AAGAAGGGGA	TGAATATAAG	3000
ATTGCC'TACT	ATAATCCTGA	AACCCAGGAA	TCAGCTCCAG	ATCAGGAAGT	CTTTAAAAAG	3060
CTAGAGCAAG	CAGCTCAGCC	ACAAGTACAG	AATTCAAAAG	AAAAGGAAAA	ATCTGAAGAG	3120
GAAAAGAACC	ATTTCGGATCA	AAAGAATCTC	CCTCAGACAG	GAGAAGGTCA	GTCAATCTTG	3180
GCAAGTCTAG	GGTTCTTGCT	ACTTGGGGCA	TTTTATCTAT	TCCGTAGAGG	AAAGAACAAC	3240
TAA						3243

(2) INFORMATION FOR SEQ ID NO:2241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2241:

TTCCAATTGA	TCATAAGAAA	TACAACTACT	GTCCAAATCA	TACCAATTAT	GAACGGTATT	60
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ACAAATTTAT	ATGTTTGTAT	TTCTAATGAT	ATCATAGCTG	ATACCATCGC	CGATACAAAT	120
GCAGACAACA	ATACTGAGGT	AACAAAATTC	CTTACCGCTT	CATCATTTTT	GACACAAC TA	180
TCATGCTCAG	CTAATATAAT	TTCTCTATAT	CTAGCTAAAT	ATTCTATTGG	AATATTATCA	240
ATAAAATCTT	TTGATGTTCT	ATAG				264

(2) INFORMATION FOR SEQ ID NO:2242:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1416 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1416
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2242:

CGAGAATTGA	TGATGAAATA	CCTCGAAGGT	GAAGAAATCA	CTAACGAAGA	ATTGAAAGCT	60
GGTATCCGTA	AAGCGACTAT	CAACGTTGAA	TTCTTCCCAG	TATTGTGTGG	TTCAGCCTTC	120
AAAAACAAAG	GTGTTCAATT	GATGCTTGAT	GCGGTTATCG	ACTACCTTCC	AAGTCCACTT	180
GACATCCCAG	CAATCAAAGG	TATTAACCCA	GATACAGACG	CTGAAGAAAC	TCGTCCAGCA	240
TCTGACGAAG	AGCCATTTGC	AGCTCTTGCC	TTCAAGATCA	TGACTGACCC	ATTTCGTAGGT	300
CGTTTGACAT	TCTTCCGTGT	TTACTCAGGT	GTTCTTCAAT	CAGGTTTATA	CGTATTGAAT	360
ACTTCTAAAG	GTAAACGTGA	ACGTATCGGA	CGTATCCTTC	AAATGCACGC	TAACAGCCGT	420
CAAGAAATCG	ACACTGTTTA	CTCAGGTGAT	ATCGCTGCTG	CCGTTGGTTT	GAAAGATACT	480
ACAACTGGTG	ACTCATTGAC	AGATGAAAAA	TCTAAAAATCA	TCCTTGAGTC	AATCAACGTT	540
CCAGAACCAG	TTATCCAATT	GATGGTTGAA	CCAAAACTTA	AAGCTGACCA	AGACAAGATG	600
GGTATCGCCC	TTCAAAAAAT	GGCTGAAGAA	GATCCAACAT	TCCGCGTTGA	AACAAACGTT	660
GAAACTGGTG	AAACAGTTAT	CTCAGGTATG	GGTGAACTTC	ACCTTGACGT	CCTTGTTGAT	720
CGTATGCGTC	GTGAGTTCAA	AGTTGAAGCG	AACGTAGGTG	CGCCTCAAGT	ATCTTACCGT	780
GAAACATTCC	GCGCTTCTAC	TCAAGCACGT	GGATTCTTCA	AACGTCAGTC	TGGTGGTAAA	840
GGTCAATTTCG	GTGATGTATG	GATTGAATTT	ACTCCAAACG	AAGAAGGTAA	AGGATTCGAA	900
TTTCGAAAACG	CAATCGTCGG	TGGTGTGGTT	CCTCGTGAAAT	TTATCCCAGC	GGTTGAAAAA	960
GGTTTGGTAG	AATCTATGGC	TAACGGTGTG	CTTGACGGTT	ACCCAATGGT	TGACGTTAAA	1020
GCTAAGCTTT	ATGATGGTTC	ATATCACGAT	GTCGACTCAT	CTGAAACTGC	CTTCAAGATT	1080
GCGGCTTCAC	TTTCCCTTAA	AGAAGCTGCT	AAATCAGCAC	AACCAGCTAT	CCTTGAACCA	1140
ATGATGCTTG	TAACAATCAC	TGTTCCAGAA	GAAAACCTTG	GTGATGTTAT	GGGTCACGTA	1200
ACTGCTCGTC	GTGGACGTGT	AGATGGTATG	GAAGCACACG	GTAACAGCCA	AATCGTTCGT	1260
GCTTACGTTT	CACCTGCTGA	AATGTTCCGT	TACGCAACAG	TTCTTCGTTT	TGCATCTCAA	1320
GGACGTGGTA	CATTATGATG	GGTATTTGAC	CACTACGAAG	ATGTACCTAA	GTCAGTACAA	1380
GAAGAAATTA	TTAAGAAAAA	TAAAGGTGAA	GAATAA			1416

(2) INFORMATION FOR SEQ ID NO:2243:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 609 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2243:

ACACAGTTGA	TGAGTATATC	CCAGAACCAG	AACGTGACAC	TGACAAACCA	TTGCTTCTTC	60
CAGTCGAGGA	CGTATTCTCA	ATCACTGGAC	GTGGTACAGT	TGCTTCAGGA	CGTATCGACC	120
GTGGTATCGT	TAAAGTCAAC	GACGAAAAC	ATATTGTTGG	TATCAAAGAA	GAAAACCTCG	180
AACCCCTTGT	TTCCGGGTGT	TGAAATGTTT	CGTAAACAAC	TTGACGAAGG	TCTTGCTGGA	240
GATAACGTAG	GTGTCCTTCT	TCGTGGTGTT	CAACGTGATG	AAATCGAACG	TGGACAAGTT	300
ATCGCTAAAC	CAGGTTCAAT	CAACCCACAC	ACTAAATTCA	AAGGTGAAGT	CTACATCCTT	360
ACTAAAGAAG	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGTCC	ACAATTCTAC	420
TTCCGTACTA	CTGACGTTAC	AGGTTCAATC	GAACTTCCAG	CAGGTACTGA	AATGGTAATG	480
CCTGGTGATA	ACGTGACAAT	CGACGTTGAG	TTGATTACAC	CAATCGCCGT	AGAACAAGGT	540
ACTACATTCT	CTATCCGTGA	GGGTGGACGT	ACTGTTGGTT	CAGGTATGGT	TACAGAAATC	600
GAAGCTTAA						609

(2) INFORMATION FOR SEQ ID NO:2244:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3510 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...3510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2244:

ATGGTGACCT	TATTAGATTT	ATTCTCAGAA	AATGATCAGA	TTAAAAAATG	GCATCAAAAT	60
TTAACAGATA	AGAAAAGACA	ACTAATACTT	GGTTTATCAA	CATCTACTAA	GGCTCTTGCA	120
ATTGCAAGCA	GTTTAGAAAA	AGAAGATAGG	ATTGTGTTAT	TGATGTCAAC	TTATGGAGAA	180

GCAGAAGGAC	TTGTTAGTGA	TCTTATATCT	ATCTTGGGTG	AGGAACTCGT	CTATCCATTT	240
TTGGTAGATG	ATGCTCCTAT	GGTGGAGTTT	TTGATGTCTT	CACAGGAAAA	AATTATTTCA	300
CGGGTTGAAG	CCTTGCCTTT	TTTGA CTGAT	TCATCTAAGA	AAGGGATTTT	AGTTTGTAAT	360
ATCGCAGCAA	GTCGATTGAT	TTTACCGTCT	CCCAATGCAT	TCAAAGATAG	TATTGTAAAA	420
ATCTCAGTTG	GTGAAGAATA	TGATCAACAC	GCGTTTATCC	ATCAGTTAAA	GGAAAATGGC	480
TATCGAAAAAG	TTACTCAAGT	ACAAACTCAG	GGCGAATTTA	GTCTTCGAGG	AGATATTTTA	540
GATATTTTTG	AAATATCCCA	GTTAGAACCCT	TGTCGAATTG	AGTTTTTTGG	TGATGAAATT	600
GATGGTATCA	GGTCATTTGA	AGTAGAAACA	CAATTATCGA	AAGAAAATAA	GACAGAACCT	660
ACTATCTTTC	CAGCTAGTGA	TATGCTTTTG	AGAGAAAAGG	ATTATCAACG	AGGACAGTCA	720
GCTTTAGAAA	AACAAATTTT	AAAAACTTTA	TCACCTATTT	TGAAATCATA	CCTAGAAGAA	780
ATTCTTTCAA	GTTTTTCACCA	AAAACAAAGT	CATGCAGACT	CTCGGAAGTT	TTTATCTTTG	840
TGCTATGATA	AGACATGGAC	TGTCTTTGAT	TATATTGAAA	AAGATACTCC	AATATTCTTT	900
GATGATTATC	AAAAATTGAT	GAATCAGTAT	GAAGTCTTTG	AAAGAGAATT	AGCGCAGTAC	960
TTTACAGAAG	AATTACAGAA	TAGTAAAGCA	TTTTCTGATA	TGCAGTATTT	TTCTGATATT	1020
GAACAAATCT	ATAAAAAACA	AAGTCCAGTG	ACCTTTTTTTT	CTAATCTTCA	AAAGGGTTTTA	1080
GGAAATCTCA	AATTTGACAA	AATTTATCAA	TTCAATCAAT	ATCCTATGCA	GGAAATTTTTT	1140
AATCAGTTTT	CTTTTCTAAA	AGAAGAAATT	GAACGATATA	AAAAAATGGA	TTACACCATT	1200
ATTCTGCAGT	CTAGCAATTC	AATGGGAAGT	AAAACATTGG	AGGATATGTT	AGAGGAATAT	1260
CAGATTAAAT	TGGATTCTAG	AGATAAGACA	AATATCTGTA	AAGAATCTGT	AAACTTAATA	1320
GAGGGTAAATC	TCAGACATGG	TTTTCATTTT	GTAGATGAAA	AGATTTTATT	GATAACTGAA	1380
CATGAGATTT	TTCAAAAAGAA	ATTAAAGCGT	CGTTTTTCGAA	GACAACATGT	TTCAAATGCA	1440
GAGAGATTAA	AAGATTACAA	TGAAC TTGAA	AAAGGGGACT	ATGTTGTCCA	TCATATCCAT	1500
GGGATTGGTC	AATATCTAGG	AAT TGAAACC	ATTGAAATCA	AGGGAATTCA	TCGTGATTAT	1560
GTCAGTGTCC	AATACCAAAA	TGGTGATCAA	ATTTCTATTCT	CCGTGGAACA	GATT CATCTA	1620
CTGTCCAAAT	ATATTTCAAG	TGATGGTAAA	GCTCCAAAAC	TCAATAAATT	AAATGACGGT	1680
CATTTTAAAA	AGGCCAAGCA	AAAGGTTAAG	AACCAGGTAG	AGGATATAGC	TGATGATTTA	1740
ATCAAACCTCT	ACTCTGAACG	TAGTCAGTTG	AAGGGTTTTG	CTTTCTCAGC	TGATGATGAT	1800
GATCAAGATG	CTTTTGATGA	TGCTTTCCCT	TATGTTGAAA	CGGATGATCA	ACTTCGTAGT	1860
ATTGAGGAAA	TCAAAGAGGA	TATGCAGGCT	TCTCAGCCAA	TGGATCGACT	TTTAGTTGGG	1920
GATGTTGGTT	TTGGAAAGAC	TGAAGTTGCT	ATGCGTG CAG	CCTTTAAAGC	AGTCAATGAT	1980
CACAAACAGG	TTGTCAATTCT	AGTTCCGACG	ACGGTTTTTAG	CGCAACAGCA	CTATACGAAT	2040
TTTAAGGAAC	GATTCCAAAA	TTTTGCAGTT	AATATTGATG	TGTTGAGTCG	CTTTAGAAGT	2100
AAAAAAGAGC	AGACTGCAAC	ACTTGAAAAA	TTGAAAAACG	GTCAAGTCGA	TATTTTGATT	2160
GGAACACATC	GTGTTTTGTC	AAAAGATGTT	GTGTTTGCTG	ATTTGGGCTT	GATGATTATT	2220
GATGAGGAAC	AGCGATTTGG	TGTCAAGCAT	AAGGAACTT	TGAAAGAACT	GAAGAAACAA	2280
GTGGATGTCC	TAACCTTGAC	CGCTACGCCA	ATCCCTCGTA	CCCTCCATAT	GTCTATGCTG	2340
GGAATCAGAG	ATTTATCTGT	TATTGAAACT	CCGCCGACTA	ATCGCTATCC	TGTT CAGACC	2400
TATGTTTTGG	AAAAGAATGA	TAGTGTCATT	CGTGATGCTG	TCTTGCGTGA	AATGGAGCGT	2460
GGAGGTC AAG	TTTATTATCT	TTACAACAAA	GTTGACACAA	TTGTT CAGAA	GGTTTCAGAA	2520
TTACAGGAGT	TGATTCCGGA	GGCTTCGATT	GGATATGTTT	ATGGTCGAAT	GAGTGAAGTC	2580
CAGTTGGAAA	ATACTCTATT	AGACTTTATT	GAGGGACAAT	ACGATATCTT	GGTGACGACT	2640
ACTATTATTG	AGACAGGGGT	GGACATTCCA	AATGCTAATA	CTTTATTTAT	TGAAAATGCG	2700
GACCATATGG	GCTTGTC AAC	CTTATATCAG	TTAAGAGGAA	GAGTCGGTCG	TAGTAATCGT	2760
ATTGCTTATG	CTTATCTCAT	GTATCGTCCA	GAAAAATCAA	TCAGTGAAGT	CTCTGAAAAG	2820
AGATTAG AAG	CGATTAAAGG	ATTTACAGAA	TTGGGCTCTG	GC'TTTAAGAT	TGCAATGCGA	2880
GATCTTTTCGA	TTCGTGGAGC	AGGAAATCTT	TTAGGAAAAAT	CCCAGTCTGG	TTTCATTGAT	2940
TCTGTTGGTT	TTGAATTGTA	TTCGCAGTTA	TTAGAGGAAG	CTATTGCTAA	ACGAAACGGT	3000
AATGCTAACG	CTAACACAAG	AACCAAAGGG	AATGCTGAGT	TGATTTTGCA	AATTGATGCC	3060
TATCTTCCTG	ATACTTATAT	TTCTGATCAA	CGACATAAGA	TTGAAATTTA	CAAGAAAATT	3120
CGTCAAATTG	ACAACCGTGT	CAATTATGAA	GAGTTACAAG	AGGAGTTGAT	AGACCGTTTTT	3180
GGAGAATACC	CAGATGTAGT	AGCCTATCTG	TTAGAGATTG	GTTTGGTCAA	ATCATACTTG	3240
GACAAGGTCT	TTGTTCAACG	TGTGGAAAGA	AAAGATAATA	AAATTACAAT	TCAATTTGAA	3300
AAAGTCACTC	AACGACTGTT	TTTAGCTCAA	GATTATTTTA	AAGCTTTATC	CGTAACGAAC	3360
TTAAAAGCAG	GCATCGCTGA	GAATAAGGGA	TTAATGGAGC	TTGTATTTGA	TGTCCAAAAT	3420
AAGAAAGATT	ATGAAATTTT	AGAAGGTTTG	CTGATTTTTG	GAGAAAGTTT	ATTAGAGATA	3480
AAAGAGTCTA	AGGAAGAAAA	TTCCATTTGA				3510

(2) INFORMATION FOR SEQ ID NO:2245:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 438 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...438
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2245:

ACTAAACTGA TAGTAACATG TAGCGAAAGG GGTAGGTACA TGATTAAAAT TTATACAGTC	60
TCAAGTTGTA CTAGCTGTAA AAAAGCAAAA ACCTGGCTCA ATGCCCACCA GTTAAGTTAT	120
AAAGAACAAA ACCTTGGTAA AGAAGGAATT ACGAGAGAAG AATTACTGGA TATTCTAACC	180
AAAACAGATA ACGGAATAGC CAGCATCGTT TCGTCTAAAA ATCGCTATGC CAAAGCCCTT	240
GGAGTGGATA TTGAAGATTT GAGTGTCAAT GAAGTTCTCA ATCTGATTAT GGAAACACCG	300
AGAATTTTAA AGAGCCCAAT CCTTG TAGAT GAAAAACGCC TGCAAGTTGG CTACAAGGAA	360
GACGATATTC GTACCTTCCT ACCACGCTCT GTCCGTAATG TAGAAAATGC AGAAGCACGT	420
TTGCGTGCAG CTCTATAA	438

(2) INFORMATION FOR SEQ ID NO:2246:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...234
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2246:

AAGTCTATGA TACACATTAT CGTTAATACA TTTATAGAAA AGGATATGAC TGGAGCAGTT	60
GTTGAAGTGT TGTATGCCAG TGCTGACCAA GATAAGGTAC AAGCTAAATA TGAAGAACTA	120

GCTGCACAAT ACCCCGAAAA TTATTTAGCT ATCTATGATG TACCGCTGGA TACGGATTTG	180
AATACACTAG ATCATTACCC GTCTGTGTTT ATTGAAAAAG AGGAGTTTGA GTAG	234

(2) INFORMATION FOR SEQ ID NO:2247:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 444 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...444
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2247:

ACGCCTATGA TAGAAATCAA GCGAATTCAA CAACAGCCTG ACCTAGCTCA AGCCATCTAC	60
GCTGTTATGG CAGCTGTTTA CCTAGTCAGT CCTTGGACTC TGGAGCAAAT CCAAGCAGAT	120
CTGTCCCAAG ACCAGACTTG GTATGCATTG GCTTATGATG GGGCAGAAGT GATTGGATTT	180
CTAGCTGTGC AGGAGAATCT TTTTGAAGCA GAAGTCCTGC AAATCGCTGT CAAAGGAGCT	240
TATCAGGGTC AGGGAATTGC GTCAGCCTTG TTTGCTCAAT TGCCGACAGA TAAGGAGATT	300
TTCTTCGAAG TCAGAAAGTC AAATCAACGA GCGCAAGCAT TTTACAAGAA AGAAAAAATG	360
GCGGTCATCG CTGATCGAAA GGCCTACTAC CATGACCCAG TCGAGGACGC CATTATCATG	420
AAGAGAGAAA TAGATGAAGG ATAG	444

(2) INFORMATION FOR SEQ ID NO:2248:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 531 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...531
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2248:

ATAGATATGA	TGTCCGAAGT	ACAAAGAGCT	GCACGTATTC	TATATATGTT	GAGAGTGAAC	60
TTTAATGGTC	TATATCGTGT	GAATTCTAAG	AACCAATTTA	ATGTTCCATA	TGGACGTTAT	120
AAGAATCCTA	AAATTGTTGA	TGAGGAATTG	ATATCTGCTA	TTTCAGTTTA	TCTAAATAAC	180
AATCAACTAG	AAATTAAAAGT	GGGAGATTTT	GAAAAGGCAA	TTGTAGATGT	TCGAACAGGA	240
GATTTTGTGT	ATTTTGACCC	TCCATATATT	CCATTGTCTG	AGACGAGTGC	ATTTACGTCT	300
TATACTCATG	AGGGATTCTC	TTTTGCAGAT	CAAGTAAGAT	TAAGAGATGC	CTTTAAGAGA	360
CTGAGTGATA	CAGGAGCTTA	TGTTATGTTA	TCAAATTCTT	CTAGTGCTTT	AGTAGAGGAG	420
TTGTATAAGG	ATTTTAATAT	ACATTATGTT	GAAGCTACCC	GAACTAATGG	AGCAAAATCT	480
TCAAGTCGAG	GAAAAATTTT	TGAAATTATA	GTCACAAATT	ATGAAAAATA	A	531

(2) INFORMATION FOR SEQ ID NO:2249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2249:

ATAAGTATGA	TTGATTTTTA	TTTTTTTTCTC	GTCGGGAGCA	TTCTCGCTTC	CTTTCTTGGT	60
TTGGTCATTG	ACCGTTTTTC	AGAGCAATCC	ATTATCAGTT	CAGCCAGTCA	CTGCGATTCC	120
TGTCAGACTC	GCTTGCGTCC	CTTAGATTTG	ATTCCGATTC	TCTCACAGGT	CTTCAATCGC	180
TTTCGCTGTC	GCTACTGCAA	AGTTCGCTAT	CCTGCTGGT	ATGCCCTCTT	TGAATTAGTC	240
TTAGGACTCC	TCTTCTGCT	TTACTCTTGG	GAATTGCTTT	CCTTGGGGCA	AGTCGTCCTA	300
ATCACCGCTG	GTTTGACCTT	GGGTATCTAC	GACTTTCACC	ATCAGGAATA	TCCCTTACTG	360
GTCTGGATGA	CTTTCACCT	AATCCTAATA	GCTTCCTCTG	GCTGGAATCT	GGTCATGGTC	420
TCCTTCCTTG	CTCTTGGAAT	TTTGGCTCAT	TTTATCGATA	TCCGCATGGG	CGCAGGAGAT	480
TTCTCTTTT	TAGCTTCTTG	TGCTCTAGTC	TTTAGCGTAA	CGGAGTTACT	GATCTTGATT	540
CAGTTCGCTT	CTGCGACGGG	TATTCTGGCC	TTTCTCCTGC	AAAAGAAAAA	GGAAAGACTT	600
CCTTTCGTGC	CTTTCCTCTT	ACTTGCTACT	TGTTTGATTA	TTTTTGGTAA	GCTACTGCTT	660
GTTTGA						666

(2) INFORMATION FOR SEQ ID NO:2250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 744 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2250:

AATAAGATGA	TACTAAAGAA	GGAAATAACT	ATGAAACCAG	AAACATTTTA	CAACTTGCTT	60
GCCGAGCAGA	ATCTTCCACT	TTCGAACCAG	CAAAAAGAAC	AATTTGAACG	TTATTTTGAG	120
CTCTTGGTG	AGTGGAATGA	GAAGATTAAT	TTGACGGCGA	TTACGGACAA	GGAAGAAGTT	180
TATCTCAAAC	ATTTTTACGA	TTCGATTGCA	CCCATTCTTC	AAGGTTTGAT	TCCCAATGAA	240
ACTATCAAAC	TTCTTGATAT	CGGGGCTGGG	GCAGGATTTC	CTAGTCTACC	AATGAAAATT	300
CTCTATCCGG	AGTTAGATGT	GACCATTATT	GATTCACTCA	ATAAGCGCAT	CAACTTCCTA	360
CAACTCTTGG	CTCAAGAACT	GGATTTGAAC	GGAGTTCATT	TCTACCACGG	ACGTGCCGAA	420
GATTTTGCCC	AAGACAAGAA	CTTCCGTGCT	CAATATGATT	TTGTAACAGC	TCGTGCGGTT	480
GCCCGTATGC	AGGTCCATATC	TGAATTGACT	ATTCCCTACC	TTAAGGTTGG	TGGCAAACATA	540
TTGGCACTCA	AGGCCAGCAA	TGCGCCTGAG	GAATTATTAG	AAGCTAAGAA	TGCCCTCAAT	600
CTCCTTTTTTA	GTAAGGTCGA	AGACAATCTC	AGNTACGCCC	TACCGAATAG	AGATCCGCGC	660
TATATCACAG	TGGTAGAAAA	GAAAAAAGAA	ACACCAAATA	AATATCCACG	TAAGGCTGGT	720
ATGCCAAATA	AACGCCCACT	TTAA				744

(2) INFORMATION FOR SEQ ID NO:2251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1014 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2251:

GTCAAGATGA	TTGCTGTTAA	AACTTGCGGA	AACTCTATT	GGGCAGGTGA	ATATGCTATT	60
TTAGAGCCAG	GGCAGTTAGC	TTTGATAAAG	GATATTCCCA	TCTATATGAG	GGCTGAAATT	120
GCTTTTTCTG	ACAGCTACCG	TATCTATTCA	GATATGTTTG	ATTTCGCAGT	GGACTTAAGG	180
CCTAATCCTG	ACTACAGCTT	GATTCAAGAA	ACGATTGCTT	TGATGGGAGA	CTTCCTCGCT	240
GTTCCGCGTC	AGAATTTAAG	ACCTTTTTTC	CTAAAAATCT	GTGGCAAAAT	GGAACGAGAA	300
GGGAAAAAGT	TTGGTCTAGG	TTCTAGTGGC	AGCGTCGTTG	TCTTGGTTGT	CAAGGCTTTA	360
CTGGCTCTCT	ATAATCTTTC	GGTTGATCAG	AATCTCTTGT	TCAAGCTGAC	TAGCGCTGTC	420

TTGCTCAAGC	GAGGAGACAA	TGGTTCCATG	GGCGACCTTG	CCTGTATTGT	GGCAGAGGAT	480
TTGGTTCTCT	ACCAATCATT	TGATCGCCAG	AAGGTGGCTG	CTTGGTTAGA	AGAAGAAAAC	540
TTGGCGACAG	TTCTGGAGCG	TGATTGGGGA	TTTTTTATCT	CACAAGTGAA	ACCAACTTTA	600
GAATGTGATT	TCTTAGTGGG	ATGGACCAAG	GAAGTGGCTG	TATCGAGTCA	CATGGTCCAG	660
CAAATCAAGC	AAAAATATCAA	TCAAAATTTT	TTAAGTTCCCT	CAAAAGAAAC	GGTGGTTTCT	720
TTGGTCGAAG	CCTTGGAGCA	GGGGAAAGCC	GAAAAAGTTA	TCGAGCAAGT	AGAAGTAGCC	780
AGCAAGCTTT	TAGAAGGCTT	GAGTACAGAT	ATTTACACGC	CTTTGCTTAG	ACAGTTGAAA	840
GAAGCCAGTC	AAGATTTTGA	GGCCGTTGCC	AAGAGTAGTG	GTGCTGGTGG	TGGTGACTGT	900
GGCATCGCCC	TGAGTTTTGA	TGCGCAATCA	ACCGAAACCT	TAAAAAATCG	TTGGGCCGAT	960
CTGGGGATTG	AGCTCTTATA	TCAAGAAAGG	ATAGGACATG	ACGACAAATC	GTAA	1014

(2) INFORMATION FOR SEQ ID NO:2252:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 732 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...732
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2252:

GAGAAGATGA	TAATGTCAAT	ATATAAACTT	TATAAAGATA	TTGAAAGAAA	AACGATGTCG	60
CCTGCTAAAA	AAGCAATGGC	TAAAAATGAT	TATTTTGCGT	TTTATGTTGG	AAGACCGTTA	120
TCCTATCTTT	TAACAGTTCC	TTTTTTAAAA	ACGAATATTA	CTCCCAATCA	AGTATCTTAT	180
TTATCTATAG	CCCCTTTGAT	TCTTGGATTT	CTGACAATGA	CATTTACAAC	TAATTTTCATT	240
CTATTATTGC	TGGCATGGTT	TCTATTTTTT	TTATGGAAC	TACTAGATGG	AGTAGATGGG	300
AACTTAGCTA	GATATCGGGA	GCAATACTCG	AAGGATGGAA	GTGTAGTAGA	TGCAATGGCA	360
GGCTATGTGG	CTATGGTGCT	GACGTATTTT	GGTGCAGGAA	TAGTAGCAAC	TCATCTAAAT	420
GGCTCAGATA	TGTATGTGAT	TTTGGGTGCT	TTATCTGGAA	TTTCTTTGAT	TTTTCCAAGA	480
TTGGTGATGC	ATAAGTATAT	CAACACAGTA	GCACGAAATG	AGTCTGTCAA	TAACATTAAA	540
GATAAAATCAA	ATTTTAGTAC	TATAAAACTA	CTGGCTTTAA	ATATGACATC	AATTACAGGT	600
ATTCCCTCAGG	TTTTACTACT	AGTAACGATT	TTAACAAATC	AGTGGAATT	TTTTACTTTA	660
GTATATTTCA	CGATTAATTT	TTTATTAATG	ATATTTTCGT	TATATTCATT	ATTTAAAAAG	720
GAGAATGTTT	AG					732

(2) INFORMATION FOR SEQ ID NO:2253:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 684 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2253:

GAGAAGATGA	TTTCAAAGAG	ATTAGAAATTG	GTAGCTTCCT	TTGTGTCACA	GGGGGCTATT	60
TTACTAGATG	TGGGAAGTGA	CCATGCTTAT	CTGCCTATCG	AGTTGGTTGA	GAGAGGCCAA	120
ATCAAAAGCG	CTATTGCAGG	TGAGGTGGTG	GAAGGTCCCT	ATCAGTCTGC	GGTTAAAAAT	180
GTTGAGGCTC	ACGGCCTAAA	GGAGAAAATC	CAAGTCCGTT	TAGCCAATGG	CTTGGCAGCT	240
TTTGAAGAGA	CTGACCAAGT	GTCTGTCAAT	ACCATTGCTG	GCATGGGTGG	TCGTTTGATT	300
GCTAGGATTT	TAGAAGAAGG	TTTGGGGGAA	TTAGCTAATG	TAGAGCGTTT	GATCCTCCAG	360
CCCAATAATC	GTGAAGACGA	CTTGCGTATC	TGGCTACAGG	ATCATGGATT	CCAGATTGTA	420
GCAGAAAGCA	TCTTAGAAGA	AGCTGGAAAAG	TTTTATGAGA	TTTTGGTGGT	GGAAGCAGGA	480
CAAATGAAGC	TATCAGCCAG	TGATGTTTCGC	TTTGGTCCCT	TCTTGTCCAA	AGAAGTCAGT	540
CCAGTATTTG	TCCAAAAATG	GCAAAAAGAA	GCTGAGAAGC	TAGAGTTCGC	CCTCGGACAA	600
ATCCCAGAAA	AAAATCTGGA	AGAACGTCAA	GTTCTAGTAG	ATAAGATTCA	AGCTATCAAG	660
GAGGTGCTCC	ATGTTAGCAA	GTGA				684

(2) INFORMATION FOR SEQ ID NO:2254:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2254:

CTTATGGTGA	TGATAAAACT	CTTGAAGCTT	TACAAAAAGG	ATCCTCTTTT	AGGTAAAATA	60
AATGCAATTA	AAAATGGTGC	CGTTGCTGTA	ATTCCAGATA	ATACACCGTT	AGCAGCCTCA	120
TGCACTCCAG	CACCACTTTC	AATAAACTAT	ACTATTGAAG	AATACCTAAA	TCTTTTAGGA	180
AATGCATGCA	AAAATGCGAA	ATAA				204

(2) INFORMATION FOR SEQ ID NO:2255:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 204 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...204
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2255:

CTTGAGGTGA	TGAAAATGGC	AACCGATAAA	AATAGAATAA	TGATTAGCTT	GGATGATAAA	60
AATCTAGAGA	AACCTGAAAA	TTTAGTAGAA	GATGCTAGAG	ATAGAAGGGG	AATGCGACTA	120
ACAAAGTCCC	AGGTATTGA	ATTACTCCTA	AATACCGTTG	ATTATTTCTGA	TGATATTATG	180
GGGGCTATTT	ACTCAAAAAA	ATAA				204

(2) INFORMATION FOR SEQ ID NO:2256:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...3309
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2256:

TATAGGGTGA	TGAAAAATTC	CAACGAGGCT	GAGATGAAAT	TACTTTATAC	TGATATTCGG	60
ACTTCTTTGA	CAGAAATCT	AACAAGAGAG	GCAGAAGAGC	TAGTTGCAGC	TGGCAAGCGG	120
GTCTTCTACA	TTGCCCCCAA	CTCTCTTTCT	TTTGAAAAGG	AACGCGCCGT	GCTAGAATAC	180
TTGTCCCAGC	AGGCTTCTTT	TTCGATTACC	GTCACGCGCT	TTGCTCAAAT	GGCTCGCTAT	240
CTGGTCTTGA	ATGATTTACC	AGCTAAAAC	ACTCTTGATG	ATATCGGTCT	TGGGTTGGCC	300
TTTACAAAT	GCCTTGCCGA	ACTCGATCCC	AAGGACTTGC	GTGTTTATGG	CGCTATTAAG	360
CAGGATCCTC	AATTGATCCA	GCAGTTAATT	GAGCTTTACC	ATGAGATGAC	CAAATCTCAG	420
ATGAGTTTTT	TGGACTTGGA	GAATTTAACA	GATGAGGATA	AGAGGGCGGA	TTTACTCTTG	480

ATTTTTGAGA	AAGTAACAGC	CTATCTTAAT	CAAGGTCAGT	TAGCCCAGGG	AAGTCAGTTG	540
TCCCATTGTA	TTGAGGCTAT	TGAGAATGAC	AAGGTAAGTA	GTGATTTTAA	TCAAATCGCC	600
TTGGTCATTG	ACGGCTTTAC	TCGTTTTTCT	GCTGAGGAAG	AGCGGGTTGT	GGACTTACTT	660
CACGGCAAAG	GTGTTGAGAT	TGTTATCGGG	GCTTATGCTA	GTAAGAAAGC	CTATACCAGT	720
CCTTTTAGCG	AGGGCAATCT	CTACCAAGCC	AGCGTAAAT	TTCTCCATCA	TCTGGCTTCT	780
AAATACCAAA	CGCCTGCTCA	GGACTGTTCT	CAAACTCATG	AGAAGATGGA	TAGTTTTGAC	840
AAGGCCCTCTC	GTTTGTGGA	GTCTTCTTAT	GACTTTTCAG	AACTCGCTTT	GGATGTCGAT	900
GAGAAAGACC	GTGAAAATTT	ACAAATCTGG	TCTTGTGTTGA	CGCAAAAGGA	GGAGTTGGAG	960
CTAGTAGCCC	GTAGTATTCG	TCAGAAAATTA	CATGAGAACT	CAGACCTGAG	CTACAAGCAT	1020
TTTCGTATTC	TCTTGGGGGA	TGTAGCTTCT	TACCAGTTAT	CTCTCAAAAC	CATTTTTGAC	1080
CAGTATCAGA	TTCTTTTTTA	TCTTGGTAGA	AGCGAAGCCA	TGGCTCATCA	TCCCTTGACT	1140
CAGTTTGTCTG	AGTCTATTTT	AGCTTTAAAA	CGTTACCGTT	TTCGTCAGGA	GGATTTGATC	1200
AATCTTCTTA	GAACGTATTT	GTATACTGAC	CTCAGTCAGT	CTGATATTGA	TGCTTTTGAG	1260
CAATATATCC	GCTATCTTGG	TATCAATGGC	TTGCCAGCCT	TTCAGCAAAC	CTTCACCAAA	1320
TCCCACCATG	GAAAATTTAA	TCTTGAGCGT	TTGAATGTCC	TCCGCCTGAG	AATTTTAGCA	1380
CCTCTTGAAA	CCCTCTTTGC	CAGCCGAAAA	CAAAAGGCTG	AAAACCTCCT	ACAAAAATGG	1440
AGTGTCTTTC	TAAAAGAAGG	AGCTGTGACT	AAGCAGTTAC	AAGATTTGAC	AACCACTTTG	1500
GAAGCTGTAG	AACAGGAAAG	ACAAACCGAA	GTTTGGAAGG	CTTTCCTGCCA	TGTTTTAGAA	1560
CAATTTGCGA	CTGTTTTTGC	TGGTTCACAG	GTTAGTCTGG	AAGACTTCCT	AGCCTTGCTC	1620
CATTCTGGAA	TGAGTTTGTC	CCAATACCGT	ACCATTCCAG	CAACAGTGGA	CAGTGTCTG	1680
GTGCAGAGTT	ACGATTTGAT	TGCACCATTG	ACTGCTGACT	TTGTCTATGC	TATTGGACTA	1740
ACTCAGGACA	ATTTACCAAA	AATTTCTCAA	AACACCAGTC	TTCTGACAGA	TGAAGAAAGG	1800
CAAAACCTAA	ACCAACGAC	CGAAGAAGGC	GTTCAATTAC	TGATTGCCAG	CAGTGAAGAT	1860
CTCAAGAAAA	ATCGCTACAC	TATGCTTTCC	TTGGTCAATT	CTGCTCGTAA	GCAGTTGTTT	1920
TTGTTCGGCTC	CAAGCCTTTT	TAACGAAAGT	GAAAGTAAGG	AATCTGCCTA	TCTTCAAGAG	1980
TTGATCCATT	TTGGATTTAG	GCGGAGAGAG	AAGAGGATGA	ATCACAAAGG	ACTGTCTAAG	2040
GAGGATATGG	GGTCCTATCA	CAGTCTTTTG	TCTAGTCTGG	TTGCCATATCA	CCAGCAGGGT	2100
GAGATGAGCG	ATACTGAGCA	AGATTTGACT	TTTGTCAAGG	TTCTGTTCGCG	TGTCATAGGT	2160
AAAAAACTAG	ATCTGCAAGG	TCTGGAAAAAT	CCAGCTATCC	CAACCAGTCC	AAGCAGCAAG	2220
ACCTTAACCA	AGGACACCTT	GCAAGCTCTC	TATCCTGCCA	AACAGGAGTT	TTACCTGTCT	2280
ACGTTCGGGTT	TGACAGAGTT	CTATCTCAAT	GAATACAGTT	ATTTCTTACG	CTACGTTTTTA	2340
GGCTTGACAG	AGGAATTACG	TTTGCGTCCCT	GATGCCCGTA	GTCACGGGAA	TTTCTTGTCAT	2400
CGTATCTTTG	AACGCGCCTT	ACAGTTGCCT	AATGAAGATT	CCTTTGACCA	ACGTCTAGAA	2460
CAAGCTATTC	AAGAAAACAG	TCAAGAACGC	GAATTTGAAG	CTATTTATCA	AGAAAGTTTG	2520
GAAGCCAGT	TTACCAAGGA	AGTTTTGCTT	GATGTTGCAC	GGACGACTGG	ACATATTCTC	2580
CGACACAATC	CAGCCATCGA	AACCATCAAA	GAAGAAGCAA	ATTTTGGTGG	AAAAGACCAA	2640
GCCTTTATTC	AATTAGACAA	TGGACGCAGT	GTCTTTGTAC	GAGGCAAGGT	GGACCGGATT	2700
GACCGTTTGA	AAGCTAATGG	AGCGATAGGA	GTAGTAGACT	ACAAATCCAG	TCTGACTCAG	2760
TTCCAGTTTC	CTCATTTCTT	TAATGGGCTC	AATTCTCAGT	TACCAACCTA	TCTTGCTGCC	2820
CTAAAAAGAG	AAGGGGAGCA	GAACTTTTTC	GGCGCCATGT	ACTTGGAAT	GGCTGAACCT	2880
ATCCAATCTC	TGATGGCGGT	AAAAAGTCTG	GCAGGAGCAG	TGGTAGAAGC	CAGCAAATCT	2940
ATGAAATACC	AAGGGCTCTT	CTTGGAAGAA	GAAAGCAGTT	ATTTAGGCGA	ATTTTATAAC	3000
AAAAACAAGG	CTAATCAACT	GACAGATGAG	GAATTTGAGC	TCCTACTGGA	CTACAATGCC	3060
TATCTTTACA	AGAAAGCTGC	TGAGAAGATT	TTAGCAGGCC	GGTTCGCCAT	CAATCCTTAT	3120
ACTGAAAAATG	GCAGAAGCAT	TGCCCCATAC	GTCCAGCAAC	ATCAGGC'TAT	TACAGGC'TTT	3180
GAAGCCAATT	ACCATCTGGG	CCAAGCCCGT	TTCCTAGAAA	AGTTGGACCT	AGCTGATGGC	3240
AAGCGTCTGG	TCGGAGAAAA	ACTCAAGCAA	GCTTGG'TTTG	AAAAAATAAG	AGAGGAGTTA	3300
AATCGATGA						3309

(2) INFORMATION FOR SEQ ID NO:2257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 867 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2257:

AACGATACGA	TAGAAAGAAT	AATGAACAAT	ATGACTGATT	TAAAAGCAAT	TCAGGCTTGT	60
AGTTTGGAGA	TGGCTGAATA	TTTTGTGGCC	TTTTGCAAGG	AACATGATTT	ACTTTGCTAT	120
CTCTGTGGGG	GAGGCGCTAT	TGGTGCCCTT	CGAAACAAGG	GGTTCATTCC	TTGGGACGAC	180
GACCTAGACT	TTTTTATGCC	TCGTAAAGAT	TATGAGAAAT	TAGCAGAATT	ATGGCCTCGT	240
TATGCAGATG	AACGTTATTT	CTTGTCAAAG	AGTTACAAGG	ATTTTGTGTA	TCGTAATCTT	300
TTTATTACCA	TTCGTGACAA	GGAAACCACC	TGTATCAAGC	CTTATCAGCA	GGATTTGGAT	360
TTGCCACATG	GTCTGGCCTT	GGATGTTTTG	CCTTTGGATT	ATTATCCGAA	AGATCCAGCT	420
GAGCGGAAAA	AACAGGTTTC	TTGGGCCTTG	ATTTATTCAC	TCTTTTGTGC	GCAAACCTATT	480
CCAGAAAAGC	ATGGTGCTCT	CATGAAATGG	GGAAGTCGCA	TTTTACTGGG	TTTGACTCCA	540
AAATCTCTCC	GTTATCGCAT	CTGGAAAAAA	GCTGAGAAAAG	AAATGACTAA	GTATGATTTG	600
GCTGATTGTG	ATGGCATTAC	AGAATTATGC	TCAGGTCCTG	GCTACATGAG	AAACAAGTAC	660
CCAATCACAT	CTTTTGAAGA	CAATCTTTTC	TTGCCATTTG	AAGGAACAAA	GATGCCTATT	720
CCAATCGGCT	ATGATGTCTA	TCTCAGAACT	GCTTTTGGGG	ATTATATGAC	GCCTCCACCA	780
GCAGACAAGC	AGGTACCGCA	TCATGATGTT	GTCATCGCTG	ATATGGATAA	GTCTTATACA	840
GAATACAAGG	GAGAATATGG	TGGCTAA				867

(2) INFORMATION FOR SEQ ID NO:2258:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1215 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2258:

TATAGAACGA	TTTTTTACAT	GAATGATAAA	ACAGAGGTAA	ATATGACAAT	CGGTATTGAT	60
AAGATTGGTT	TTGCGACCAG	TCAATATGTC	TTGAAATTAC	AAGACTTAGC	AGAAGCGAGG	120
GGAATTGACC	CTGAAAAATT	AAGTAAAGGA	CTCTTACTCA	AGGAATTGAG	TATTGCGCCC	180

CTAACTGAGG	ACATCGTGAC	CTTGGCGGCC	AGTGCTAGTG	ACTCTATTTT	AACTGAGCAA	240
GAAAGACAAG	AAGTTGACAT	GGTCATTGTG	GCTACCGAGT	CAGGAATTGA	CCAGAGTAAG	300
GCTGCGGCCG	TCTTTGTGCA	TGGCTTGCTG	GGCATCCAGC	CCTTTGCTCG	TAGTTTCGAG	360
ATTAAAGAAG	CCTGCTATGG	GGCGACAGCT	GCCCTCCATT	ATGCCAAATT	GCATGTGGAA	420
AATTCCTCCG	AGTCCAAGGT	ATTGGTCATT	GCCAGTGATA	TTGCCAAATA	TGGTATTGAA	480
ACTCCGGGAG	AACCAACTCA	AGGTGCTGGA	AGTGTAGCTA	TGTTGATTAC	ACAAAATCCA	540
CGCATGATGG	CCTTTAATAA	TGACAATGTA	GCTCAGACCC	GTGACATCAT	GGATTTCTGG	600
CGACCAAATT	ACTCGACAAC	TCCTCATGTA	AATGGTGTCT	ATTCTACCCA	ACAATACTTG	660
GATAGTTTGA	AAACGACTTG	GCTTGAATAT	CAAAAACGCT	ACCAGCTTAC	TTTGGATGAT	720
TTTGCTGCTG	TTTGTTTCCA	CTTGCCTTAT	CCTAAATTAG	CGCTAAAAGG	C'TTGAAAAAA	780
ATCATGGATA	AGAGCCTGCC	TCAAGAGAAA	AAAGACCTCT	TACAAAAGCA	TTTTGACCAG	840
TCTATTCTCT	ACAGTCAAAA	GGTGGGGAAT	ATCTACACAG	GTTCACTTTT	CCTTGGACTT	900
TTGTCTCTCT	TGGAAAATAC	AGATAGCTTG	AAAGCTGGGG	ATAAAATCGC	CCTTTATAGT	960
TACGGAAGTG	GAGCTGTGGC	TGAGTCTTTC	AGTGGTGAAT	TGGTTGAAGG	ATATGAAGCT	1020
TATTTGGATA	AAGACCGCTT	GAACAAGCTC	AACCAACGAA	CTGCCCTATC	CGTTGCAGAC	1080
TATGAAAAGG	TCTTTTTTGA	GGAAGTAAAC	TTGGATGAAA	CAAACCTCTG	CCAGTTTGCT	1140
GGCTATGAAA	ATCAAGATTT	TGCCTTGGTT	GAAATTCCTG	ACCACCAACG	CCGTTATAGC	1200
AAGGTTGAAA	AATAA					1215

(2) INFORMATION FOR SEQ ID NO:2259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 954 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2259:

CTATTAGCGA	TTGTCACTGT	AAATAATATC	CTTGTAGCAA	GCAATTTTTTC	TCCTAGACTT	60
GAAATAAAGC	GCATTTCTCT	ATATAATAAA	TACTTATATA	GAAAACACCT	TTTAGAAAGA	120
TACCTATGCT	TCCATATCCA	TTTTCCTTTT	TTTCATGTAT	TTGGTTGGTA	TCGTAAGCCC	180
CTGTCCAAAC	GTTTCGAGCT	CAACTGGTTC	CAACTTCTCT	TTACCAGTAT	CTTCCTTATC	240
AGCTTGTCTA	TGGTACCCAT	TGCTATCCAA	AACAGCTCCC	AGGAGACCTA	TCCGCTAGAA	300
ACTTTTATCG	ATAATGTCTA	TGAACCTCTG	ACAGATAAGG	TTGTCCAGGA	TCTCTCTGAA	360
CATGCTACAA	TTGTGATGG	CACATTAACT	TATACTGGAA	CAGTTAGTCA	AGCCTCTTCT	420
ATTGTGATTG	GTCCAAGTCA	AATCAAGGAA	TTACCTAAGG	ACTTGCAACT	GCATTTTCGAT	480
ACAAATGAGC	TAGTCATCAG	CAAGGAAAGC	AAGGAACTGA	CCCGCATCTC	TTACCGAGCC	540
ATTCAAGCTG	AGAGTTTCAA	AAGCAAAGAC	AGCTTGACCC	AAGCAATTTT	TAAAGACTGG	600
TACCAACAAA	ATCGTGTCTA	TATCAGCCTC	TTCCTAGTTC	TCGGTGCGAG	CTTCCTCTTT	660
GGTTTGAATT	TCTTTATCGT	CTCTCTAGGA	GCTAGTCTTC	TCCTTTTATAT	CACTAAGAAA	720
TCACGCCTCT	TTTCATTTAG	AACCTTTAAA	GAGTGCATAT	ACCTTTATCTT	GAAGTGTTTA	780
GGATTGCCGA	CTCTAATTAC	ACTTATTTTG	GGATTATTTG	GCCAAAATAT	GACAACCTTG	840
ATTACTGTAC	AAAATATTCT	TTTTGTCTCT	TATCTGGTCA	CTATCTTTTA	TAAAACACAT	900

TTCCGTGATC CAAATTACCA TAAATACGGA GATTTTTATG CCCGTTACGA TTAA

954

(2) INFORMATION FOR SEQ ID NO:2260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2260:

AAATCAGCCT TTTTTTCAAC AAAAATACGT TTATCCATCA ATTCTTATTC CTTTATTTCA	60
GCTCTTGCAA TATTCCCAAA CAGCCTTGAG GTTGTTATTT TAAACCCTGC AACTTTTCCC	120
AGACAAATTC GTAAACATCT GTTAGTTCAC CTAGTTCTCT ACAGAGTGAA AAGGTCTGGG	180
GGACCTTTTC AGCCTGAGTC CTTTTAG	207

(2) INFORMATION FOR SEQ ID NO:2261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2261:

GTTTGTGAGA TGAAAAGCTG GAAGAATTGG CTGATAAAAA TCAATTATTG CGTTTACAAG	60
AAGAAAAGGA AAGGAAGAAT GCGTAAATTC TTAATTATTT TGTTGCTACC AAGTTTTTTG	120
ACCATTTCAA AAGTCGTTAG CACAGAAAAA GAAGTCGTCT ATACTTCGAA AGAAATTTAT	180
TACCTTTCAC AATCTGACTT TGGTATTTAT TTAGAGAAA AATTAAGTTC TCCCATGGTT	240

TATGGAGAGG	TTCCTGTTTA	TGCGAATGAA	GATTTAGTAG	TGGAATCTGG	GAAATTGACT	300
CCCAAAACAA	GTTTTCAAAT	AACCGAGTGG	CGCTTAAATA	AACAAGGAAT	TCCAGTATTT	360
AAGCTATCAA	ATCATCAATT	TATAGCTGCG	GACAAACGAT	TTTTATATGA	TCAATCAGAG	420
GTAACCCAA	CAATAAAAAA	AGTATGGTTA	GAATCTGACT	TTAAACTGTA	CAATAGTCCT	480
TATGATTTAA	AAGAAGTGAA	ATCATCCCTA	TCAGCTTATT	CGCAAGTATC	AATCGACAAG	540
ACCATGTTTG	TAGAAGGAAG	AGAATTTCTA	CATATTGATC	AGGCTGGATG	GGTAGCTAAA	600
GAATCAACTT	CTGAAGAAGA	TAATCGGATG	AGTAAAGTTC	AAGAAATGTT	ATCTGAAAAA	660
TATCAGAAAAG	ATTCTTTCTC	TATTTATGTT	AAGCAACTGA	CTACTGGAAA	AGAAGCTGGT	720
ATCAATCAAG	ATGAAAAGAT	GTATGCAGCC	AGCGTTTTGA	AACCTCCCTA	TCTCTATTAT	780
ACGCAAGAAA	AAATAAATGA	GGGTCTTTAT	CAGTTAGATA	CGACTGTAAA	ATACGTATCT	840
GCAGTCAATG	ATTTTCCAGG	TTCTTATAAA	CCAGAGGGAA	GTGGTAGTCT	TCCTAAAAAA	900
GAAGATAATA	AAGAATATTC	TTTAAAGGAT	TTAATTACGA	AAGTATCAAA	AGAATCTGAT	960
AATGTAGCTC	ATAATCTATT	GGGATATTAC	ATTTCAAACC	AATCTGATGC	CACATTCAAA	1020
TCCAAAATGT	CTGCCATTAT	GGGAGATGAT	TGGGATCCAA	AAGAAAAATT	GATTTCTTCT	1080
AAGATGGCCG	GGAAGTTTAT	GGAAGCTATT	TATAATCAAA	ATGGATTTGT	GCTAGAGTCT	1140
TTGACTAAAA	CAGATTTTGA	TAGTCAGCGA	ATTGCCAAAG	GTGTTTCTGT	TAAAGTAGCT	1200
CATAAAATTG	GAGATGCGGA	TGAATTTAAG	CATGATACGG	GTGTTGTCTA	TGCAGATTCT	1260
CCATTTATTC	TTTCTATTTT	CACTAAGAAAT	TCTGATTATG	ATACGATTTT	TAAGATAGCC	1320
AAGGATGTTT	ATGAGGTTCT	AAAATGA				1347

(2) INFORMATION FOR SEQ ID NO:2262:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 888 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...888
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2262:

AGGTGTCAGA	TGGCAGTGTC	TCTAAATGAT	ATTAAAACAA	AAATCGCCTC	AACAAAAAAT	60
ACGAGTCAAA	TCACTAATGC	CATGCAAATG	GTATCGGCTG	CTAAGCTAGG	TCGCTCTGAA	120
GAAGCTGCTC	GCAACTTCCA	AGTTTACGCT	CAGAAAGTGC	GTAAACTTTT	GACAGATATC	180
CTTCATGGTA	ATGGAGCTGG	TGCTTCAACT	AATCCGATGT	TGATTAGCCG	TTCTGTGAAG	240
AAGACAGGCT	ATATCGTTAT	CACTTCAGAC	CGCGGTTTGG	TTGGAGGTTA	TAATTCCTCT	300
ATTTTGAAAAG	CTGTTATGGA	GTTGAAAAGAA	GAATACCACC	CAGACGGTAA	AGGTTTTGAA	360
ATGATCTGTA	TCGGTGGGAT	GGGAGCTGAT	TTCTTTAAGG	CTCGCGGTAT	TCAACCACTT	420
TATGAATTAC	GTGGCTTGGC	AGACCAACCT	AGCTTTGATC	AAGTTCGTAA	GATTATTTCA	480
AAAACGTGTG	AAATGTACCA	AAATGAACTC	TTTGATGAGC	TTTATGTTTG	CTACAACCAC	540
CATGTCAATA	CGCTAACCA	TCAAATGCGT	GTGGAACAAA	TGCTTCCGAT	TGTTGACTTG	600
GATCCAAATG	AAGCGGATGA	AGAGTACAGC	TTGACTTTTG	AATTGGAAAC	CAGCCGAGAA	660
GAAATPCTGG	AGCAGTTGTT	GCCTCAGTTT	GCAGAAAGTA	TGATTTACGG	TGCCATTATC	720
GATGCCAAGA	CAGCTGAGAA	TGCTGCGGGT	ATGACAGCCA	TGCAAACAGC	GACAGATAAT	780
GCTAAGAAAAG	TCATCAATGA	TTTGACAATT	CAGTATAACC	GTGCCAGACA	GGCGGCTATT	840

(2) INFORMATION FOR SEQ ID NO:2263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 909 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2263:

GTGACTAAGA	TGTTGTTTGA	TCAAATTGCA	AGCAATAAAC	GAAAAACCTG	GATTTTGTTG	60
CTGGTATTTT	TCCTACTCTT	AGCTCTTGTT	GGTTATGCGG	TTGGTTATCT	CTTTATAAGA	120
TCTGGACTTG	GTGGTTTGGT	TATCGCACTG	ATTATCGGCT	TTATCTACGC	TTTGTCTATG	180
ATTTTTCAAT	CGACAGAGAT	TGTCATGTCC	ATGAATGGAG	CGCGTGAGGT	GGATGAGCAA	240
ACGGCACCAG	ACCTCTACCA	TGTAGTGGAA	GATATGGCTC	TGGTCGCTCA	GATTCCTATG	300
CCCCGTGTTT	TCATCATTTGA	TGATCCAGCC	TTAAATGCCT	TTGCGACAGG	TTCTAATCCT	360
CAAAATGCGG	CTGTTGCTGC	GACTTCAGGT	CTACTAGCTA	TCATGAATCG	TGAAGAACTA	420
GAAGCTGTTA	TGGGACATGA	AGTCAGTCAT	ATTCGTAATT	ATGATATCCG	TATTTCTGACT	480
ATTGCAGTTG	CCCTTGCTAG	TGCTATCACC	ATGCTTTCTG	GTATGGCAGG	TCGTATGATG	540
TGGTGGGGTG	GAGCAGGTCG	CAGACGAAGT	GATGATGACC	GAGATGGAAA	TGGTCTTGAA	600
ATCATTATGC	TAGTGGTTTC	CCTACTAGCT	ATTGTACTGG	CACCTCTCGC	TGCAACCTTG	660
GTTTCAGCTCG	CTATTTCTCG	TCAGAGGGAA	TTTCTGGCAG	ATGCATCTAG	TGTTGAGCTG	720
ACTCGCAATC	CCCAGGGAAT	GATTAATGCC	CTAGATAAGT	TGGACAATAG	CAAACCGATG	780
AGTCGCCACG	TCGATGATGC	TAGCAGTGCT	CTTTATATCA	ATGATCCCAA	GAAAGGTGGG	840
GGGTTCCAAA	AACTCTTTTA	TACCCACCCA	CCTATCTCAG	AACGGATTGA	ACGTTTAAAA	900
CAGATGTAA						909

(2) INFORMATION FOR SEQ ID NO:2264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2264:

GAGAATAAGA	TGGCATTAT	TGAAAAAGGT	CAAGAAATCG	ATATGGAAGT	CATCAAGGCT	60
GAAACCCAAT	TGTCTGCGGA	AGCCTTGAGA	CTCAAGGAAA	GCCGTGACAG	GGAATTGGCA	120
GATATTATTT	CAGGGGAAGA	TGACCGTATT	CTCTTGGTGA	TTGGTCCCTG	CTCTTCTGAT	180
AATGAAGAGG	CGGTCTTGGA	ATATGCTCGC	CGTTTATCCG	CCTTGCAAAA	GAAGGTAGCG	240
GATAAGATTT	TCATGGTCAT	GCGCGTGTAT	ACTGCTAAGC	CTCGTACCAA	TGGAGACGGC	300
TATAAAGGAT	TAGTTCACCA	GCCAGATACT	TCTAAGGCTC	CAAGCCTGAT	TAATGGCTTG	360
CAGGCTGTGC	GCCAGTTGCA	CTACCGCGTG	ATTACAGAGA	CTGGTTTGAC	AACGGCAGAT	420
GAGATGCTTT	ATCCGTCAAA	TCTGATCTTG	GTGGATGACT	TGGTCAGCTA	CCATGCCGTT	480
GGAGCTCGTT	CTGTGGAAGA	CCAAGAGCAC	CGCTTTGTGG	CTTCTGGGAT	TGATGCACCA	540
GTAGGGATGA	AAAATCCAAC	CTCAGGAAAT	TTGGGTGTTA	TGTTTAACGC	CATCTATGCT	600
GCTCAAAACA	AGCAAAC TTC	CTTAATCATG	GGCAGGAAGT	TGGAACATCA	GTAA	654

(2) INFORMATION FOR SEQ ID NO:2265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 879 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2265:

GAGAATAAGA	TGAAGATTAT	TGTACCTGCA	ACCAGTGCCA	ATATCGGGCC	AGGTTTTTGAC	60
TCGGTTCGGTG	TAGCTGTAAC	CAAGTATCTT	CAAATTGAGG	TCTGCGAAGA	ACGAGATGAG	120
TGGCTGATTG	AACACCAGAT	TGGCAAATGG	ATTCCACATG	ATGAGCGTAA	TCTCTTGCTC	180
AAAATCGCTT	TGCAAATTGT	ACCAGACTTG	CAACCAAGAC	GCTTGAAAAT	GACCAGTGAT	240
GTCCCTTTGG	CGCGCGGTTT	GGGTTCTTCC	AGCTCGGTGA	TCGTTGCTGG	GATTGAACTA	300
GCCAACCAAC	TGGGTCAACT	CAACTTATCA	GACCATGAAA	AATTGCAGTT	AGCGACCAAG	360
ATTGAAGGGC	ATCCTGACAA	TGTGGCTCCA	GCCATTTATG	GTAATCTCGT	TATTGCAAGT	420
TCTGTTGAAG	GGCAAGTCTC	TGCTATCGTA	GCAGACTTTC	CAGAGTGTGA	TTTTCTAGCT	480
TACATTCCAA	ACTATGAATT	ACGTACTCGC	GACAGCCGTA	GTGTCTTGCC	TAAAAAATTG	540
TCTTATAAGG	AAGCTGTTGC	TGCAAGTTCT	ATCGCCAATG	TAGCGGTTGC	TGCCTTGTTG	600
GCAGGAGACA	TGGTGACCGC	TGGGCAAGCA	ATCGAGGGAG	ACCTCTTCCA	TGAGCGCTAT	660
CGTCAGGACT	TGGTAAGAGA	ATTTGCGATG	ATTAAGCAAG	TGACCAAAGA	AAATGGGGCC	720
TATGCAACCT	ACCTTTCTGG	TGCTGGGCCG	ACAGTTATGG	TTCTGGCTTC	TCATGACAAG	780

ATGCCAACAA TTAAGGCAGA ATTGGAAAAG CAACCTTTCA AAGGAAAAC	GCATGACTTG	840
AGAGTTGATA CCCAAGGTGT CCGTGTAGAA GCAAAATAA		879

(2) INFORMATION FOR SEQ ID NO:2266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2266:

AAAAGTAAGA TAGGAGCATT CATGCAGTAT TCAGAAATTA TGATTGCTA CGGTGAGCTG	60
TCAACCAAGG GCAAAAATCG TATGCGTTTC ATCAATAAAC TTCGCAATAA TATTTAGAC	120
GTTTTGTCTA TCTATCCCCA AGTTAAGGTA ACAGCAGATC GCGACCGTGC CCACGCTTAC	180
CTCAATGGAG CAGATTACAC AGCAGTAGCA GAATCGCTCA AACAAGTATT TGGAATTCAA	240
AACTTTTCCC CTGTTTATAA GGTGAAAAA TCTGTAGAAG TTCTGAAGTC TGCTGTCCAA	300
GAGATTATGC AGGACATCTA CAAGGAAGGC ATGACCTTTA AAATCTCTAG CAAGCGTAGC	360
GACCACACCT TTGAATTGGA CAGTCGTGAA CTCAACCAAA CGCTTGGAAG GGCTGTATTC	420
GAAGCCATTC CAAACGTACA AGCTCAAATG AAAAGTCCTG ACATCAATCT TCAGGTGGAG	480
ATACGTGAAG AAGCAGCCTA TCTTTCTTAT GAAACCGTTC GAGGGGCAGG TGGATTACCA	540
GTGGGAACCT CTGGTAAGGG CATGCTCATG TTGTCAGGGG GAATCGATTG CCCTGTAGCT	600
GGCTATCTAG CGCTTAAACG AGGGGTAGAT ATAGAGGCAG TTCACCTTGC CAGCCCACCT	660
TACACGAGTC CTGGTGCTCT TAAAAAAGCC CAAGATTTGA CCCGTAAAT AACCAGATTT	720
GGGGGAAATA TCCAGTTTAT CGAAGTTCCT TTTACAGAGA TTCAAGAGGA AATCAAAGCC	780
AAAGCGCCAG AAGCCTACCT TATGACCTTG ACGCGTCGTT TTATGATGCG TATTACTGAC	840
CGTATTCGTG AGGTACGAAA TGGTTTAGTT ATCATCAATG GGGAAAGTCT AGGTCAAGTA	900
GCCAGCCAAA CCCTTGAAAG TATGAAGGCT ATCAATGCTG TTACCAACAC TCCCATCATT	960
CGTCCTGTGG TTACCATGGA CAAGTTGGAA ATCATTGACA TCGCCCAGGA AATCGATACC	1020
TTTGACATTT CAATCCAACC GTTTGAAGAC TGTGTACCA TTTTGCACC AGATCGTCCA	1080
AAAACAAATC CTAAAAATTAA GAATGCGGAG CAGTACGAAG CGCGTATGGA TGTGAAGGC	1140
TTGGTTGAGC GAGCAGTGGC TGGAATCATG ATTACTGAAA TCACACCTCA AGCCGAAAAA	1200
GATGAAGTTG ATGACTTGAT TGACAATCTG CTCTAA	1236

(2) INFORMATION FOR SEQ ID NO:2267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2267:

GGGGGTAAGA TTATGAAATA TGATTTATAT GATAATTGTA TTGAACTTCT AAAAGAACGC	60
GAAGTTACAA TTGAAGATAT GGCAGCGTTA GTAATATTTT CACAACAAAA ATATTACCCT	120
GAATTAACTC TTGACGACGC TTCATATGCA ATTCAACGTG TACTAAAAAA ACGTGAAGTT	180
CAGAAATGTAA TTATGACAGG AATTGAGTTA GATAAGTTAG CTGAAGCACA AAAACTATCT	240
CCAGAATTTT AAAAGATTAT GGAGAAAGAT AATCCATTGT ATGGGATTGA TGAAGTAATC	300
GTCTTATCGA TATTGAATTT ATATGGTTCT ATTGCCTTTA CAAATTATGG CTATTTAGAT	360
AAATTAAAC CACTGATTTT AGAAAGATTG AATGAGAATC ACGAAGGTGT TTGTAATGTA	420
TTTCTAGATG ATATTGTTGG TGCAATAGCC GCAGCAGCAT GTAGTAAAAT TGCACACAAT	480
CATGCTAGTG ATGAAATATA A	501

(2) INFORMATION FOR SEQ ID NO:2268:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 222 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2268:

AGGTTAAAGA TGTCAAAACA AAAGAAATTT GAGGAAAATC TAGCAGAACT GGAAACCATT	60
GTCCAAAGTT TGGAAAATGG TGAAATTGCT CTGGAAGATG CGATTACTGC CTTTCAAAAG	120
GGCATGGTCT TGTCAAAAGA GCTCCAAGCT ACGCTGGACA AGGCTGAAAA GACCTTGGTC	180
AAGGTCATGC AAGAAGACGG AACAGAAAGT GATTTTGAAT GA	222

(2) INFORMATION FOR SEQ ID NO:2269:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1791 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2269:

TGTCAAAAAGA	TACAAGGTAT	AAGAGCCTGC	AAGAGATGTT	TAACATTGCG	AATGAATGGA	60
GGGTTTCAAA	TGAAAGAGTT	TTATAAAAAA	AGATTTGCTC	TTACAGATGG	AGGAGCAAGA	120
AATTTAAGTA	AAGCAACACT	GGCTTCATTT	TTCGTTTATT	GTATAAACAT	GCTTCCTGCC	180
ATATTACTTA	TGATTTTTGC	TCAGGAAGTT	TTGGAAAATA	TGGGCAAAAG	CAATGGCTTT	240
TATATAGTAT	TCTCAGTTTT	GATTTTGATA	GCAATGTATA	TTTTGCTTTC	TATCGAATAC	300
GATAAATTAT	ATAACACAAC	CTATCAAGAA	AGTGCAGATT	TAAGAATAAG	GACAGCGGAG	360
AATTTATCAA	AATTACCTCT	ATCTTACTTT	TCTAAACATG	ACATTTCCGA	CATTTACAAA	420
ACAATCATGG	CTGATATTGA	AGGCATAGAG	CATGCAATGA	GCCACTCAAT	ACCAAAGGTG	480
GGCGGCATGG	TACTGTTTTT	CCCATTAATA	TCTGTAATGA	TGCTAGCGGG	CAATGTCAAG	540
ATGGGTTTAG	CTGTAATTAT	TCCATCTATT	TTAAGCTTTA	TATTTATACC	TTTATCTAAA	600
AAATATCAGG	TTAATGGACA	GAATAGATAT	TATGATGTCT	TAAGAAAAAA	CTCAGAAAGC	660
TTTCAAGAAA	ATATCGAAAT	GCAAATGGAG	ATTAAAGCAT	ATAATTTATC	GAAGGATATT	720
AAAGATGACT	TATATAAAAA	AATGGAAGAT	AGTGAGAAAG	TACACTTAAA	GGCGGAAGTA	780
ACTACAATTT	TAACTTTGTC	TATATCTTCA	ATATTTAGCT	TTATATCTCT	TGCTGTTGTG	840
ATATTTGTCT	GCGTAAATCT	AATTATTAAT	AAAGAGATAA	ATTCTCTCTA	CCTTATAGGA	900
TATTTACTAG	CTGCTATGAA	GATAAAAGAC	TCTTTAGATG	CATCTAAAGA	GGGCTTGATG	960
GAAATATTTT	ATTTATCGCC	CAAAATAGAA	AGATTTAAAG	AAATTCAAAA	TCAAGATTTA	1020
CAAGAAGGCG	ATGACTATAG	CTTAAAAAAA	TTTGATATTG	ATCTAAAAGA	TGTTGAGTTT	1080
GCCTACAATA	AAGACGAAAA	AGTTTTTAAAT	GGTGTAAGTT	TTAAAGCTAA	GCAGGGAGAG	1140
GTCACGTGCT	TGGTAGGTGC	AAGTGGCTGC	GGTAAAACAA	CTATCTTGAA	ACTTATATCA	1200
AGACTTTATG	ATTATGACAA	GGGACAAATC	TTAATCGATG	GCAAAGATAT	AAAGGAAATA	1260
TCAACAGAAAT	CCCTTTTTGA	TAAGGTGTCT	ATTGTTTTCC	AAGATGTGGT	TCTCTTTAAT	1320
CAAAGCGTTA	TGGAAAATAT	TAGAATCGGT	AAGCAAGATG	CAAGTGACGA	AGAGGTTAAA	1380
AGAGCAGCAA	AACTTGCAAA	TTGCACAGAT	TTTATAGAAA	AAATGGATAA	AGGTTTCGAT	1440
ACAGTTATTG	GTGAAAACGG	AGCTGAGCTA	TCAGGAGGAG	AAAGACAAAAG	ATTATCAATA	1500
GCCAGAGCCT	TCTTAAAAGA	TGCGCCGATA	TTGATCTTAG	ATGAGATAAC	AGCAAGCCTT	1560
GATGTTAACA	ACGAGAAAAA	GATTCAAGAG	TCTTTAAATA	ATTTAGTTAA	AGATAAAACT	1620
GTTGTAATCA	TTTCACATAG	AATGAAATCC	ATAGAAAATG	CAGACAAGAT	AGTAGTTCTT	1680
CAAAACGGAA	GAGTAGAAAG	CGAAGGTAAG	CATGAAGAGC	TTTTACAAAA	ATCAAAAATT	1740
TACAAAAATT	TAATAGAAAA	GACAAAAATG	GCAGAAGAAT	TTATTTATTA	G	1791

(2) INFORMATION FOR SEQ ID NO:2270:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2270:

GTCAAAAAGA	TGTTCAAAGA	TTTTATCCAA	TCTATTTATG	AAAAAGTTTA	TATTATAAAT	60
TTCGAAAAAT	GCTCTCAAAT	ACCGTGTTTG	ACGAGTGAAG	AATTGAAAAG	TC'TTGGAAAA	120
TGGTATGTCT	CGACTGGTAA	AGAATGGATT	TGTCATTTCAG	ATGCTGATCT	GGAAGAATTT	180
AAAAATCTAT	TTTTAAATTT	TATCAATCCT	GAAGAATGGG	ATACTATCTC	CTTTGATTCA	240
GATTTTATGC	CGTTTCAATA	A				261

(2) INFORMATION FOR SEQ ID NO:2271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 885 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2271:

GAGAAAAAGA	TGAGAAATGT	AAGAGTTGCA	ACCATTTCAGA	TGCAATGCGC	TAAGGATGTG	60
GCAACAAATA	TCCAAACCGC	AGAGCGTTTA	GTACGTCAGG	CTGCTGAGCA	AGGAGCCCAA	120
ATTATTCTCT	TGCCCGAGTT	GTTTGAACAT	CCCTATTTCT	GTCAGGAACG	TCAGTATGAC	180
TACTACCAGT	ATGCCCAATC	TGTAGCGGAA	AATACTGCCA	TTCAGCATTT	TAAGGTGATT	240
GCTAAGGAAC	TACAAGTTGT	TTTACCAATC	AGTTTCTATG	AAAAAGATGG	TAATGTCTTG	300
TATAACTCTA	TTGCCGTCAT	TGATGCAGAT	GGGGAAGTGC	TGGGCGTTTA	TCGAAAGACC	360
CACATACCAG	ATGACCATTA	TTATCAAGAA	AAATTCCTATT	TCACGCCTGG	TAACACTGGT	420
TTCAAGGTCT	GGAATACTCG	CTATGCTAAG	ATTGGTATCG	GTATCTGTTG	GGATCAATGG	480
TTCCCCGAAA	CAGCCCGCTG	TCTTGCTCTG	AATGGGGCAG	AATTGCTCTT	TTATCCAACA	540
GCCATCGGTT	CAGAGCCGAT	TTTGGATACA	GATAGTTGTG	GTCAC TGGCA	ACGTACTATG	600
CAAGGGCACG	CAGCAGCGAA	TATTGTTCCA	GTCATCGCAG	CCAATCGTTA	TGGTTTAGAG	660

GAGGTTACTC	CTAGTGAGGA	AAATGGCGGA	CAGAGTTCCA	GTCTTGACTT	CTACGGTTCC	720
TCCTTTTATGA	CGGATGAAAC	AGGAGCTATT	CTAGAACGAG	CTGAAAGACA	AGAAGAAGCT	780
GTTCTGTTAG	CTACTTATGA	CCTAGACAAG	GGAGCAAGTG	AACGCCATAA	CTGGGGCTTG	840
TTTCGAGATA	GAAGACCAGA	AATGTATAGA	CAAATTACAG	ATTAG		885

(2) INFORMATION FOR SEQ ID NO:2272:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 768 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...768
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2272:

AATAGAAAGA	TTGATACTAT	GACAAAAATT	AAGATTGTAA	CCGATTCATC	TGTTACTATT	60
GAACCTGAAC	TAGTAAAGCA	ATTAGATATT	ACAATTGTTC	CATTATCTGT	AATGATTGAT	120
AATGTTGTTT	ATTCTGATGC	GGATTTGAAA	GAAGAAGGTA	AATTTCTTCA	GTTGATGCAA	180
GAAAGTAAGA	ATCTTCCGAA	AACAAGTCAG	CCACCTGTAG	GTGTCTTTGC	TGAGATTTTT	240
GAAGACCTAT	GCAAAGATGG	TGGCCAGATT	CTTGCTATTG	ATATGTCCCA	TGCTCTTTTCG	300
GGTACGGTAG	AAGCAGCACG	CCAAGGTGCT	AGCCTATCTA	CTGCAGATGT	GAAGTTTGTG	360
GATAGTTCCT	TCCTGACCA	AGCCCTGAAA	TTCCAAGTTG	TTGAGGCTGC	GAAGTTAGCT	420
CAAGAAGGTA	AAGATATGGA	GGCAATTTTA	TCTCATGTAG	AAGAGGTTAA	AAACCATACA	480
GAGCTTTATA	TTGGTGTTTC	AACTTTGGAA	AATCTTGTC	AAGGTGGACG	AATTAGCCGT	540
GTAAGTGGCT	TGTTGAGCTC	TCTTCTCAAT	ATCCGTGTTG	TCATGCAAAT	GAAAGACCAT	600
GAATTGCAGC	CAATGGTTAA	AGGTCGTGGA	ACTAAAACAT	TTAAAAAATG	GTTAGATGAG	660
TTGATAACAT	CGCTTCTGA	ACGTGCTGTA	GCAGAGATTG	GAATTTTCATA	TTCTGGTAGT	720
GATNGATTGG	GCAAAAGAGA	TGAAAGAAAAG	CTTACAAGCT	TATGTTGA		768

(2) INFORMATION FOR SEQ ID NO:2273:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2273:

AGAGGAAAGA	TGAGTACTTT	AGCAAAAATA	GAAGCGCTCT	TGTTTGTAGC	GGGTGAAGAT	60
GGGATTCGGG	TCCGCCAGTT	AGCTGAACTC	CTCTCTCTGC	CACCGACAGG	CATCCAGCAA	120
AGTTTAGGAA	AATTAGCCCA	GAAGTATGAA	AAGGACCCAG	ATTCCAGTTT	GGCTTTGATT	180
GAGACAAGTG	GTGCTTATAG	ATTGGTGACC	AAGCCTCAAT	TTGCAGAGAT	TTTGAAGGAA	240
TACTCTAAGG	CGCCTATCAA	CCAGAGCTTG	TCTCGGGCTG	CCCTTGAGAC	CTTGTCCATT	300
ATTGCCCTACA	AACAGCCGAT	TACGCGGATA	GAAATTGATG	CCATCCGTGG	AGTTAACTCG	360
AGTGGAGCCT	TGGCAAAGTT	GCAGGCTTTT	GACCTGATAA	AGGAAGACGG	GAAAAAGGAA	420
GTATTGGGGC	GCCCCAACCT	CTATGTGACT	ACGGATTATT	TCCTAGATTA	CATGGGGATA	480
AACCATTTAG	AAGAATTACC	AGTGATTGAT	GAGCTTGAGA	TTCAAGCCCA	AGAAAGCCAA	540
TTATTTGGTG	AAAGGATAGA	AGAAGATGAG	AATCAATAA			579

(2) INFORMATION FOR SEQ ID NO:2274:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 795 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2274:

TTTATGAAGA	TTCTCTCTT	AACTTTTGCA	AGGCATAAAAT	TTGTTTATGT	CTTGCTTACT	60
TTGCTTTTTT	TTGCTTTGGT	TTATCGTGAT	GTTTTGATGA	CTTATTTCTT	TTTTGATATT	120
CATGCGCCCG	ATCTAGCTAA	ATTTCGATGGA	CAAGCAATTA	AAAATGACTT	ATTAAAATCA	180
GCATTAGATT	TTTCGTATTCT	CCAGTTCAAT	CTAGGTTTTT	ATCAATCATT	TATTATTCCA	240
ATCATCATTG	TTTTGCTAGG	TTTTCAATAT	ATTGAGCTGA	AAAATAAAGT	TTTACGATTG	300
AGTATTGGAA	GAGAAGTGAG	CTATCAAGGG	TTAAAAAGAA	AGTTGACTTT	GCAAGTTGCA	360
AGTATCCCTT	GTTTGATATA	TTTAGTGACT	GTGCTGATAA	TTGCAATTAT	AACCTATTTT	420
CTTGGGACTT	TTTCTCCTCT	TGGATGGAAT	TCTCTATTTT	CTGATGGAAG	TGGTTTACAA	480
AGACTCCTAG	ATGGAGAGAT	AAAAAGCTAT	TTGTTCTTTA	CTTGTGTCCT	ACTAATCGGT	540
ATTTTCATCA	ATGCAATCTA	TTTTTTTACAA	ATAGTTGATT	ATGTGGGGAA	TGTGACTCGT	600
TCGGCAATCA	CCTATTTGAT	GTTTCTTTTG	CTTGGTTCTA	TGCTGCTCTA	TAGTGCCCTG	660
CCTTACTATA	TGGTTCCCTAT	GACGAGTTTG	ATGCAAGCTA	GCTATGGGGA	TGTAAGTTTG	720
ATGAAACTCT	TTACTCCTTA	TATCCTTTAT	ATTGTCCTTT	ATATGGTGCT	TGAAAAATAT	780
GAAGATAATG	TTTAA					795

(2) INFORMATION FOR SEQ ID NO:2275:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 723 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...723
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2275:

ACGATGAAGA	TTGATATTTT	AACCCTCTTT	CCAGAGATGT	TTTCTCCACT	GGAGCACTCA	60
ATCGTTGGAA	AGGCTCGAGA	AAAAGGGCTC	TTGGATATCC	AGTATCATAA	TTTTCGAGAA	120
AATGCTGAAA	AGGCCCGTCA	TGTAGATGAT	GAGCCCTACG	GAGGCGGTCA	GGGCATGTTG	180
CTCAGAGCAC	AACCTATTTT	CGATTCTTTT	GATGCTATTG	AAAAGAAAAA	TCCGCGCGTT	240
ATTCTCCTCG	ATCCTGCTGG	AAAGCAGTTT	GATCAGGCTT	ATGCTGAAGA	TTTGGCTCAA	300
GAGGAAGAGC	TAATCTTTAT	CTGTGGGCAC	TATGAGGGTT	ATGATGAGCG	CATTAAGACC	360
TTGGTAACAG	ATGAGATTTT	CCTAGGCGAC	TATGTCCTCA	CTGGTGGAGA	ATTGGCAGCT	420
ATGACCATGA	TTGATGCTAC	AGTTCGCCTG	ATTCCAGAAG	TGATTGGCAA	GGAGTCTAGC	480
CACCAAGATG	ATAGTTTTTC	TTCAGGTCTT	TTAGAATATC	ATCAGTACAC	ACGTCCCTAT	540
GATTATCGAG	GCATGGTCGT	GCCAGATGTA	TTGATGAGTG	GCCATCATGA	AAAGATTCGT	600
CAGTGGCGAT	TGTACGAGAG	TTTAAAGAAA	ACCTACGAGC	GCAGACCGGA	TTTACTTGAA	660
CATTATCAAC	TGACAGTAGA	AGAAGAAAAA	ATGCTGGCAG	AAATCAAAGA	AAACAAAGAA	720
TAA						723

(2) INFORMATION FOR SEQ ID NO:2276:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2276:

AAGATGAAGA	TTATGCTGCT	AAATATACAC	GAGCGAAGTA	CTATTATTCT	AAGTCGAGGG	60
AAAAAGTTTA	TACGATTCCCT	GACTTGCTTC	AAAGGTGATA	AAATGGAAAA	TTTATTAGAC	120
GTAATAGAGC	AATTTTTGAG	TTTGTGAGAT	GAAAAGCTGG	AAGAATTGGC	TGATAAAAAT	180
CAATTATTGC	GTTTACAAGA	AGAAAAGGAA	AGGAAGAATG	CGTAA		225

(2) INFORMATION FOR SEQ ID NO:2277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2277:

GAGATGAAGA	TTGGATTTAT	CGGTTTGGGG	AATATGGGTG	CTAGCTTGGC	AAAATCTGTC	60
TTGCAGACTA	GGACGTCAGA	TGAGATTCTC	CTTGCCAATC	GTAAGTCAAGC	TAAGGTAGAT	120
GCTTTCATTG	CAGACTTTGG	TGGTCAGGCT	TCCAGCAATG	AAAAAATGTT	TGCAGAAGCA	180
GATGTGATTT	TTCTAGGAGT	TAAGCCTGCT	CAGTTTCTCTG	AACTGCTTTC	TCAATACCAG	240
ACCATCCTTG	AAAAAAGAGA	AAGTCTTCTT	TTGATTTCGA	TGGCAGCTGG	ATTGACCTTA	300
GAAAAACTAG	CAAGTCTTAT	CCCAAGCCAA	CACCGAATTA	TTCGTATGAT	GCCTAATACC	360
CCTGCTTCTA	TCGGGCAAGG	AGTGATTAGT	TATGCCCTGT	CTCCTAATTG	CAGGGCTGAG	420
GACAGTGAGA	TCTTTTGTC	GCTTTTAGCC	AAGGCTGGTC	TCTTGGTTGA	ATTAGGAGAA	480
AGCTTAATCA	ATGCAGCGAC	AGGTCTTGCA	GGTTGTGGAC	CAGCCTTGT	CTATCTCTTT	540
ATTGAGGCCT	TGGCAGATGC	AGGTGTTTCA	ACGGGATTAC	CACGAGAAAC	AGCCTTGAAA	600
ATGGCAGCCC	AAACTGTGGT	AGGAGCTGGG	CAATTGGTCC	TAGAAAGCCA	GCAACATCCT	660
GGAGTTTGA	AAGATCAAGT	TTGTAGTCCA	GGCGGTTTCA	CTATTGCTGG	CGTAGCAAGC	720
CTAGAAGCGC	ATGCTTTTCG	AGGCACAGTC	ATGGAGGCAG	TTCATCAAGC	CTATAAACGA	780
ACACAAGAAC	TAGGTAAATA	A				801

(2) INFORMATION FOR SEQ ID NO:2278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...198
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2278:

TTGGATGAGA TAGGATTCCA AGGTGCTAGC GCTCCCTCAC GTAAGGTTTT GCTGGCATCT	60
GGCACTACCA AATCAGTATC CACCTCCAGC TTGATGCCCA AGCCGTCACA CTCACTACAA	120
GAGCCAAAAG GAGCATTGAA AGAGAAGAGA CGAGGCTCTA ACTCTGGGAC AGTAAAACCA	180
CAAACCTGGAC AGGCATAA	198

(2) INFORMATION FOR SEQ ID NO:2279:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 540 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...540
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2279:

AAAGTGAGAG TTATGAGTTA TTTTAAAAAA TATAAATTCG ATAAATCCCA GTTCAAACCTT	60
GGTATGCGAA CCTTTAAAC AGGTATTGCT GTTTTTCTAG TTCTCTTGAT TTTTGGCTTT	120
TTTGGCTGGA AAGGTCTTCA AATTGGTGCT TTGACAGCCG TTTTTCAGCCT GAGGGAGAGT	180
TTTGATGAGA GTGTTCAATTT TGGGACTTCG CGTATTCTAG GAAATAGTAT CGGTGGACTC	240
TATGCCTTGG TCTTCTTCTT ATTAAATACT TTTTTCACAG AAGCCTTTTG GGTGACCTTG	300
GTAGTTGTTC CAATCTGCAC CATGTTAACC ATTATGACAA ATGTAGCCAT GAATAACAAA	360
GCAGGGGTTA TTGGTGGTGT AGCAGCTATG TTAATCATT A CCCTATCAAT TCCAAGTGGC	420
GAGACAATTT TGTACGTGTT TGTGCGTGTA TTAGAAACGT TTATGGGAGT TTTTGTTCGCA	480
ATTATCGTAA ATTACGATAT TGATCGTATT CGTCTCTTTT TAGAGAAAAA AGAAAAATAA	540

(2) INFORMATION FOR SEQ ID NO:2280:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5904 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...5904

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2280:

ATAAAGGAGA	TAAAAGTGTT	TAAAAAAGAC	CGTTTTTTC	TTCGTAAGAT	TAAGGGAGTT	60
GTAGGCTCTG	TATTTCTTGG	AAGCCTTTTT	ATGGCTCCTT	CTGTAGTGGA	CGCAGCCACC	120
TATCACTATG	TAAATAAAGA	GATTATTTCA	CAAGAAGCTA	AAGATTTAAT	TCAGACAGGA	180
AAGCCTGACA	GGAATGAAGT	TGTATATGGT	TTGGTGATC	AAAAAGATCA	GTTGCCCTCAA	240
ACAGGGACAG	AAGCATCTGT	TTTGACAGCT	TTTGGTTTGC	TGACTGTTGG	GAGCTTGCTT	300
TTAATCTACA	AGAGAAAGAA	AAATTGCTAGC	GTCCTTCTAG	TTGGAGCTAT	GGGATTGGTA	360
GTTCTTCCTA	GTGCAGGGGC	TGTAGACCCA	GTTGCGACCC	TAGCGCTGGC	TAGTCGAGAG	420
GGTGTTGTTG	AAATGGAGGG	CTATCGCTAT	GTTGGTTATC	TATCAGGTGA	CATCCTCAAA	480
ACGCTTGGCT	TGGACTAGGT	TTTAGAAAAA	ACCTCAGCAA	AACCTGGAGA	GGTGACTGTA	540
GTGGAAGTTG	AGACTCCTCA	ATCAACAACA	AATCAGGAGC	AAGCTAGGAC	AGAAAAACCAA	600
GTAGTAGAGA	CAGAGGAAGC	ACCTAAAACA	GAAGAAAGTC	CAAAGGAAGA	ACCAAAATCG	660
GAGATAAAAC	CTACTGACGA	CACCCCTCCT	AAAGTAGAAA	AGGGAAAGAA	AATCCNCNNA	720
ACCGCTCCAG	TTGAAGAAAGT	AGGTGGAGAA	GTTGAGTCAA	AACCAGAGGA	AAAAGTAGCA	780
GTTAAGCCAG	AAAGTCAACC	ATCAGACAAA	CCAGCTGAGG	AATCAAAAGT	TGAACCACCA	840
GTAGAACAAG	CAAAAGGCCC	AGAACAACCC	GTGCAACCTA	CACAAGCTGA	GCAACCAAGG	900
ATACCAAAAG	ATTATCACA	ACCAGAAGAT	CCTAAAGAAG	ATAGGGGAGC	GGAAGATACA	960
CCGAAACAAG	AAGATACACA	GCCAGAAGTA	GTAGAAACAA	AAGATGAGGC	TGCTAATCAA	1020
CCTGTTGAAG	AACCAAAAGT	TGAAACGCCT	GCTGTAGAAA	AACAAACGGA	ACCAAAAGTT	1080
GAACAAGTAG	GTGAACCAGT	CGAGCCAAGT	GAAGACGAAA	AGGCACCAGT	CTCTCCAGAA	1140
AAGCAACCAG	AAGCTCCTGA	AGAGAAGGCT	GTAGAGGAAA	CACCGAAACC	AGAAGATAAA	1200
ATAAAGGGTA	TTGGTACTAA	AGAACCAGTT	GATAAAAGTG	AGTTAAATAA	TCAAATTGAT	1260
AAAGCTAGTT	CAGTTTCTCC	TACTGATTAT	TCTACAGCAA	GTTACAATGC	TCTTGGACCT	1320
GTTTTAGAAA	CTGCAAAAGG	TGTCTATGCT	TCAGAGCCTG	TAAACAGCC	TGAGGTAAAT	1380
AGCGAGACAA	ATAAACTTAA	AACGGCTATT	GACGCTCTAA	ACGTTGATAA	AAGTGAATTA	1440
CAGGAACAAT	TAAGAGTTGC	TGAACAAAAA	CAACAAGCTG	ACTATAGCGC	TAAAACCTTG	1500
AGGGAATTCA	AAATTGCTGA	ACTTCAAGCT	AAAGAAATCA	ACAACCAAAC	TACACCACTT	1560
CCTAAACAAA	GTGAAATAGA	TGCAGCTACT	AAGGCTCTTC	AAGACGCTCT	TCAAGCTCTT	1620
GCTGTAGATA	AAACTGTATT	ACAAAACGCT	ATTAACACAG	CTAATAGCAA	ACGTGAAGAA	1680
GAGTATACTG	CTCAGACATG	GAAAGCGTTA	GAAGATGCTC	TTACAGCAGT	GAATCCTGTT	1740
AATGAAGATG	AAACTGCAAC	TCAAAGCAAA	GTAGACGAAG	CTACTAGAAA	CTTAGAAGAA	1800
GCTATCAATA	ACCTAGTTCT	ATTAAGTGAA	AAACCGGTAT	TAACATTTAT	TGAGACTGAT	1860
AAGAAAGCAT	TAGAACGTGA	AGTAGTTGCT	AAGTATTCTC	TAGAAAACCA	AAATAAAACA	1920
AAAATTAAT	CAATCACAGC	TACTCTGAAA	AAAGGAGAAA	CAGTTGTTAG	CACTGTAGAG	1980
CTTATAGGCG	ATGATGTAAC	TAATGAAACT	ATAACCTCTG	CATTTAAGAA	TCTAGAGTAC	2040
TACAAAGAAT	ACACCTATC	TACAACTATG	GTTTACGATA	GAGGTGACGG	TGATGTAACA	2100
GAAATCTTAG	ATAATCAACC	AATCCAACCTA	GATCTTAAAA	AAGTTGAGCT	TAAAAATATT	2160
AAACGTACAG	ATTTAATCAA	ATACGAAAAAT	GGAAAAAGAA	CTAATGAATC	ACTAATAACA	2220
ACTGTTCCCTG	ATGATAAGCG	GAATTATTAT	TTAAAAATAA	CTTCAAAGAA	TCAAAAAACT	2280

ACATTACTAG	CTGTTAAAAA	TATAGAAGAA	ACTACGGTTA	ACGGAACACC	TGTATATAAA	2340
GTTACAGCAA	TCGCAGACAA	TTTAGTCTCT	AGAACTGCTG	ATAATAAATT	TGAAGAAGAA	2400
TACGTTCACT	ATATTGAAAA	ACCTAAAGTC	CACGAAGATA	ATGTATATTA	TAACCTCAAA	2460
GAATTAGTGG	AGGCTATTCA	AAACGATCCT	TCAAAAAGAA	ATCGTCTGGG	ACAATCAATG	2520
AGCGCTAGAA	ATGTTGTTCC	TAATGGAAAA	TCATATATCA	CTAAAAGAA	TACAGGAAAA	2580
CTTTTAAGTT	CTGAAGGAAA	ACAATTTGCT	ATCACTGAGT	TGGAACATCC	ATTATTTAAT	2640
GTGATAACAA	ACGCAACGAT	AAATAATGTG	AATTTTGAAA	ATGTAGAGAT	AGAACGTTCT	2700
GGTCAAGATA	ATATTGCATC	ATTAGCCAA	ACTATGAAAG	GTTCTTCAGT	TATTACAAAT	2760
GTCAAAATTA	CAGGCACACT	TTCAGGTCGT	AATAATGTTG	CTGGATTTGT	AAATAATATG	2820
AATGATGGAA	CTCGTATTGA	AAATGTTGCT	TTCTTTGGCA	AACCTACACTC	TACAAGTGGA	2880
AATGGCTCTC	ATACAGGGGG	AATTGTCAGGT	ACAAACTATA	GAGGAATTGT	TAGAAAAGCA	2940
TATGTTGATG	CTACTATTAC	AGGAAACAAA	ACACGCGCCA	GCTTGTTAGT	TCCTAAAGTA	3000
GATTATGGAT	TAACCTAGTA	CCATCTTATT	GGTACAAAAG	CTCTCCTAAC	TGAGTCGGTT	3060
GTAAAAGGTA	AAATAGATGT	TTCAAATCCA	GTAGAAGTTG	GAGCAATAGC	AAGTAAGACT	3120
TGGCCTGTAG	GTACGGTAAG	TAATTCTGTC	AGCTATGCTA	AGATTATCCG	TGGAGAGGAG	3180
TTATTCGGCT	CTAACGACGT	TGATGATTCT	GATTATGCTA	GTGCTCATAT	AAAAGATTTA	3240
TATGCGGTAG	AGGGATATTC	GTCAGGTAAT	AGATCATTTA	GGAAATCTAA	AACATTTACT	3300
AAATTAACCTA	AAGAACAAGC	TGATGCTAAA	GTTACTACTT	TCAATATTAC	TGCTGATAAA	3360
TTAGAAAAGTG	ATCTATCTCC	TCTTGCAAAA	CTTAATGAAG	AAAAAGCCTA	TTCTAGTATT	3420
CAAGATTATA	ACGCTGAATA	TAACCAAGCC	TATAAAAAATC	TTGAAAAATT	AATACCATTTC	3480
TACAATAAAG	ATTATATTGT	ATATCAAGGT	AATAAAATTA	ATAAAGAACA	CCATCTAAAT	3540
ACTAAAGAA	TTCTTTCTGT	TACCGCGATG	AACAACAATG	AGTTTATCAC	AAACCTAGAT	3600
GAAGCTAATA	AAATTATTGT	TCACTATGCG	GACGGTACAA	AAGATTACTT	TAACCTGTCT	3660
TCTAGCAGTG	AAGGTTTAAG	TAATGTAAAA	GAATATACTA	TAAGTACTTT	AGGAATTTAA	3720
TATACACCTA	ATATCGTTCA	AAAAGATAAC	ACTACTCTTG	TTAATGATAT	AAAATCTATT	3780
TTAGAACTAG	TAGAGCTTCA	GTCTCAAACG	ATGTATCAGC	ATCTAAATCG	ATTAGGTGAC	3840
TATAGAGTTA	ATGCAATCAA	AGATTTATAT	TTAGAAGAAA	GCTTCACAGA	TGTTAAAGAA	3900
AACCTTAACAA	ACCTTAATCAC	AAAATTAGTT	TAAAACGAAG	AACATCAACT	AAATGATTCT	3960
CCAGCTGCTC	GTCAAAATGAT	TCGTGATAAA	GTCGAGAAAA	ACAAAGCAGC	TTTATTACTA	4020
GGTTTAACTT	ACCTAAATCG	TTACTATGGA	GTTAAATTTG	GTGATGTTAA	TATTAAAGAA	4080
TTAATGCTAT	TCAAACCAGA	TTTCTATGGT	GAAAAAGTTA	GCGTATTAGA	CAGATTAAAT	4140
GAAATCGGTT	CTAAAGAGAA	CAACATTAAA	GGTTCACGTA	CATTTCGACGC	ATTTCGGTCAA	4200
GTATTGGCTA	AATATACTAA	ATCAGGTAAT	TTAGATGCAT	TTTTAAATTA	TAATAGACAA	4260
TTGTTACAAA	ATATAGACAA	TATGAACGAT	TGGTTTATTG	ATGCTACAGA	AGACCATGTC	4320
TACATCGCAG	AACGCGCTTC	TGAGGTCGAA	GAAATTAATA	ATTCTAAACA	TCGTGCATTTC	4380
GATAATTTAA	AACGAAGTCA	CCTTAGAAAT	ACTATACTCC	CACTACTGAA	TATTGATAAA	4440
GCACATCTTT	ATTTAATTTTC	AAATTTATAAT	GCAATTGCGCT	TTGGTAGTGC	AGAGCGATTA	4500
GGTAAAAAAT	CATTAGAAGA	TATTAAAGAT	ATCGTTAACA	AAGCTGCAGA	TGGTTATAGA	4560
AACTATTATG	ATTTCTGGTA	TCGTCTAGCG	TCTGATAACG	TTAAACAACG	ACTACTAAGA	4620
GATGCTGTTA	TTCTTATTTG	GGAAAGGTTAT	AACGCTCCTG	GTGGATGGGT	TGAAAAATAT	4680
GGCCGCTATA	ATACCGACAA	AGTATATACT	CCTCTTAGAG	AATTCTTTGG	TCCTATGGAT	4740
AAGTATTATA	ATTATAATGG	AACAGGAGCT	TATGCTGCTA	TATATCCTAA	CTCTGATGAT	4800
ATTAGAACTG	ATGTAAAAA	TGTTCAATTA	GAAATGGTTG	GTGAATACGG	TATTTCAAGTT	4860
TACACACATG	AAACAACACA	CGTCAACGAC	CGTGCGATTT	ACTTAGGTGG	CTTTGGACAC	4920
CGTGAAGGTA	CTGATGCTGA	AGCATATGCT	CAGGGTATGC	TACAAACTCC	TGTTACTGGT	4980
AGTGGATTTG	ATGAGTTTGG	TTCTTTAGGT	ATTAATATGG	TATTTAAACG	CAAAAATGAT	5040
GGGAATCAGT	GGTATATTAC	AGATCCAAAA	ACTCTAAAAA	CACGAGAAGA	TATTAATAGA	5100
TATATGAAGG	GTTATAATGA	CACTTTAACT	CTTCTTGATG	AAATTGAGGC	TGAATCTGTG	5160
ATTTCTCAAC	AAAAATAAGA	TTTAAATAGT	GCATGGTTCA	AAAAAATAGA	TAGAGAATAC	5220
CGTGATAACA	ATAAATTAATA	TCAATGGGAT	AAAAATTCGAA	ATCTAAGTCA	AGAAGAGAAA	5280
AATGAATTAA	ATATTCAATC	TGTTAATGAT	TTAGTTGATC	AACAATTAAT	GACTAATCGC	5340
AATCCAGGTA	ATGGTATCTA	TAAACCCGAA	GCAATTAGCT	ATAACGATCA	ATCACCTTAT	5400
GTAGGTGTTA	GAATGATGAC	CGGTATCTAC	GGAGGTAATA	CTAGTAAAGG	TGCTCCTGGA	5460
GCTGTTTCAT	TCAAACATAA	TGCTTTTAGA	TTATGGGGTT	ACTACGGATA	CGAAAAATGGG	5520
TTCTTAGGTT	ATGCTTCAAA	TAAATATAAA	CAACAATCTA	AAACAGATGG	TGAGTCTGTT	5580
CTAAGTGATG	AATATATTAT	CAAGAAAAATA	TCTAACATAA	CATTTAATAC	TATTGAAGAA	5640
TTTAAAAAAG	CTTACTTCAA	AGAAGTTAAA	GATAAAGCAA	CGAAAGGATT	AACAACATTC	5700

GAAGTAAATG	GTTCTTCCGT	TTCATCATAC	GATGATTTAC	TGACATTGTT	TAAAGAAGCT	5760
GTTAAAAAAG	ATGCCGAAAC	TCTTAAACAA	GAAGCAAACG	GTAATAAAAC	AGTATCTATG	5820
AATAATACAG	TTAAATTAAA	AGAAGCTGTT	TATAAGAAAC	TTCTTCAACA	AACAGATAGC	5880
TTTAAAACTT	CAATCTTTAA	ATAA				5904

(2) INFORMATION FOR SEQ ID NO:2281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2281:

GAGAAGGAGA	TGAGTTCAGG	TAAAATTGCT	CAGGTTATCG	GTCCCGTTGT	AGACGTTTTG	60
TTTGCAGCAG	GGGAAAAACT	TCCTGAGATT	AATAATGCAC	TTGTCGTCTA	CAAAAATGAC	120
GAAAGAAAAA	CAAAAATCGT	CCTTGAAGTA	GCCTTGGAGT	TAGGAGATGG	TATGGTTCGT	180
ACTATCGCCA	TGGAATCAAC	AGATGGGTTG	ACTCGTGGAA	TGGAAGTATT	GGACACAGGT	240
CGTCCAATCT	CTGTACCAGT	AGGTAAAGAA	ACTTTGGGAC	GTGTCTTCAA	CGTTTTGGGA	300
GATACCATTG	ACTTGGAAGC	TCCTTTTACA	GAAGACGCAG	AGCGTCAGCC	AATTCATAAA	360
AAAGCTCCAA	CTTTTGATGA	GTTGTCTACC	TCTTCTGAAA	TCCTTGAAAC	AGGGATCAAG	420
GTTATTGACC	TTCTTGCCCC	TTACCTTAAA	GGTGGTAAAG	TTGGACTTTT	CGGTGGTGCC	480
GGAGTTGGTA	AAACTGTCTT	AATCCAAGAA	TTGATTCAACA	ACATTGCCCA	AGAGCACGGT	540
GGTATTTTCA	TATTTGCTGG	TGTTGGGGAA	CGTACTCGTG	AGGGGAATGA	CCTTTACTGG	600
GAAATGAAAG	AATCAGGCGT	TATCGAGAAA	ACAGCCATGG	TCTTTGGTCA	GATGAATGAG	660
CCACCAGGAG	CACGTATGCG	TGTTGCCCTT	ACTGGTTTGA	CAATCGCTGA	ATACTTCCGT	720
GATGTGGAAG	GCCAAGACGT	GCTTCTCTTT	ATCGATAATA	TCTTCCGTTT	CACTCAGGCT	780
GGTTCAGAA	TATCTGCCCT	TTTGGGTCGT	ATGCCATCAG	CCGTTGGTTA	CCAACCAACA	840
CTTGCTACGG	AAATGGGTCA	ATTGCAAGAA	CGTATCACAT	CAACCAAGAA	GGGTTCTGTA	900
ACCTCTATCC	AGGCTATCTA	TGTGCCAGCG	GATGACTATA	CTGACCCAGC	GCCAGCAACA	960
GCCTTCGCTC	ACTTAGATT	AACAACAAAC	TTGGAACGTA	AGTTGGTACA	ATTGGGTATC	1020
TACCCAGCCG	TTGACCCACT	TGCTTCAAGC	TCACGTGCCT	TGGCACCTGA	AATCGTTGGA	1080
GAAGAGCACT	ATGCAGTTGC	TGCTGAAGTA	AAACGTGTTT	TTCAACGTTA	CCATGAATTG	1140
CAAGATATCA	TTGCTATCCT	TGGTATGGAT	GAGCTTTCTG	ATGAAGAAAA	GACCTTGGTT	1200
GCTCGCGCCC	GTCGTATCCA	GTTCTTCTTG	TCACAAAACT	TCAACGTTGC	GGAACAATTT	1260
ACTGGTCAGC	CAGGTTCTTA	TGTTCCAGTT	GCTGAAACTG	TACGTGGCTT	TAAGGAAATC	1320
CTTGATGGTA	AATACGACCA	CTTGCCAGAA	GATGCCTTCC	GTGGTGTAGG	TTCTATCGAA	1380
GATGTGATTG	CAAAAGCTGA	AAAAATGGGA	TTTTTAA			1416

(2) INFORMATION FOR SEQ ID NO:2282:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 858 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...858

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2282:

AACGAGGAGA	TGGATATGAC	GAAAATAGCT	CTTCTTTTCAG	ATATTCATGG	AAATACCACC	60
GCCTTGGAGG	CTGTTTGGG	AGATGCTCAG	CAGCTAGGAG	TGGATGAATA	CTGGCTTTTG	120
GGAGATATTC	TCATGCCAGG	GACAGGACGT	AGGAGGATTT	TGGACTTGTT	GGATCAACTA	180
CCGATTACGG	CTAGAGTTTT	GGGAAACTGG	GAAGACAGTC	TTTGGCATGG	TGTCCGTAAG	240
GAATTGGACA	GTACTCGCCC	CAGTCAACGC	TATCTCTTGC	GCCAGTGCCA	GTATGTTTTA	300
GAGGAAATTT	CCCTAGAAGA	AATTGAAGTG	CTCCACAATC	AACCTCTTCA	AATTCATCGT	360
CAGTTTGGGG	ATTTGACGGT	GGGAATTAGC	CATCATCTGC	CTGATAAGAA	CTGGGGGCGA	420
GAGTTGATTC	ATACTGGCAA	ACAAGAGGAG	TTTGACCGCT	TGGTGACTCA	TCCTCCCTGT	480
GATATTGCTG	TTTATGGACA	TATTCACCAG	CAGTTGCTTC	GTTACGGGAC	TGGTGGGCAA	540
TTGATTGTCA	ATCCGGGTTC	GATTGGCCAA	CCTTTCTTTT	TGGACGCTCA	GCTACGGAAG	600
GACTTGCGGG	CCCAGTATAT	GATTTTGGAG	TTTGATGACA	AAGGCCTGGT	AGATATGGAC	660
TTCCGACGGG	TAGACTACGA	TGTGGCAGCG	GAATTGCAGC	TGGCTAAAGA	CCTGAGACTT	720
CCCTATTTTG	AGGTTTACTA	TGAAAGTCTG	GTCAATGGGA	TCCACCATAC	TCATCATCAG	780
GAATTTTTGA	GAGAATTGGC	TCAGAAAGAG	GGCTGCGACC	GGGAGTTAGA	CGACTGGTTG	840
AAAAGTGGTA	ACGATTGA					858

(2) INFORMATION FOR SEQ ID NO:2283:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 462 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2283:

AAGGGGGAGA	TTATGGGTAA	ACCGATGTTA	GTCTTTAAGC	GTTTTGGTCA	TCAAATTCAC	60
CTGATGGTGC	AAAAGGAAGC	CAAACGTTGC	GGCATTGAAT	TTATGGGTGG	GCCGCAAGGT	120
CAGGTTGTGC	ATTTTTTGA	TAATCGCGAG	AAAAACCAAG	ACTTGGTCTT	GATTAAAGAT	180
ATCGATCAGG	AACTCAATAT	TACCAAGTCT	GTTGCTAGTA	ATCTGGTTAA	GCGTATAGTG	240
CAAAATTGTT	TGGTGGAATT	GGAGGCGAGT	CCTGTTGATA	AGCGGGCTAA	GTTTGTTCGT	300
CTGACGGACA	AAGCACGTTT	TCAGATGCAA	CAGGTTAAGG	CTTTTTTTGA	ACGCATAGAC	360
AAGCAGTTGA	TGGAAGATAT	TGATGAAGAT	GAATTACTGA	TTTTTGAGAA	GGTCTCGGT	420
CAACTACAGG	CAAAATATCA	AGGGAATAGG	AGGAGAGAAT	AA		462

(2) INFORMATION FOR SEQ ID NO:2284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2284:

GACTTATGGA	TAATCCTAAA	CTCAGAGGAA	ACCTGTCATT	ATTGGAAGCG	ACCTCGGCAA	60
ACAGGTGGAC	GGGGAGTCGT	TTCTACCTGT	AGTTATGAGG	CAAGAGCTTT	TGGTGTCCAT	120
TCTGCCATGA	GTTCCAAGGA	AGCTTATGAA	CGTTGTCCCC	AGGCTGTCTT	TATCTCAGGG	180
AATTATGAGA	AATACAAGTC	TGTGGGACTC	CGGATTCGAG	CTATTTTTAA	GCGCTATACA	240
GATTTGATTG	AACCCATGAG	CATTGACGAA	GCCTATTTGG	ATGTGACAGA	AAATAAACTC	300
GGTATCAAGT	CAGCGGTCAA	AATTGCTCGC	CTCATTCAAA	AAGATATCTG	GAAAGAACTC	360
CATCTAACTG	CTTCCGCAGG	CGTTTCTTAC	AACAAATTCT	TAGCTAAAAT	GGCGAGTGAT	420
TATCAAAAAC	CACATGGTTT	GACAGTGATT	CTACCTGAAC	AGGCTGAGGA	TTTTCTCAAA	480
CAAATGGATA	TTTCCAAATT	TCATGGAGTA	GGAAAAAGA	CAGTAGAACG	TCTTCATCAA	540
ATGGGCGTTT	TTACTGGTGC	TGATTTACTT	GAAGTTCCGT	AGGTAACCC	AATAGACCGT	600
TTTGGTAGAC	TAGGCTATGA	TCTGTATCGA	AAGGCTCGTG	GCATTCACAA	CTCTCCAGTC	660
AAATCCAATC	GCATCCGTAA	ATCAATCGGC	AAGGAGAAAA	CCTACGGGAA	GATTCTCCGT	720
GCCGAGGAAG	ATATCAAAAA	AGAGCTGACT	CTTCTATCAG	AAAAAGTCGC	TCTCAATCTA	780
CATCAACAAG	AAAAAGCTGG	AAAAATTGTC	ATTTTGAAAA	TCCGCTACGA	AGACTTTTCA	840
ACTCTTACCA	AACGAAAAAG	TCTTGCTCAA	AAAACACAAG	ATGCTAGTCA	GATAAGCCAA	900
ATAGCCCTGC	AACTCTATGA	AGAATTAAGC	GAGAAAGAAA	GAGGTGTCCG	CCTATTGGGG	960
ATTACCCTGA	CTGGATTTTA	A				981

(2) INFORMATION FOR SEQ ID NO:2285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...222
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2285:

CGCAAATGGA TCTGGCCTCC ACAAGCTGGG CAGGTGTATG CTTGCTTCTC AAGTTTATCC	60
TCTAACACAT TTACCAATTC TCCCTAGTA TCTCTCGCAA CAAACATGAA TTCCCTCCTT	120
TTCTATATCA TTCGTAAAAA AGAAAAAAGA TCAGGAAAAT TCCTAATCTT CATGTGTGTT	180
TACTTGATTT TCTTAGCTAG TAAGGTCGCA AAGCGTAGTT GA	222

(2) INFORMATION FOR SEQ ID NO:2286:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...357
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2286:

ACGCCGTGGA TACGGCTCCG CTCGTGTCGT CCGACACCCC TGCCCCCCTT CCGCCGCTGC	60
GCGCGCAGCA GATCGCCTTC GAACAGGCCC TGCCCGCGCA CCGACCGCCG GCGCCCAGGC	120
CACCGTTCGA CAAGGGCGAC GAAACGACAG AGGCCGAAGA GCCCGCCGCG AACAGCGACG	180
CGCCGACCTC GACGCTCTC GCCGACCAGC CCGCGGCGCC TGCCGCCGAC CGGCCGCCGA	240
CCAATNGGCA AGCCCCGTG CCAGTTGCCG CGGAAGCAAC GCCAACGCCA ACGCCAACGC	300
CAACGCCAAC GCCAACGCCA ACGCCAACGC CAACAGTGTG GCCGTCCGGA TCGGTAG	357

(2) INFORMATION FOR SEQ ID NO:2287:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2287:

AGAACGTGGA	TATCAACGGC	TGGTTGGTTG	TCTGCTGCTG	TTGAGAAGAC	TTGTGATTTA	60
GATGTTGGGA	TTGTAGTGTT	GCGATCGATA	AGTTTTGTAA	ATACTCCACC	CATTGTTTCG	120
ATACCAAGTG	ACAATGGCGT	TACATCAAGA	AGGACAACAT	CCTTGACATC	ACCAGTAATC	180
ACACCACCTT	GGATAGCCGC	ACCCATAGCA	ACTACTTCAT	CAGGGTTTAC	TGATTTGTTT	240
GGTTCCTTAC	CAGTTTCAGC	TTTAACAGCT	TCAACAACGG	CAGGGATACG	AGTTGAACCA	300
CCAACAAGGA	TAACCTCGTC	GATTTCTGAC	AAGCTCAAAC	CTGCATCTGA	AAGGGCTTGA	360

(2) INFORMATION FOR SEQ ID NO:2288:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 282 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2288:

CTCGAGTGGA	TATCCACATC	AGCGCTTTTT	ACCTTGGCAT	CAAAGGTCAC	AATCCCCCTTA	60
TTGCCACCAG	AAATTTCCAG	TTGTTCCAAG	GCATTTTTTG	TCCCTTGTTT	CCAGACCAAC	120
AAATCCGCCC	CATGGAGTTT	GTCTGCATGC	TTTTCCAAAT	ACTTATCTAG	GTCTGTTGAA	180
GCCGATTCCT	CCGCTCCCTC	CATGATAAAG	CTGATATTGA	CAGGTAAATC	ATCATGGTGC	240
TGCATATATT	TTCTCAAAGC	ACTCAAGCGA	GCTGTGATAT	GA		282

(2) INFORMATION FOR SEQ ID NO:2289:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 879 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...879
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2289:

AGATGGTGGA	TACGGATATT	GAGGATATTA	TCCGTCGCTT	CTACCGAAAG	GAGCTCTAGG	60
ATGATCAAAT	TGTGGAGACG	TTATAAACCC	TTTATCAATG	CAGGGGTTCA	GGAGTTGATT	120
ACTTACCGAG	TCAACTTTAT	TCTCTATCGG	ATTGGCGATG	TCATGGGGGC	TTTTGTGGCC	180
TTTTATCTCT	GGAAGGCTGT	CTTTGATTCT	TCGCAAGAGT	CTTTGATTCA	GGGCTTCAGT	240
ATGGCGGATA	TCACCTCTA	CATCATCATG	AGTTTTGTGA	CCAATCTTCT	GACTAGATCC	300
GATTTCGTCT	TTATGATTGG	GGAGGAGGTC	AAGGATGGCT	CCATTATCAT	GCGTTTGTTG	360
CGACCAGTGC	ATTTTGCGGC	CTCCTATCTT	TTCACCGAGC	TTGGTTCCAA	GTGGTTGATT	420
TTTATCAGCG	TTGGCCTTCC	ATTTTAAAGT	GTCATTGTCT	TGATGAAAAT	CATATCGGGT	480
CAAGGTATTG	TAGAGGTGCT	AGGATTAACT	GTCCTTTATC	TTTTTAGCTT	AACGCTCGCC	540
TATCTGATTA	ACTTTTTCTT	TAATATTTGC	TTTGGATTTT	CAGCCTTTGT	GTTTAAAAAT	600
CTTTGGGGTT	CCAACCTACT	TAAGACTTCC	ATAGTGGCTT	TTATGTCGGG	GAGTTTGATT	660
CCCTTGGCAT	TCTTTCCAAA	GGTTGTTTCA	GATATCTTTT	CCTTTTTGCC	TTTTTCATCC	720
TTGATTTATA	CTCCAGTTAT	GATCATTGTT	GGAAAATACG	ATGCCAGTCA	GATTCTTCAG	780
GCACTCCTTT	TGCAGTTCTT	CTGGCTCTTA	GTGATGGTGG	GATTGTCTCA	GTTGATTTGG	840
AAACGGGTCC	AGTCCTTTAT	CACCATTCAA	GGAGGTTAG			879

(2) INFORMATION FOR SEQ ID NO:2290:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2290:

GCTTGTCGGA TTGCCCAACT GCGCTCCACT AATTCTTGCA ACTCCATAAT TAGTATCCTA	60
ATAAAAAAAT GCGACATCCT CGAAAGGACG TCGCAACGTG GTTCCACCTT CATTTATGTA	120
CCTCAAAAGA GAGGGACACC TCTGATCGGC TCTAACGTGG CCACCGTTTT ATGTTTTTCAT	180
AAAAAACTCA AGAGTAGTAT C	201

(2) INFORMATION FOR SEQ ID NO:2291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2291:

AAAAC TAGGA TTTTATACTC AATGAAAATC AAAGAGCAAA C TAGGAAGCT AGCCGCAGGT	60
TGCTCAAAAC ACTGTTTTGA GGTGTGGAT AGAACTGACG AAGTCAGCTC AAAACATGGT	120
TTTGAGGTTG TAGATGAAAC TGACGAAGTC AGTAACCATA CCTATGGCAA GGTGAAGCTG	180
ACGTGGTTTTG AAGATATTTT AGAAGAGTAT TAA	213

(2) INFORMATION FOR SEQ ID NO:2292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1041 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2292:

TGTTGGAGGA	TATATAAAAT	GAAGCTTTTT	AAAAAATGA	TGCAAGTCGT	ACTAGCCACA	60
TTTTTCTTCG	GTTTGCTAGG	GACTAGTACA	GTATGTGCAG	ATGATTCTGA	AGGATGGCAG	120
TTTGTCCAAA	AAAATGGTAG	AACCTACTAC	AAAAAGGGGG	ATCTAAAAGA	AACCTACTGG	180
AGAGTGATAG	ATGGGAAATA	CTATTATTTT	GATCCTTTAT	CCGGAGAGAT	GGTTGTCGGC	240
TGGCAATATA	TACCTGCTCC	ACACAAGGGG	GTTACGATTG	GTCCTTCTCC	AAGACAAGAG	300
ATTGCTTTTA	GACCAGATTG	GTTTTACTTT	GGTCAAGATG	GGGTACTACA	AGAATTTGTT	360
GGCAAGCAAG	TGTTAGAAGC	AAAAACTGCT	ACAAATACCA	ACAAACATCA	TGGGGAAGAA	420
TATGATAGCC	CAGCAGAGAA	ACGAGTCTAT	TATTTTGAAG	ATCAGCGTAG	TTATCATACT	480
TTAAAACTG	GTTGGGTTTA	TGATGATGGG	GACTGGTATT	ATTTGCAGAA	GGATGGTGGC	540
TTTGATTCTC	GCATCAACAG	ATTGACGGTT	GGAGAGCTAG	CACGTGGTTG	GGTTAAGGAT	600
TACCCCTCTTA	CCTATGATGA	AGAGAAGCTC	AAACCTGCTC	CATGGTACTA	CCTAGATCCA	660
GCAACTGGCA	TCATGCAAAC	AGGTTGGCAA	CATCTTGGTA	ATAAATGGTA	CTATCTCCGT	720
TCATCAGGAG	CTATGGCAAC	TGGCTGGTAT	CAAGATGGTT	CAACTTGGTA	CTATTTAGAT	780
GCTGAAAATG	GCGATATGAA	AAC TGGTTGG	CAAAACCTTG	GGAACAAATG	GTACTATCTC	840
CGTTCATCAG	GAGCTATGGC	AAC TGGTTGG	TATCAGGAAG	GTTCGACTTG	GTACTATCTA	900
AATGCAAGTA	ATGGAGATAT	GAAAACAGGC	TGGTTCCAAG	TCAATGGTAA	CTGGTACTAT	960
GCCTATGATT	CAGGTGCTTT	AGCTGTTAAT	ACCACAGTAG	GTGGTTACTA	CTTAAACTAT	1020
AATGGTGAAT	GGGTAAAGTA	A				1041

(2) INFORMATION FOR SEQ ID NO:2293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2293:

AAAGAAGGGA	TGACAAGTAT	GAGAAAAAAA	ACAATTGGAG	AGGTTTTTACG	ATTAGATAGA	60
ATCAATCAGG	GATTGAGTTT	AGATGAATTG	CAGAAAAAGA	CAGAAATCCA	GTTAGATATG	120
TTGGAAGCAA	TGGAAGCAGA	CGATTTCGAT	CAACTTCCAA	GTCTTTTTTA	CACGCGTTCT	180
TTCTTGAAAA	AATATGCATG	GGCTGTTGAG	TTAGATGACC	AAATTGTTTT	GGATGCTTAT	240
GATTCTGGGA	GTATGATTAC	TTATGAGGAA	GTAGATGTTG	ATGAAGATGA	GTTGACAGGT	300
CGTAGACGTT	CAAATAAGAA	AAAGAAGAAA	AAAACATCAT	TTTTACCTTT	ATTTTATTTT	360
ATCCTTTTTG	CTTTATCGAT	TTTAATTTTT	GTGACTTATT	ATGTTTGGAA	CTATATTCAA	420
ACTCAACCAG	AGGAGCCTTC	TCTTTCTAAT	TACAGTGTGG	TTCAATCAAC	AAGTTCAACT	480
AGCTCTGTTC	CCCCTCCTC	AAGTAGTAGT	TCTTCTAGTA	TAGAATCAGC	TATAAGTGTA	540
TCAGGCGAAG	GAAATCATGT	AGAAATCGCT	TATAAGACAA	GTAAGGAAAC	AGTTAAATTG	600
CAATTGGCAG	TTTCAGATGT	TAGCAAGTTG	GGTCAGTGTT	TCAGAAAGCG	AACTTGA	657

(2) INFORMATION FOR SEQ ID NO:2294:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 741 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...741
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2294:

AGTAGAGGGA	TAATGGAAC	ATTTAAACA	TGGAAGAAAA	ATATGGTTCT	CTATGGTCTT	60
AAATCTCAAA	TTGGAACGT	CTACCGAAAC	AATGATAGGA	CAACAAGCTT	TTATGATGTT	120
GGGAATTTTC	TATACCTAGC	AGGGGAGTTG	GATTCCAGAT	TTTGGGAAGA	TTTTGTTAGA	180
AAATATGGTT	TAGATTATAA	GATTATTATT	TCAGAAAATA	CTAATTGGCA	AGATTTTCTG	240
CATCGAAAAG	TGGGGCTAAA	TTCTTTTACT	CGCTATTCTT	TTAAAGATAA	GGCAAATTTT	300
CAAGTTGAAT	TTTTAAATAA	TCTAGTTACT	CATTTAGAGG	AAGGTTACAA	TATTGTGCCT	360
ATTGATAATC	ATATTTATAA	CTGCTTTTCT	ACGGAAGAAT	GGTCACAGGA	TTTACAGGGG	420
GATTTTGAGT	CCTATCAGGA	TTTTGTTTTA	AAAGGTGGAT	TTGGCTTTGT	GATTCTTAAA	480
AATAATGAAC	TGATTGCTGG	GATTTCCCTCA	GGGTAGTTT	ACCGTAAAGC	AGTTGAAGTG	540
GAAGTTGCAA	CTAGACCAAA	CGAACAAGGA	AATGGATTTG	CTAAAAAGCT	TGGTGCTGCA	600
ATGATTCTAG	AGAGTTTAAA	TAGAGATATG	TTTCCACTTT	GGGATGCTCA	TAATGAGGCT	660
TCCAAAAAAG	TAGCAGAATT	TTTAGGATAT	GAGTTATCTG	AACCTTATGA	AGCTTTTGAA	720
CTAGAGGAAA	TTTTGATATA	A				741

(2) INFORMATION FOR SEQ ID NO:2295:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1452 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2295:

AACGTGGGGA	TTATAATAAA	GTTAATCAAG	GACGAAGAGA	GAAGAAAAAT	GGAAGCGGTT	60
TTAGCAATAG	ATTTAGGTGC	GACTTCTGGA	AGAGCAATCG	TTGGTTACCT	TTCTGAAAAT	120
AAACTAGTAA	TGGAAGAAAT	AAATCGCTTT	TCTAATCTAC	CTATTAGAGT	AAAAGGGCAT	180
TTATCTTGGG	ATATTGACTT	TCTACTAGCT	AAAATTCTTG	AAAGTATCCG	CTTGGCTAAT	240
ACTAGTTACA	AGATTTTATC	TATCGGTATT	GACACATGGG	GAGTTGATTT	TGGACTGATT	300
GATAATGAAG	GTAAGCTGTT	ATTACAACCT	GTTTCATTATC	GTGATGAAAG	AACAAAGGGA	360
GTGTTAAAGG	AAATATCTGA	AATGACTGAA	TTAGAAAAAC	TGTATTCAGA	GACAGGAAAT	420
CAGATTATGG	AGATAAAATAC	CTTGTTTCAA	CTCTTTAAGG	CACGTCAAGA	ATCTCCTGAC	480
TCTTTCTATA	AGACCAATAA	GATTCTTTTA	ATGCCAGATT	TGTTTAATTA	TCTCTTGACA	540
GGTAAGTTTG	CTACAGAAAA	AAGCATTGCT	TCAACAACCTC	AATTATTTGA	TCCTAGGAGT	600
CAAAATTGGA	ATCAGAATAT	CTTAAAACTA	TTTGAATTGG	ATTCATCTTT	ACTTCCTGAA	660
ATTGTTTCAG	AGGGAAATGT	TCTTGGAAGG	ATAAAAGAGG	AGTATGGTTT	AGGCGATATT	720
CCTGTTGTGA	ATGTTTGTAG	TCATGATACA	GCAAGCGCGA	TTGTCTCAGT	ACC'TAAGACA	780
GAAGGTAGTT	TATTTATTTT	ATCAGGTACT	TGGTCTTTGG	TTGGAGTGGA	ACTTACTTCA	840
CCGATTCTTA	CTACCGAATC	CTTCAGTTAT	GGATTTACAA	ATGAAGTCGG	TAAAGATGGA	900
GTGATTACAT	TTCTGAAGAA	TTGTACAGGG	TTGTGGATCA	TAGAGGAACT	AAGACGTTCA	960
TTTGAACGAA	GAGGGAAAAGC	CTATTCTTTT	GATGATATTA	GGACAATGGT	GGAGAAAGAA	1020
AAAGAAAATC	TTCCCTCTGAT	TGATACTGAA	TCAACTGAAT	TTGCAACAGA	ATCTGATATG	1080
CACAAGACTT	TGACAGAATA	TCTAGCTTAT	CATCATGAAA	CTAGAGAGTG	GACAGATGGA	1140
CAACTATTTA	AGATTGTTTA	TGAAAGCCTA	GCTGAAACGT	ATAGGAAAGC	GATAGAGTTA	1200
CTAGAAGAAC	TAACTCATAA	GGTTTATAAG	AGGATATATG	TGATTGGAGG	AGGTGCTAGA	1260
GCCAGTTACT	TTAACCAAAT	GATTGCTGAT	AGAACTGGTA	AAGAGGTTCT	TACAGGTTCTG	1320
ACTGAGGGTA	CAGTGTGGG	GAATATTGTT	GTGCAGCTAT	TGAGTCAAGG	TAAAATAAAC	1380
GAGGATACAG	AGTTAAAGGA	TATTATGACA	AATATTGCTG	ATACACAATA	TTATTATCCT	1440
CAGCTATCAT	AA					1452

(2) INFORMATION FOR SEQ ID NO:2296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2296:

GAAAAGGGGA	TAAAGATTNT	GCGCGGAAGA	AAGCGACGAA	GGAATCTTGA	CTATGTACTT	60
GTCCAAGCGG	AAGCAACCGC	CATTGTAAAG	TGCGTGGGGA	GCGGGATTTC	GAAGGAGTTC	120
CCAAAAAAGC	GGGAAGTTAT	TCGACCGCAA	CCCGCCAAGG	GGAGTTACGC	AAGGGCCGAT	180
AAAACATCCT	GGGGGTAG					198

(2) INFORMATION FOR SEQ ID NO:2297:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 753 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2297:

ATGAAAGTTT	TAATTTTAGA	AGATGTTATT	GAACATCAAG	TGAGACTAGA	GAGAATATTG	60
GATGAAATTT	CGAAAGAATC	GAATATTCCA	ATATCATACA	AGACAACGGG	AAAAGTCCGT	120
GAATTTGAAG	AATACATTGA	AAATGATGAA	GTAAATCAAC	TTTATTTCCCT	AGATATCGAT	180
ATTCATGGAA	TTGAGAAAAA	GGGATTTGAA	GTGGCTCAGC	TCATTTCGTCA	TTACAATCCT	240
TACGCTATTA	TCGTCTTTAT	CACTAGTCGA	TCAGAGTTTG	CGACTCTAAC	CTATAAATAC	300
CAGGTATCAG	CCCTAGATTT	TGTTGATAAG	GATATCAATG	ATGAGATGTT	TAAGAAGAGA	360
ATTGAGCAAA	ATATCTTCTA	CACGAAGAGT	ATGTTACTTG	AAAATGAAGA	TGTTGTAGAT	420
TATTTTCGACT	ACAATTACAA	GGGAAATGAT	TTAAAAATTC	CTTACCATGA	TATTTTGTAT	480
ATTGAAACAA	CAGGGGTATC	TCATAAATTG	CGCATTATTG	GTAAGAATTT	TGCAAAAGAG	540
TTTTATGGTA	CCATGACAGA	TATTCAGGAA	AAGGACAAAC	ATACTCAGCG	ATTTTATTCT	600
CCTCACAAAGT	CATTTTGGT	AAATATAGGC	AATATCAGAG	AAATTGATCG	AAAAAACTTA	660
GAAATTGTTT	TCTATGAAGA	CCATCGTTGT	CCTATTTCAA	GATTAAAAAT	TAGAAAATTA	720
AAAGATATTT	TAGAGAAAAA	ATCTCAAAAG	TGA			753

(2) INFORMATION FOR SEQ ID NO:2298:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1095 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2298:

TATACTTACT	TATGGAGAAA	ATACATGAAA	CGTGAGATTT	TACTGGAACG	AATCGACAAA	60
CTAAAACAAC	TCATGCCCTG	GTATGTTCTG	GAATACTACC	AATCTAAGCT	GGCTGTGCCC	120
TACAGTTTTA	CAACCCTGTA	CGAATACCTT	AAGGAATATG	ACCGATTTTT	CAGCTGGGTT	180
TTGGAGTCTG	GTATTTCAAA	CGCTGATAAA	ATATCCGATA	TTCTTTTATC	AGTTTTGGAA	240
AATATGTCTA	AGAAAGACAT	GGAATCCTTT	ATCCTTTATC	TACGTGAACG	TCCCTTGCTG	300
AATGCTAATA	CAACAAAACA	AGGTGTTTCA	CAGACAACTA	TCAATCGAAC	CTTATCAGCA	360
CTTTCTAGTC	TTTACAAGTA	TCTAACCAGG	GAGGTTGAAA	ACGATCAGGG	GGAACCTTAT	420
TTCTATCGTA	ATGTAATGAA	AAAAGTTTCA	ACCAAGAAAA	AGAAAGAAAC	CCTTGCTGCC	480
AGAGCTGAAA	ATATCAAGCA	AAAACCTCTT	CTAGGTGATG	AAACAGAAGG	TTTTCTAACT	540
TATATCGATC	AAGAGCACCC	ACAACAGCTT	TCAAATCGAG	CTCTCTCATC	ATTCAACAAA	600
AATAAAGAAC	GAGATTTAGC	CATTATTGCC	CTTCTCTTGG	CATCTGGTGT	TCGCTTATCT	660
GAAGCTGTTA	ATCTAGATCT	AAGAGATCTC	AATCTAAAAA	TGATGGTTAT	TAATGTTACT	720
CGAAAAGGTG	GCAAACGTGA	CTCAGTCAAT	GTCGCTGCTT	TTGCTAAACC	TTATTTAGAG	780
AATTATCTGG	CCATTTCGAA	TCAACGCTAT	AAAACGGAAA	AAACAGATAC	AGCCCTTTTT	840
TTAACTCTCT	ACAGAGGTGT	TCCTAATCGT	ATCGATGCTT	CTAGCGTTGA	GAAAATGGTT	900
GCTAAATACT	CAGAGGATTT	TAAAGTACGT	GTAACACCCC	ATAAACTGCG	CCATACGCTA	960
GCAACTAGGC	TCTATGATGC	GACTAAATCA	CAAGTTTTAG	TCAGTCACCA	ACTAGGACAT	1020
GCCAGCACAC	AAGTCACTGA	CCTCTATACC	CATATTGTTA	ATGATGAACA	AAAGAATGCT	1080
CTAGATAGTT	TATGA					1095

(2) INFORMATION FOR SEQ ID NO:2299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2299:

AATGATTACT	TGTCATTTCA	GAGCATTTTT	GTTAATCGCA	TAAGTTTTCT	TTTGTATGCC	60
TTGAGTAGTC	CCCTATTCAA	GGTATATTTT	TTTGGAGGTA	GTGAGATGAG	CGATTCAAAA	120
TATATGAAAT	TAGCAATAAA	ACTGGCACAA	AAAGGGGCTG	GTTACGTCAA	TCCCAATCCT	180
ATGGTTGGCG	CAATTATTGT	AAAAGATAAT	CACATTATCG	GACAAGGTTA	TCATGAGTTT	240
TTTGGTGGCC	CACATGCTGA	GAGAAATGCT	CTTAAAAACT	GTAGAAAATC	CCCTGTGCGA	300
GCGACGCTTT	ATGTAACACT	TGAACCCTGT	TGTCACCTCG	GGAAAACACC	TCCCTGTATA	360
GATGCTATAA	TCGATAGTGG	TATTACAAGA	GTAGTCATTG	GAAGCCTAGA	CTGTAATCCT	420
ATTGTATCTG	GAAAAGGAGT	AAAGATACTT	GAGGAAAATA	ATCTTCAAGT	TACTGTTGGA	480
ATTTTtagaaa	ATGAGTGTCT	TAACTTAATA	AAAAGTTTTA	GAAAGTATAT	TACCCAGCAT	540
GTACCCtATG	TTTTTATGAA	ATATGCAATG	TCAATGGATG	GAAAAATAGC	CACTAAAACA	600
AATCAATCCA	AATGGATTAC	TGAAGAAGAA	GCAAGAAAGC	ATGTGCATCA	GTTACGACAC	660

CATGTTAGTG CAATTATGGT GGGAGTCAAT ACTGTTATTC AAGACGATCC TTTGCTGACA	720
TGTAGATTGG AGGAAGGGAA AAATCCTATC CGTATCATAT GCGATACACA TTTACGAACT	780
CCTCTTACCT CTAAAATCGT AAAAACAGCA AATGATATTA AAACCTTACAT TGCCACTTCC	840
TCTGAAGACA AAAATAAAAT GAAGCTATAT CAAAATCATG GCTGTGAAAT ACTTTCCATA	900
AAGAAAAAAG GCAATCATAT AGACTTATCG AGTTTAATGC AACATCTAGG AAACATGCAG	960
ATTGATAGCC TAGTTCTAGA AGGGGGCAGT CTAATGAATT GGAGTGCTTT GGAACAACAA	1020
ATTGTTGATG AGCTGAAAAT ATATATTGCA CCAAAAATTT TTGGAGGCAG TGCCAAGTTT	1080
CCTGTCGGAG GTGAAGGCAT TTCTTTGCCA AATGACGCTA TTAGATTGAA ACCTTATGCT	1140
TTTTCTCAAA TAGGAAATGA CTATCTCATA GAAAGTGAAG TGATTTATCC ATGTTACAG	1200
GAATAA	1206

(2) INFORMATION FOR SEQ ID NO:2300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2300:

TGGAGTTACT TAAAAAAGA TGTCAAGCAG CCGTTAGCTG TTAATCAGCT ACAATTGAGT	60
GCGGCTTTTA CTCCAGGATT TGAATCAGCT TTTCATGTTA ATATGGAAGA TAGTCAAGCA	120
GCTATGCGAG ATGGCAGCAT TTTTGAATAT TGCAAATTAC ACGATGTGGT CATTCAAGCA	180
TGGTCTGTCT TACAATTCGG GTATTTTAAA GGGAAATTTG TTGGAAATGA GAAATTTCAA	240
GCTTTAAATC AAGTACTTGA TCGTTTAGCT ATTAAATATG GAGTAACCTC TTCAACTATT	300
GCCATTTCTT GGATATTGCG TTATCCAGCA AAAATGCAGG CAGTTGTAGG TACCACAAAT	360
CCTAAGCACT TGAGAGAAGT TAGCCAAGCG CAACTTTAG CTTAA	405

(2) INFORMATION FOR SEQ ID NO:2301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2301:

ATTTTCTACT	TCTTCTGCCA	AGGATTGTCT	GATTCCTTCT	TCATGGATTT	GTTCCAAGAG	60
TTGATTTGCC	TTGCTCAAAA	GACTTTCTAC	TTCTTCCTTG	CTATCTGTCG	CAGATTATTG	120
GTTGCTATCT	ACCATGTACT	CCTAAAACAG	GAGAGTTATA	ATCCAAGATT	ACAAGGCCTT	180
ACAGAAATAA	GAAATCCAGA	TAAGACAATG	TTCGTCCAAG	ACGCTATTCT	CTTCGCACAA	240
CAGCACGGAT	TCAATATGCT	TTAA				264

(2) INFORMATION FOR SEQ ID NO:2302:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 822 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2302:

GTTCAATACT	TCATTGATAA	AGGTGTTCAA	GGTCTTTATG	TCAATGGTTC	TTCTGGTGAA	60
TGTATCTACC	AAAGCGTTGA	AGATCGCAAG	TTGATTTTGG	AAGAAGTCAT	GGCGGTAGCC	120
AAAGGTAAAT	TGACCATAT	TGCCCATGTT	GCTTGCAATA	ATACTAAAGA	TAGTATGGAA	180
CTTGCTCGCC	ATGCTGAAAG	CTTGGGAGTA	GATGCTATTG	CAACGATTCC	ACCAATTTAC	240
TTCCGCTTGC	CAGAATACTC	AGTTGCCAAA	TACTGGAACG	ATATCAGTTC	TGCAGCTCCA	300
AACACAGACT	ACGTGATTTA	CAACATTCCCT	CAATTGGCAG	GGGTTGCTTT	GACTCCAAGC	360
CTTTACACAG	AAATGTTGAA	AAATCCTCGT	GTTATCGGTG	TTAAGAAGTC	TTCTATGCCA	420
GTTCAAGATA	TCCAAACCTT	TGTCAGCCTT	GGTGGGGAAG	ACCATATCGT	CTTTAATGGT	480
CCTGATGAGC	AGTTTCTAGG	AGGACGCCTC	ATGGGTGCTA	GGGCTGGTAT	CGGTGGTACT	540
TATGGTGCTA	TGCCAGAACT	CTTCTTGAAA	CTCAATCAGT	TGATTGCGGA	TAAGGACCTA	600
GAAACAGCGC	GTGAATTGCA	GTATGCTATC	AACGCAATCA	TTGGTAAACT	CACCTCTGTT	660
CATGGAAATA	TGTACGGTGT	CATCAAAGAA	GTTTTTGAAA	TCAATGAAGG	CTTGACTATT	720
GGATCTGTTC	GTTCAACATT	GACACCAGTG	ACTGAAGAAG	ATCGTCCAGT	TGTAGAAGAA	780
GCTGCTGCCT	TGATTCTGTA	AACCAAGGAG	CGCTTCCTCT	AA		822

(2) INFORMATION FOR SEQ ID NO:2303:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1443 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1443
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2303:

ATTTCGATACT	TCAGTAGACG	AATACGGTTC	TTATGGAAGT	TATGGGAAAA	AGAAAAAATA	60
GGTTGGGGGA	TAGAGATGAA	TGGAAACTA	GTAAAGCCTT	CATTGGCCAT	AGTCCAGAGT	120
TTTCTTGTTA	TTTTATTGGC	TTATCTACTT	AGCACTGTGA	GAGAAACAGA	GATTGTTTCA	180
ACAACAGCTA	TTGTACTTTA	TATCCTCCAC	TATTTTGCCT	TTTATATCAG	TGATTATGGA	240
CAGGATTTCT	TTAAAAGGGG	ATATTTGATT	GAACTTGTCC	AGACATTGAA	ATATATCCTA	300
TTCTTTGCGC	TAGCGATTAG	TATTTCTAAT	TTTTTCTTAG	AAGATCGATT	TAGTATTTCC	360
AGAAGAGGCA	TGATTTACTT	CCTCCTATTA	CATGTTCTCT	TAGTCTATGT	GCTAAACCGA	420
TTTATCAAGT	GGTATTGGAA	GCGGGCTTAT	CCCAACTTTA	AAGGAAGTAA	GAAGATTCTC	480
CTACTTACAG	CAACTTCTCG	TGTCGAAAAG	GTATTGGATA	GACTAATAGA	ATCAGATGAT	540
GTTGTTGGGG	AGTTGGTAGC	CGTCAGTGTT	TTAGATAAAC	CAGATTTTCA	GCATGATTAT	600
TTAAAGGTTG	TAGCAGAGGG	GGAGATCGTA	AACTTTGCGA	CTCATGAGGT	GGTCGATGAA	660
GTCTTTATCA	ATCTTCCAAG	TGAAAAATAC	AATATTGGAG	AGCTTGTTCTC	TCAGTTTGAA	720
ACGATGGGAG	TTGATGTAAC	AGTCAATCTA	AATGCTTTTCG	ATTGTATCTT	GGCACATAAC	780
AAGCAAATTT	GTGAGATGGC	AGGACTAAAC	GTTGTGACTT	TTTCTACAAC	ATTTTATAAG	840
ACTAGCCATG	TGATTGCTAA	GCGGGTTATT	GATATTATCG	GTTCCCTGGT	AGGTTTGATA	900
CTATGTGGTC	TAGTCAGTAT	TGTACTGGTT	CCTTTGATTG	GAAAGGATGG	GGGCTCTGCT	960
ATTTTGTGCTC	AGACGCGTAT	TGGGAAAAAT	GGTCGCCATT	TCACTTTTTTA	CAAGTTTCGC	1020
TCTATGTGTG	TGGATGCTGA	GGAGAAAAAA	AGAGAACTCA	TGGAACAAAA	TACCATGCAG	1080
GGTGGAATGT	TTAAGGTGGA	TGAGGATCCA	CGTATCACGA	AAATTGGTCA	TTTTATACGG	1140
AAGACGAGCT	TGGACGAGCT	ACCACAGTTT	TACAATGTTC	TAAAGGGAGA	TATGAGTTTG	1200
GTAGGGACAC	GACCACCAAC	AGTGGACGAG	TATGAGCACT	ATACCCAGAG	ACAAAAACGT	1260
CGCCTAAGTT	TTAAACCTGG	CATAACAGGT	CTATGGCAGG	TCAGCGGACG	AAGCGAGATC	1320
AAGAATTTTCG	ATGAGGTTGT	CAAATTAGAT	GTGGCCTATA	TAGACGGTTG	GACAATTTGG	1380
AAAGATATTG	AAATTTTATT	GAAGACAGTT	AAAGTTGTAT	TGATGAAGGA	TGGAGCGAAG	1440
TAG						1443

(2) INFORMATION FOR SEQ ID NO:2304:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2304:

AGAATGTACT	TCGTCATCGC	AGAGTTCAAT	GCTAATTGGT	TTACACATCG	GAAGTCCAAG	60
AGAAGCTACT	TTCTCCATCA	TATCAAATTC	AAATTTTTTT	ATAATCTAAC	TTCGACTTAT	120
CAGAAACACG	CAAGAAATAT	TTTTACTGAT	TTTGATCTGT	CACACAATAT	TTTTTATCAT	180
CTGACCAGCC	TTTATTTATG	GCTATCTTAC	TACTAA			216

(2) INFORMATION FOR SEQ ID NO:2305:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2305:

GAAACACACT	TTATATCTTT	GTTTTTTGTG	ACTACTGTCG	ATGGCAACTT	GCGAGGTTAC	60
CCAACGACAA	AAGTTAAAAT	TTGTAAAGCG	AGCAAAGATT	TCTTGGAGAA	TCCCTCCCTT	120
CTTTTGGCG	TGAAAATTGA	CCAAGCCAAT	ACTGTATTTC	AGGTCACGAA	AACTAGTCTC	180
TATGCCCCAT	CTACTGGCGT	AGAGATTTTT	TAA			213

(2) INFORMATION FOR SEQ ID NO:2306:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2306:

GAAACACACT TTATATCTTT GTTTTTTGTG ACTACTGTCG ATGGCAACTT GCGAGGTTAC	60
CCAACGACAA AAGTTAAAAAT TTGTAAAGCG AGCAAAGATT TCTTGGAGAA TCCCTCCCTT	120
CTTTTTGGCG TGAAAATTGA CCAAGCCAAT ACTGTATTTC AGGTCACGAA AACTAGTCTC	180
TATGCCCCAT CTA CTACTGGCGT AGAGATTTTTT TAA	213

(2) INFORMATION FOR SEQ ID NO:2307:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2307:

GAAACACACT TTATATCTTT GTTTTTTGTG ACTACTGTCG ATGGCAACTT GCGAGGTTAC	60
CCAACGACAA AAGTTAAAAAT TTGTAAAGCG AGCAAAGATT TCTTGGAGAA TCCCTCCCTT	120
CTTTTTGGCG TGAAAATTGA CCAAGCCAAT ACTGTATTTC AGGTCACGAA AACTAGTCTC	180
TATGCCCCAT CTA CTACTGGCGT AGAGATTTTTT TAA	213

(2) INFORMATION FOR SEQ ID NO:2308:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 909 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2308:

CAGACGCACT	TAAAGGGCAA	GGACTCTAAG	ATGCAGGGAC	AAATCATTAA	AGCCTTGGCT	60
GGGTTCTACT	ATGTAGAGAG	TGATGGCCAA	GTCTATCAAA	CACGCGCGCG	TGGGAATTTTC	120
CGTAAAAAAG	GGCATACCCC	TTACGTTGGG	GA CTGGGTAG	ATTTCTCTGC	CGAGGAAAAT	180
TCAGAAGGCT	ATATTCTCAA	GATTCACGAA	CGGAAAAACA	GTCTGGTCCG	TCCGCCTATT	240
GTCAATATCG	ACCAAGCTGT	AGTAATCATG	TCCGTCAAGG	AACCTGATTT	TAACAGCAAT	300
TTGCTGGATC	GTTTCTTGGT	TCTTTTGGAG	CACAAGGGCA	TCCATCCCAT	TGCTATATTT	360
TCCAAAATGG	ATTTGTTGGA	AGATAGGGGA	GA ACTGGATT	TTTACCAGCA	GACCTATGGT	420
GACATCGGCT	ATGACTTTGT	GACCAGTAAA	GAGGAACTCC	TGTCTTTGTT	AACAGGCAAG	480
GTTACGGTCT	TTATGGGGCA	GACAGGTGTT	GGGAAGTCAA	CTCTTCTCAA	TAAAATCGCA	540
CCAGACCTCA	ATCTTGAAAC	GGGAGAAATT	TCAGACAGTC	TAGGTCGCGG	TCGCCATACC	600
ACTCGAGCTG	TTAGTTTTTA	CAATCTCAAC	GGGGGTAAAA	TCGCAGATAC	ACCAGGATTT	660
TCATCCTTGG	ACTATGAAGT	ATCAAGGGCT	GAAGACCTCA	ATCAGGCTTT	CCCAGAGATT	720
GCTACTGTTA	GCCGAGATTG	TAAGTTCCGT	ACTTGTACCC	ATACCCATGA	GCCGCTTGT	780
GCCGTCAAAC	CAGCTGTTGA	AGAGGGTGTT	ATTGCAACCT	TCCGTTTTGA	CAATTACCTG	840
CAATTCCTTA	GTGAAATTGA	AAATCGTAGA	GAAACCTATA	AAAAAGTCAG	CAAAAAAATT	900
CCAAAATAA						909

(2) INFORMATION FOR SEQ ID NO:2309:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2309:

AAGTATAACT	TATACTCTTT	GAAAATCTCT	TCAAACCACG	TCAGCTTCGC	CTTGCTGTAT	60
ATATGGTTAC	TGACTTCGTC	AGTTCTATCC	ACAACCTCAA	AACAGTGTTT	TGAGCTGACT	120
TCGTCA GTTC	TATCCACAAC	CTCAAAACAG	TGTTTTGAGC	TGACTGCGGC	TAGCTTTCTA	180
GTTTGCTCTT	TGATTTTAT	TGAGTATTAG				210

(2) INFORMATION FOR SEQ ID NO:2310:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 828 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...828
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2310:

CCAAGTAACT	TTTTGGAGGA	AATGATGAAA	CTTTTATTTA	TTTTGATTTT	AATGGTATTA	60
GTATCGCTTT	ATATGGTGAT	AACTTCCGTT	GACCATCGAG	AAGAGATTTT	ATTTGGTAAC	120
TATCCTTCTG	TTGATGTGAC	AGGAATGATG	ATAAATCAAC	CAGTAGCTAG	TCGCGAAGAG	180
GTGACAGAGG	CTTTGAGTCA	CTTGGCGGTA	GAGCACAATA	GTCTCATTGC	TCGTCGAATC	240
GTTGAGCCAA	ATGAAGCTGG	AGAAACACGC	TTTACCTATG	CCACTTATGG	TGAGGGAAAAG	300
CTTCCAGAAG	GTCTGACCAT	TTCCTCCAAG	GAGAGTGCAG	AAACGAGTGA	TTTATTAGGG	360
TCTTACTTGA	TTGTATCAGG	AAGTTTGGAT	GGAGTGAGCT	TACAGACCAC	CTTGAAAGAG	420
CTTGGTATATC	AAGGCTTTGT	TTCGAATGGA	GAAGATCCAT	TTTCGATAGT	CTTACTATTG	480
ACGGCCACCC	CTATGGTGCT	ACTGAGTTTA	GCTATTTTTC	TGCTGACCTT	TATGAGTCTG	540
ACCCTGATTT	ATCGGATCAA	ATCCCTTCGT	CAGGCAGGGA	TTCGCTTAAT	ANCTGGTGAG	600
AGCTTGTTTTG	GAGTTGCTCT	CAGACCAGTG	TTAGAAGATG	TGAGACAGCT	TATCTGCTCA	660
GTGCTGGTAT	CCAGTCTTTT	GGGATTGGGG	ATTCTCTGGT	ATCAAGGTGC	CTTGTTTATG	720
GCAACGGTGC	AACTGGTCAT	CATTGCTCTT	CTACTTTATG	GATTGCACCT	TGGCAGGGAT	780
TTCTACCTTA	CTAAGTGTCG	TCTATCTACT	TGGTTTACAG	GAAAATAG		828

(2) INFORMATION FOR SEQ ID NO:2311:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 633 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2311:

TTTTCCAAC	TTTGTGGTGA	TNANGGCCCC	ATCGTGAGTG	ATGACGTCTA	TTTCGCGAGT	60
ACTCTCAGGC	GTGGAGTACC	TGCAGCAGAA	GCAGGTATGG	ACCGTGTTC	GGCAGATTAC	120
ACTGGAATGC	TTGGGACTGT	TATGAATGCT	CTTGTGATGG	CAGATTCATT	GCAACAAGTT	180
GGGGTTGATA	CGCGTGTACA	AACAGCTATT	GCTATGCAAC	AAGTGGCAGA	GCCTTATGTC	240
CGTGGACGTG	CCCTTCGTCA	CCTTGAAAA	GGCCGTATCG	TTATCTTTGG	TGCTGGAATT	300
GGTTCACCAT	ACTTCTCGAC	AGATACAACA	GCGGCCCTTC	GTGCAGCTGA	AATCGAAGCA	360
GATGCCATCC	TCATGGCTAA	AAATGGCGTC	GATGGTGTGT	ACAATGCCGA	TCCTAAGAAG	420
GACAAGACAG	CCGTAAAGTT	TGAAGAATTG	ACCCACCGTG	ATGTTATCAA	CAAAGGTCTT	480
CGTATCATGG	ACTCAACAGC	CTCAACCCTC	TCAATGGACA	ACGACATTGA	CTTGGTTGTC	540
TTCAACATGA	ACCAATCAGG	CAACATCAAA	CGTGTGTAT	TTGGTGAAAA	TATCGGAACA	600
ACAGTTTCAA	ATAATATCGA	AGAAAAGGAA	TAA			633

(2) INFORMATION FOR SEQ ID NO:2312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2312:

ATGAAAAACT	TTACAAATAT	TAAGTTCAAA	GAGAATGGGG	AATTTAATCA	TTTCCCTGGG	60
AATACAGTTG	TAGCAAATCT	TTATACTAAA	CAAGATTTGA	TGGAAGTTGT	TGATATTATT	120
CAATCACGTT	ATAGAGAATT	ACCATTTATC	GATAAGTTTA	CTTTAACTCC	AAGGAATTCT	180
ATTCACATGA	CTGTAATTGA	ATTGTTGTGC	CATGAAAATC	GTGAAACGGA	GTTTTGGAGC	240
AGTAATCTTC	CTCTAGATAC	ACCTTTACAG	GAAATACATG	ATTACTTTGC	TAAACAACTT	300
GAAATTTTTC	CATTGTTGGA	TGAAGAAATT	CATATGCGTA	TAACTGAAAT	GGGAAAACAA	360
AACATACTAG	TTGAACCTGC	AGATGAAGCT	TCTGCAAAGA	GATTAGAAGA	AATTCGTACT	420
TATGTCTCAG	AAAAAGCAGG	TGTTTGTTTC	CCTAATCATG	ATAGATATCA	ATTCCATATT	480
TCAATTGGGT	ATCTTCGGAT	TCCTCTAACC	GAAGAGGAGG	AAGAAGAGTT	TACTAAAGTC	540
AGAGCAGAAAT	TAACTGAAAT	TTTATTAGAG	AAGATTCCAA	CTATTACTGT	AAACCGTATT	600
GACTATACTG	TATTTGAAGA	TATGAGACAA	TTTGTTCAT	ATCACGAAAA	ATTTAAATAA	660

(2) INFORMATION FOR SEQ ID NO:2313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1011 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2313:

ATCCACTTTG	TTACTAACCT	CATGCGTAAC	TTTCCAGTTG	TTTCAGACGG	ACCCTTTACT	60
CCTGAAGACT	ATGTTGGCCG	TATCAACTAT	GAATTGGCTA	ATGACTTTGG	GAACCTCCTT	120
AACCGTACGT	TTTCCATGAT	TAATAAGTAC	TTTGATGGAC	AAATCCCTGC	CTATGTAGAA	180
GGTGTGACTG	AATTTGATCA	TGTTCTTGCT	GAGGTTGCAG	AACAATCAAT	CGCAGACTTC	240
CATACACACA	TGGAAGCAGT	TGACTATCCA	CGTGCGCTTG	AAGCAGTCTG	GACTCTGATC	300
TCTCGTACCA	ATAAATACAT	CGATGAGACC	GCACCATGGG	TCTTGGCCAA	GGATGAAGCT	360
CTTCGTGACC	AATTGGCAAG	TGTCATGAGC	CAC TTGGCAG	CCAGCATTCG	TGTAGTTGCT	420
CACTTGATTG	AACCATTTAT	GATGGAAACT	AGTCGTGCAG	TTTTGACTCA	ACTTGGTTTG	480
GAAGAAGTTT	CTAGTCTTGA	AAACTTGAGT	TTGGCTGACT	TCCCAGCAGA	TGTGACTGTA	540
GTTGCCAAAG	GAACACCTAT	CTTTCCACGT	CTAAATATGG	AAGAAGAAAT	CGCCTATATC	600
AAGGAACAAA	TGGAAGGCAA	TAAACCAGCA	GTCGAAAAAG	AATGGAATCC	GGACGAAGTT	660
GAGCTCAAAC	TAAACAAGGA	TGAAATCAAG	TTTGAAGACT	TTGACAAGGT	TGAAATCCGT	720
GTGGCAGAAAG	TCAAAGAAGT	GTCTAAAGTA	GAAGGTTGAG	ATAAGTTGCT	TCAATTCTGC	780
TTGGATGCTG	GTGATGGAGA	AGATCGTCAG	ATTCTTTTCAG	GAATTGCCAA	ATACTATCCA	840
AATGAACAAG	AATTGGTCGG	CAAGAAAGTT	CAAATCGTTG	CTAACCTCAA	ACCACGTAAA	900
ATGATGAAAA	AATATGTCAG	CCAGGGTATG	ATTCTCTCAG	CTGAACATGA	TGGCAAATTA	960
ACCCTTCTCA	CAGTTGATCC	AGCTGTACCA	AATGGAAGTG	TGATTGGGTA	A	1011

(2) INFORMATION FOR SEQ ID NO:2314:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 915 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...915

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2314:

CCCAATCTTG	TAAAAGAAGG	GAGAAGGAGA	ATGGTTAAAG	AACGTAATTT	AACTCGCTGG	60
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ATATTTGTTT	TGCCAGCTAT	GATTATCGTA	GGATTACTCT	TTGTTTATCC	GTTTTTCTCG	120
AGTATTTTTT	ATAGCTTTAC	CAATAAGCAT	TTGATTATGC	CTAATTATAA	ATTTGTTGGT	180
TTGGCTAACT	ATAAAGCTGT	GCTATCAGAT	CCCAACTTCT	TTAATGCGTT	CTTTAATTCA	240
ATTAAGTGGA	CCGTTTTCTC	ATTAGTTGGT	CAAGTTTTAG	TAGGGTTTGT	ATTGGCTTTA	300
GCTCTTCACA	GAGTACGCCA	CTTCAAGAAA	TTATATAGGA	CCTTATTGAT	TGTTCCCTTG	360
GCATTTCCCTA	CCATCGTTAT	TGCCTTTTCT	TGGCAGTGGA	TTCTAAACGG	GGTTTATGGC	420
TACTTACCTA	ATCTAATCGT	AAAATTAGGT	TTAATGGAAC	ATACACCTGC	ATTTTTGACA	480
GATAGTACAT	GGGCATTCCT	ATGTTTGGTG	TTTATCAACA	TTTGGTTTGG	AGCACCAATG	540
ATTATGGTTA	ATGTGCTTTC	AGCTTTGCAA	ACAGTACCAG	AAGAACAATT	TGAGGCTGCT	600
AAGATAGATG	GTGCTTCAAG	TTGGCAGGTG	TTCAAGTTTA	TCGTCTTTCC	ACATATTAAA	660
GTGGTTGTAG	GACTTCTAGT	TGTTTTGAGA	ACTGTATGGA	TCTTTAATAA	CTTTGACATT	720
ATCTACCTCA	TTACTGGTGG	TGGACCAGCC	AATGCTACAA	CGACGCTTCC	AATTTTTGCT	780
TACAACCTGG	GCTGGGGAAC	TAAATTGTTG	GGTCGTGCTT	CAGCAGTTAC	AGTATTGCTC	840
TTTATCTTCT	TGGTGGCGAT	TTGCTTTATC	TACTTTGCTA	TCATCAGTAA	GTGGGAAAAG	900
GAGGGTAGAA	AATAA					915

(2) INFORMATION FOR SEQ ID NO:2315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1047 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2315:

AAATCACTTG	TCAATTCTGC	CAAACTACTT	ACAACTTTGA	TGAAAAGGAC	CTGGAGGAAC	60
TCATTCGTGA	CAAACTTAA	TACACCTTTT	ATGATTGGCA	ATGTTGAGAT	TCCCAATCGT	120
ACCGTTTTAG	CGCCTATGGC	TGGCGTGACC	AACTCAGCCT	TTCGTACCAT	CGCAAAAGAG	180
CTCGGAGCTG	GACTCGTTGT	AATGGAAATG	GTCTCTGACA	AGGGAATCCA	ATACAACAAC	240
GAAAAAACCC	TGCACATGCT	TCATATCGAT	GAGGGCGAAA	ACCTGTCTC	TATCCAACCT	300
CTTGGTAGCG	ATGAAGACAG	CCTAGCACGC	GCAGCAGAAT	TCATCCAAGA	AAATACCAAG	360
ACCGATATCG	TCGATATCAA	CATGGGCTGC	CCTGTCAACA	AAATCGTGAA	GAACGAAGCT	420
GGTGCTATGT	GGCTCAAGGA	TCCTGACAAG	ATCTACTCTA	TCATCAACAA	GGTCCAGTCT	480
GTCTTGATA	TCCCACCTTAC	TGTCAAAATG	CGTACCGGCT	GGGCGGACCC	ATCTCTTGCA	540
GTAGAAAATG	CCCTCGCTGC	TGAGGCTGCA	GGTGTCTCTG	CCCTCGCCAT	GCATGGCCGT	600
ACCCGTGAAC	AAATGTATAC	TGGCCACGCA	GACCTTGAGA	CCCTTTACAA	GGTTGCCCAA	660
GCTCTAACCA	AGATTCCATT	CATCGCCAAC	GGTGATATCC	GTAAGTCCA	AGAAGCCAAG	720
CAACGCATCG	AAGAAGTTGG	TGCTGACGCA	GTCATGATTG	GCCGAGCTGC	CATGGGAAAT	780
CCTTACCTCT	TCAACCAAAT	CAACCATTAC	TTTGAAACAG	GAGAAATCCT	ACCTGATTTG	840
ACCTTTGAAG	ACAAGATGAA	GATCGCCTAC	GAACACTTGA	AACGATTGAT	TAACCTCAAA	900
GGAGAAAACG	TCGCAGTTCG	TGAATTCCGC	GGCCTCGCTC	CTCACTATCT	CCGGGGAAAC	960
TCTGGCGCTG	CCAAACTCCG	TGGAGCCATT	TCGCAAGCTA	GCACCCTGGC	AGAGATTGAA	1020
GCCCTCTTGC	AATTGGAAAA	AGTATAA				1047

(2) INFORMATION FOR SEQ ID NO:2316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2013 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2316:

TACCCACTTG	TTTACCAGTA	TCGTGAATTT	AAGACAAGTA	TTAGACATAT	AAGAAAAAGG	60
AATAAGATGA	CAGAAGAAAT	CAAAAATCTG	CAGGCACAGG	ATTATGATGC	CAGTCAAATT	120
CAAGTTTTAG	AGGGCTTAGA	GGCTGTTCTG	ATGCGTCCAG	GGATGTACAT	TGGATCAACC	180
TCAAAAGAAG	GTCTTCACCA	TCTAGTCTGG	GAAATTGTTG	ATAACTCAAT	TGACGAGGCC	240
TTGGCAGGAT	TTGCCAGCCA	TATTCAAGTT	TTTATTGAGC	CAGATGATTC	GATTACTGTT	300
GTGGATGATG	GGCGTGGTAT	CCCAGTCGAT	ATTCAAGAAA	AAACAGGCCG	TCCTGCTGTT	360
GAGACCGTCT	TTACAGTCCT	TCACGCTGGA	GGAAAGTTCC	GCGGTGGTGG	ATACAAGGTT	420
TCAGGTGGTC	TTCAAGGGGT	GGGGTCGTCA	GTAAGTTAAT	CCCTTTCCAC	TCAATTAGAC	480
GTTTCATGTT	ACAAAAATGG	TAAGATTCAT	TACCAAGAA	ACCGTCGTGG	TCATGTTGTC	540
GCAGATCTTG	AAATAGTTGG	AGATACGGAT	AAAACAGGAA	CAACTGTTCA	CTTCACACCG	600
GACCCAAAAA	TCTTCACTGA	AACAACAATC	TTTGATTTTG	ATAAATTAAA	TAAACGGATT	660
CAAGAGTTGG	CTTTTCTAAA	TCGCGGTCTT	CAAATTTCAA	TTACAGATAA	GCGCCAAGGT	720
TTGGAACAAA	CCAAGCATTA	TCATTATGAA	GGTGGGATTG	CTAGTTACGT	TGAATATATC	780
AACGAGAACA	AGGATGTAAT	CTTTGATACA	CCAATCTATA	CAGACGGTGA	GATGGATGAT	840
ATCACAGTTG	AGGTAGCCAT	GCAGTACACA	ACTGGTTACC	ATGAAAATGT	CATGAGTTTC	900
GCCAAATAATA	TTCATACACA	TGAAGGTGGA	ACGCATGAAC	AAGGTTTCCG	TACAGCCTTG	960
ACACGTGTTA	TCAATGATTA	TGCTCGTAAA	AATAAGTTAC	TGAAAGACAA	TGAAGACAAC	1020
CTAACAGGGG	AAGATGTTTC	CGAAGGCTTA	ACTGCAGTTA	TCTCAGTTAA	ACACCCAAAT	1080
CCACAGTTTG	AAGGACAAAC	CAAGACCAAA	TTGGGAAATA	GCGAAGTGGT	CAAGATTACC	1140
AATCGCCTCT	TCAGTGAAAG	CTTCTCCGAT	TTCTCATGG	AAAAATCCACA	GATTGCCAAA	1200
CGTATCGTGG	AAAAAGGGAT	TTTAGCTGCC	AAGGCTCGTG	TGGCTGCCAA	GCGTGCGCGT	1260
GAAGTCACAC	GTAAAAAATC	TGGTTTGGA	ATTTCCAACC	TTCCAGGGAA	ACTAGCAGAC	1320
TGTTCTTCTA	ATAACCCTGC	TGAAACAGAA	CTCTTCATCG	TCGAAGGAGA	CTCAGCTGGT	1380
GGATCAGCCA	AATCTGGTCG	TAACCGTGAG	TTTCAGGCTA	TCCTTCCAAT	TCGCGGTAAG	1440
ATTTTGAACG	TTGAAAAAGC	AAGTATGGAT	AAGATTCTAG	CTAACGAAGA	AATTTCGTAGT	1500
CTTTTCACAG	CCATGGGAAC	AGGATTTGGC	GCAGAAATTT	ATGTTTCGAA	AGCCCCTTAC	1560
CAAAAACCTCG	TTTTGATGAC	CGATGCCGAT	GTCGATGGAG	CCCACATTCG	TACCCCTTCTT	1620
TTAACCTTGA	TTTATCGTTA	TATGAAACCA	ATCCTAGAAG	CTGGTTATGT	TTATATTGCC	1680
CAACCACCAA	TCTATGGTGT	CAAGGTTGGA	AGCGAGATTA	AAGAATATAT	CCAGCCGGGT	1740
GCAGATCAAG	AAATCAAAC	CCAAGAAGCT	TTAGCCCCTT	ATAGTGAAGG	TCGTACCAAA	1800
CCGACTATTTC	AGCGTTATAA	GGGGCTAGGT	GAAATGGACG	ATCATCAGCT	GTGGGAAACA	1860
ACCATGGATC	CCGAACATCG	CTTGATGGCT	AGAGTTTCTG	TAGATGATGC	TGCAGAAGCA	1920

GATAAAATCT TTGATATGTT GATGGGGGAT CGAGTAGAGC CTCGTCGTGA GTTTATCGAA	1980
GAAAATGCTG TCTATAGTAC ACTTGATGTC TAA	2013

(2) INFORMATION FOR SEQ ID NO:2317:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 444 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...444
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2317:

GAAACTATTG TGTATACTAT TATAAAATCA AATATAAAAA AATTTTAGTTT ATTAACGATA	60
TTTATTGTTG CTGGTCAATT ATTGCTAATT TATGCAGCAA CTATTAATGC TCTGGTGTG	120
AATGAATTAA TTGCGATGAA TTTAGAGCGG TTTTGTGAAAT TGTCAATCTA CCAAATGATT	180
GTCTGGTGTG GGATAATATT CCTTGACTGG GTAGTGAAAA ATTATCAGGT TGAAGTGATC	240
CGAAAGTTTA ATCTAAAAAT TCGAAATAGA GTTGCCACAG ACATCTCTAA CTCTACCTAT	300
CAAGAATTTT ATAGTAAATC ATCAGGAACA TATCTTTCGT GGCTAAATAA TGATGTTTAC	360
ACTTTAAATG ATCAGGCTTT TAAACAACCT TTTTGTAGTAA TAAAAGGAGA TTTCTGGTAC	420
TATATTTGCA GTTGTGACTC TTAA	444

(2) INFORMATION FOR SEQ ID NO:2318:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 246 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...246
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2318:

GGAGATATTG TAGGTTTACA AAATCAGTAT TTTTGGATTA TTGGTGGAGC TACAGATTTA	60
TATAATTCTA AAGAGGAGAT AGGTTATTCA GTCTCAGAAG TTGTACATAT TTTATCAGAA	120
AGTTTGTCCG TTAATTGTAA AGAATCAAAA ACTCTTAAAC AAATATTTGA AACTGCTTTA	180
CTCGAGGTTA AAGATGAAAT CGGTTTAAAC TCATATAAAT TAACAGAGTA TAGTAAAATG	240
AAATAA	246

(2) INFORMATION FOR SEQ ID NO:2319:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 906 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2319:

CAAAGTATTG TAAAAAAGAA AAGGAGTTTC ATTATGAAGA AAAAGAATGG TAAAGCTAAA	60
AAGTGGCAAC TGTATGCAGC AATCGGTGCT GCGAGTGTAG TTGTATTGGG TGCCGGGGGG	120
ATTTTACTCT TTAGACAACC TTCTCAGACT GCTCTAAAAG ATGAGCCTAC TCATCTTGTT	180
GTTGCCAATG AAGGAAGCGT GGCATCCTCT GTTTTATTGT CAGGGACAGT AACAGCAAAA	240
AATGAACAAT ATGTTTATTT TGATGCTAGT AAGGGTGATT TAGATGAAAT CCTTGTTTCT	300
GTGGGCGATA AGGTCAGCGA AGGGCAGGCT TTAGTCAAGT ACAGTAGTTC AGAAGCGCAG	360
GCGGCCTATG ATTCAGCTAG TCGAGCAGTA GCTAAGGCAG ATCGTCATAT CAATGAACCTC	420
AATCAAGCAC GAAATGAAGC CGCTTCAGCT CAGGCTCCAC AGTTACCAGC GCCAGTAGGA	480
GGAGAAGATG CAACGGTGCA AAGCCCAACT CCAGTGGCTG GAAATTCTGT TGCTTCTATT	540
GATGCTCAAT TGGGTGATGC CCGTGATGCG CGTGCAGATG CTGCAGCGCA ATTAAGCAAG	600
GCTCAAAGTC AATTGGATGC AACAACTGTT CTCAGTACCC TAGAGGGAAC TGTAGTCGAA	660
GTCAATAGCA ATGTTTCTAA ATCTCCAACA GGGGCGAGTC AAGTTATGGT TCATATTGTC	720
AGCAATGAAA ATTTACAAGT CAAGGGAGAA TTGTCTGAGT ACAATCTANC CAACCTTTCT	780
GTAGGTCAAG AAGTAAGTTT TACTTCTAAA GTGTATCCTG ATAAAAAATG GACTGGGAAA	840
TTAAGCTATA TTTCTGACTG TCCTAAAAAC AATGGTGAAG CAGCTAGTCC AGCAGCCGCG	900
GAATAA	906

(2) INFORMATION FOR SEQ ID NO:2320:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 918 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...918

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2320:

GAGGTCATTG	TTATGATACA	ATGGTGGCAA	ATTTTACTTC	TCACTTTGTA	CTCAGCTTAT	60
CAAATCTGTG	ATGAGTTGAC	GATCGTTTCA	TCTGCAGGTT	CCCCTGTATT	TGCTGGTTTC	120
ATTACTGGTT	TAATCATGGG	AGATGTGACT	ACTGGTTTAC	TTATCGGTGG	TAACTTGCAA	180
CTGTTTCGTT	TTGGGGTTGG	TACCTTCGGT	GGTGCTTCTC	GTATCGACGC	AACTTCTGGT	240
GCGGTTCTTG	CGACAGCCTT	CTCTGTTTCA	CAAGGAATTG	ATGCACCGCT	TGCAATTACT	300
ACAATCGCTG	TACCAGTAGC	AGCTCTCTTG	ACTTACTTCG	ACGTTCTTGG	TCGTATGACT	360
ACTACCTTCT	TTGCTCACCG	TGTGGATGCT	GCAATCGAAC	GCTTTGACTA	TAAAGGTATT	420
GAACGCAACT	ACTTGCTTGG	TGCGATTCCG	TGGGCTCTAT	CTCGTGCCCT	TCCAGTCTTC	480
TTTGCCCTTG	CTTTTGGTGG	TGCCTTTGTA	CAATCAGTAG	TAGACTTCGT	TGAAGCCTAC	540
AAATGGGTTG	CAGATGGCTT	GACACTCGCA	GGACGTATGC	TTCCAGGTCT	TGGATTTGCA	600
ATCTTGCTTC	GTTACCTTCC	AGTTAAACGT	AACCTTCACT	ACCTTGCTAT	GGGATTTGGT	660
TTGACAGCTA	TGTTGACTGT	TCTTTACTCA	TATGTAACAG	GTCTTGGTGG	CGCTGTTGCT	720
GGTATCGTAG	GTACTCTTCC	TGCTGAAGTT	GCTGAAAAAA	TTGGTTTCGT	GAACAAC TTC	780
AAAGGTTTGT	CTATGATTGG	TATTTCTATC	GTAGGTATTT	TCCTTGCA GT	GCTTCACTTC	840
AAAAATAGCC	AAAAAGTAGC	TGTAGCAGCA	CCTTCTACAC	CATCAGAAAG	TGGGGAAATC	900
GAAGATGACG	AATTC TAA					918

(2) INFORMATION FOR SEQ ID NO:2321:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2321:

GATGTAATTG	TATGTAAAGG	AGACGTCATG	TTAAATAGTA	TTGTAACCAT	TATTTGTATT	60
GCCCTTATCG	CGTTTATCTT	GTTTTGGTTT	TTCAAAAAGC	CTGAAAAATC	TGGACAAATA	120
GCCCAGCAAA	AAAACGGATA	CCAAGAGATT	CGAGTGGAAG	TCATGGGAGG	CTATACTCCT	180
GAGTTGATTG	TCCTCAAGAA	ATCAGTGCCA	GCCCGCATTG	TCTTTGACCG	CAAGGATCCT	240

TCACCATGTC	TGGATCAAAT	TGTTTTTCCA	GATTTTGGTG	TACATGCGAA	CCTGCCAATG	300
GGGGAAGAGT	ATGTAGTGGA	AATCACGCCT	GAACAGGCTG	GAGAGTTTGG	CTTTGCTTGT	360
GGTATGAACA	TGATGCACGG	CAAGATGATT	GTAGAGTAG			399

(2) INFORMATION FOR SEQ ID NO:2322:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1353
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2322:

GAGGTGATTG	TGATTGGTAA	TGTAGTAAGT	ATTGACTCAC	AACCTAAGAT	GATAACGACT	60
GCCAAAGGAG	ACATCAAGGC	CAACAGTCCA	AGTAATGTGT	TGATGTCTTT	CAAAGCTGAT	120
GATCAGTTGA	GTATTTACCT	AAAGCACAAAC	GATTTTTCCC	AAGAGCATGA	ACTCCTTAAA	180
GATATCAAGA	TCGGCAACAC	TCTTTTAAAA	AAAGGTGAGC	TCCCTTCTAA	CTTTGATTCA	240
GTCGTAAAAAG	TTTACTTTGA	AAGTGTGTTA	GGTGTTGCTT	TCTCTAGCCA	GGCGATGCTG	300
GACGGCATGG	AAACTTTTTT	CTCAGAACGT	TCTTACAATC	CAGTCATTGA	GTATATGGAA	360
AAGGCTGCTG	AAAAATGGGA	TGGTCGTAAA	CGAATTGACC	GAATGCTTCA	GGTTTACCTG	420
GGGGCTGAAG	ATATCCCTTT	AGTTTCTAAA	ATCGCTCAA	TGTGGCTAGT	TGGTGCAGTT	480
GCTAAAGTTT	ATGATCCATA	CGTTAAGTTT	GACTATGTTC	TGGATCTAGT	CGGTGGACAA	540
GGAGTTGGGA	AAACATCCCT	CCTTCAAAAA	TTGGGTGGCG	AATGGTATAC	GGATGCCGTA	600
ACAGATTTCT	CTAATAAAGA	TAATTACGAC	ATTATGTTAA	AGAGTCTAAT	CGTCAACGAC	660
GACGAAATGG	TGGCCAGTAA	TCGGATGAGC	TTTGCAGAAA	CTAAGGCCCT	TATTTCTAAA	720
ACTAGCCTAC	GTTATCGTAA	ACCATACATG	AAACGCACAG	AAGAGTTTGC	CAAAAACTTC	780
ATTTTAGCTA	GAACACTAA	CCAAACAGAA	TACCTCAAGG	ACAAAACCGG	TGAACGTCGT	840
TTTCTACCAG	TTATGGCAGA	TAGTAAACGG	CAAAAAAAC	ATCCAATGGA	AATCGAGCCA	900
GAGACAATTG	AACAAATCTG	GGGCGAAGCC	GTTACAATCT	ATCGTGCTGG	TGCTGATTTG	960
ATGTTTGATG	AAAATACAGA	GGATGAACTG	AATATCTACC	GTGAACAGTT	CATGTATCGT	1020
GATGAAGTTG	AATTACAAGT	GCTTGAATAT	CTTGATATGC	CCGTCCCTGA	AAATTGGCAA	1080
AACTGGTCTA	TTCAGCAACA	ACATCAATAC	ACAAGTAAAT	ATTTTCGATA	TAGTAGCGAC	1140
TTTGATCCTG	GAAGCAAAAA	ACTAGATAAG	GTCTCAACTC	GTGAAATGAT	GTACAACTTA	1200
TTTATGAGAA	ATTTCGAATGA	CAGGAAGCTG	TCAACGAAGA	TTAACATGAT	CATGGATAAT	1260
CATCCTGATT	GGAAAAAAG	TGTTTTCCGG	GCAGGAGGTA	AAAGTACAAA	AGGGTTCGTA	1320
AGAGTGAAAG	ATTCGGAAAA	AACTAATCGG	TAG			1353

(2) INFORMATION FOR SEQ ID NO:2323:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 399 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2323:

ATAAAGATTG TAATGATTGA GATTAAAGTTC AATCCAGTTA TATTGAATAA TAATGCTGAG	60
ACAACCCCAA ATAAGGAGAT GACGGTCATG ACTGGAAGTA ATACGCTAAA TGATCTACTA	120
ACAGCTGGTG GAATATTTTC ACCAAGGTTC ATTTGTAAAG CTTTAACATT TGATAATTCA	180
ATGAATAATT CTGTTGCAAT AATCGCTACG ATAACCCCGG CGAACATTGC GCCTGTACCT	240
GTGTTGTTGA ATGAAAGAAC ACCTGAAATG TTTACAGCAT CTTTGTGCTCC GTCAGGAACT	300
ACAGAACTG TATTTGGCAT CATCACAATT AAAGAACTA ATGATAGCAT TGATGCTGCT	360
AACGGGTTTT CGAAATCTCT GTTTTGTAGCT AAGAAATAA	399

(2) INFORMATION FOR SEQ ID NO:2324:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2324:

ACAACCGTTG TTAACAATCA CATACTCATT CTGGAGGTCG AGTCCCAGTT TTTGTAGTA	60
GGGAGAGACA CCGAAAAGGG GCGACCCGT ACAGAGAACC AGTTTGACAC CTTTTCAAT	120
GGCTTGGTGA ATAGCAGCGA TGTGAGCCTG TGGGATTTC TGGCTTCAT TGAGGAGGCT	180
TCCATCCATA TCCAAGGCTA G	201

(2) INFORMATION FOR SEQ ID NO:2325:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2325:

GAAGGAGTTG	TGATGAAAGT	ATTTCTTCAA	AATAGAGATT	TTAGGCAATT	AACATCAAC	60
CAGTGGATTT	CAACGCTTGG	GGATACGATT	TTTTATCTGG	CCTTTCTGAA	TTATGTGGCA	120
GATGCGTCTT	TTGCACCTTT	GGCGATTTTA	CTCATTACGA	TTTCAGAAAC	CCTGCCCCAA	180
ATTTTACAAA	TCTTTCTGGG	AGTTTTGGCA	GATTTTCAAC	ATCATCGTGT	CTTGAAATAC	240
ACAGTCATTA	GTTTTGCAAA	ATTTTTGCTT	TACTCTATCG	TTTCTTTATC	ACTTTCAGGG	300
CAGTCTTTCT	CCTTGTTGCT	AGTAGCATT	ATTTGTCTGC	TTAACCTCTT	GTCTGACACA	360
TTGAGTTACT	TTTCAGGAGC	CATGCTCACT	CCGATTTTCA	TTAGAATTAT	TGGGCAAGAC	420
CATCTGGCAG	AAGCTATTGG	CTTTAAACAG	TCAACTGTTA	GTTTAGTGAA	AACAATCAGT	480
AATATCCTAG	GAGGAGTCTT	ACTAGGCATT	CTATCCATCC	AGTTTATTTT	CTTACTGAAC	540
GCTCTTACCT	TTTTAATCGC	ATTTTTAGGT	ATCCTCTTCA	TAAAAACTGA	CCTCTTGAAA	600
GTAGAAAAAA	CGATTAGCTA	TCAAGAAGGA	CTCTCTGTAA	AATCCTTTTG	CCAGCATTTG	660
CTCCAATCAT	CAAAATTGAT	ATGGAATATG	AATAAGGTGC	TCTTGGTTTT	GTTTATTATC	720
TCTACTAGTC	AAGCAGTGAT	AAATGTTACG	GTTCCCTATT	CCACTCTATT	TTTAAGGAAC	780
CAGCCCTTTT	TGAATTTACA	AACAGGTCAA	TCTCTTGCC	TGCTATCCAC	TTTTGAAGTG	840
TCAGCCCTGA	TTGTCGGAAG	CCTTGTAAGT	GGCTATCTGC	AACATAACCAT	TTCCATAAAA	900
ACAGCTCTCT	ATGCCTCACT	TGTCATCCAG	TTGCTTCTTC	TAGTAGGATT	TGCCACAGTT	960
CGTTTTGACT	GGATTCTCAT	CTTTAGTACC	TTGGATGCCT	TTTTCGCAGG	TGTTCTCTCT	1020
CCTAGATTGC	AAGAACTCGT	TTTTAAACAA	ATACCTGAGG	AGTCAATGGG	AGCAGTTCAA	1080
TCCTCTATCG	GTGCCATTAC	GGTTGTTTTA	CCTAGCTTAT	TTACAATAGC	TTTGGTAACC	1140
ATTGCTACTA	GCTTTGGAAC	TCTGGCAGTT	AGCTTTGTTT	TATTGCTATT	TCTTCTAGTT	1200
GCCTTTGTTA	TGCTTCTGAA	TATTCGTGAA	AGTATTTAG			1239

(2) INFORMATION FOR SEQ ID NO:2326:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2326:

CCCTCTTCTG	TCAGAAATGC	TGCAATTCCT	TCTCTAATCA	TTTCCTCGTC	ATCTGCAACT	60
AAAATGTTCA	TCTCTCTCCC	TTTCTACTAC	CAGAACTCCA	TACATCTATT	TCCTATATGC	120
TATTTGAAAA	TTTCCTACCA	GCCTATCATC	TATGATAATG	GAATGGATTT	CATTTATCCG	180
CTACTTTTTG	TCAACAACAA	CGTCAATACA	AGAAAATCAT	TCATCTTGCA	GCTTATACTC	240
TTCGAAAATC	TCTTCAAACC	ACGTCAGCTC	TATCTACAAT	CTAAAAACAG	TGTTTTGAGC	300
AACCTGCGGC	TAGCTGCCTA	G				321

(2) INFORMATION FOR SEQ ID NO:2327:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 474 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2327:

CTCCATTCTG	TGGTGAAGAG	TCTGCCTGCT	CAGACTATTC	AGATTGGAAC	TTTAGGTGTT	60
GATTTTTTCG	GTCTGATTCC	AGGGATTTTG	ATTATCTCTA	TGAATAGTGG	TGCTTATGTT	120
TCGGAGACTG	TTCGTGCCCG	AATCAATGCG	GTTCCAAAAG	GTCAGCTAGA	GGCGGCTTAT	180
TCGCTAGGGA	TTCGTCCTAA	AAATGCGATG	CGTTATGTGA	TTTTGCCACA	AGCAGTCAAA	240
AATATCTTGC	CAGCATTGGG	GAACGAATTT	ATCACCATTA	TCAAGGACAG	CTCCCTCTTA	300
TCAGCTATTG	GGGTCATGGA	GTTGTGGAAT	GGGGCTACAA	CAGTTTCTAC	AACAACCTAT	360
CTACCTTTAA	CACCACTTTT	ATTTGCAGCA	TTTTACTACT	TGATTATGAC	CTCTATTCTG	420
ACAGTAGCCT	TGAAAGCTTT	TGAAAAACAT	ATGGGACAAG	GAGATAAGAA	ATAA	474

(2) INFORMATION FOR SEQ ID NO:2328:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2328:

ATACGTTCTG	TTACTTCCAT	GACCAGATTC	ATATCGTGTT	CAATCAACAT	GATTGTAATC	60
TTAAATTCAT	CTTTGATACG	ACGAATTAAC	TCAGTCAATT	CGGCTGTTTC	CTGTGGGTTC	120
ATACCTGCTG	CTGGTTCATC	TAAGAAGAGA	ATTTTAGGTT	CCGTAGCAAG	GGCACGAACA	180
ATTTCCAAAC	GACGTTGTTG	TCCGTAG				207

(2) INFORMATION FOR SEQ ID NO:2329:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2329:

ACCGTCTCTG	TAGGCAGAAAT	GACAGCTCCA	CCCTTTTCCA	ACTCTTGTCT	AATCCTGTCC	60
ATCATCAACC	ACGACCATCC	TATCTTGACC	AAATTGGTCT	TTGAGTGTTC	GAACTTTTTTT	120
TTCAGGAAGA	TGTTTTCTAA	AAAGTTCGGG	AACACTTTGA	CCTTGCTTGT	ATCCAATTTT	180
AAGGTAAATC	TTACCACCAT	CCTTGAGATA	GTCTTTTGCA	TCTTCCGCAA	TTCTACAGTA	240
AATAGCTAG						249

(2) INFORMATION FOR SEQ ID NO:2330:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...219
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2330:

AATATATCTG	TTAAAATAAG	GATAATGAAA	AAGAAAAGGG	TTTCACGAAT	GAAGAAAAAT	60
CGTGGAATTC	AAAAATTAGC	TATATTAGTA	TTACTAGGTG	TTTTTATGTT	TAGTAATACA	120
ATTCCTTACC	AACAGTTTAT	TCAGAAGAAT	AGACAATTGG	AGATTTCGAGT	GCAATCGCAA	180
AAGAAGTCCA	ATGGTCTTGA	TGTTGGGAAG	GCTGATTGA			219

(2) INFORMATION FOR SEQ ID NO:2331:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 969 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...969
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2331:

GGTTATGACT	TATGTGCGAC	TATCTTGCGC	TATGTGCGAC	CTGACAAGGC	TGGAAATTTT	60
GCCAATGTTA	TCTTGGGATT	TGATGACTTT	GATAGTTATG	TAGGCAATAG	TCCCAAGCAT	120
GGAGCAAGTG	TAGGTCCTGT	AGCGGGTCGT	ATTGCAGGTG	CGACCTTTGA	GCTCAATGGT	180
AAGACCTATG	ACCTTGAGGT	TAATAATGCT	AGCAACTGTA	ATCACAGTGG	TTCAACTGGT	240
TGGGATTCCA	GCTTGTTTGA	AGTTGAAGAA	GTAAGCGATC	ATGGCTTGAC	TCTCTACACA	300
GAGCGTACAG	ATGGGACAGG	AGGGTTC CCT	GGAAATCTCA	AGATTTGGAT	CAGTTATCAC	360
TTGGAAGAAA	CTGGTGCCTA	TGAAATCAGC	TACAAGGTAA	CGACCGATCA	GGATACGCTG	420
GTCAATCCAA	CCAACCACAG	CTATTTCAAC	TTGTCTGGTG	ATTTACGCA	GACGATTGAC	480
CGTCATGTCT	TCCAACATAA	CACAGAGGGC	ATTTACTCAA	TCGCTCCTGA	CGGTGTT CCT	540
GCCAAAACTC	CAGAAGCCAA	CCGTGATGTG	GTCAAACACG	TCTACAATGG	TACCTTGTTG	600
AAGGATATCT	TTGCAGAAGA	AGATGAGCAA	ATCCAGCTGG	CATCAGGTTT	GGATCATCCA	660
TTTGCCCTTC	CTGCAGGCCA	TGACAATGCT	GGATTCC TTT	ATGACCAAAA	TTCAAGTTCG	720
TTCCTGCTTT	TCAAGACAGA	AGCTCCTTGC	TTTGTGGTCT	ACACAGCAAA	CTTTGTGGAT	780
GAAAGTGTC	TCATAGGAGG	TCAGCCAATG	CTACAGCACA	ATGGGATTGC	TCTTGAAGCG	840
CAAGCTTTAC	CAGATGCCAT	TCACAGTGAC	CTTAAAGGCC	AAGTCATTCT	TAAAGCTGGT	900

CAAACCTTCA CCAGTAAGAC ACGTTATGAA CTTGTTGTGA AGTCTTCACG CCACCGCGGA	960
ATTCTCAAT	969

(2) INFORMATION FOR SEQ ID NO:2332:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...225
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2332:

ATCTTTCCTG TCCAAATGTT CCAGGTAAAC CTCAGATTGC CTATGATTTT GAGACAACAG	60
ACCGGATTTT GGCAGAAGTG TTTGCTTACT TCACCAAACC TCTTGGAATT AAATTGCCAC	120
CTTATTTTGA TATTGTTTCA TTTGATCAAG CGGCAGCTAT TTTCAACAAA TATCCGCTCA	180
AGTTTGTCAA CTGCGTTAAC TCTATCGGAA ACGGCCTCTA TATAG	225

(2) INFORMATION FOR SEQ ID NO:2333:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...241
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2333:

GCAACCTGTG GTGAAGAGAG ACAAATGGC TAAGTCAAAC TTTGAAAAAG TAGAATCAGT	60
TGTTGGCTGG GTTCGTGATA AGAAAATCAC AGGCTACCGT ATCTCTAAAAG AAACGAATGC	120
CGGTGAAATG TCTATCATTG CTCTGGCGCA GGGTCGTGCA AAAGTAAAAA ATATTTTCATT	180

TGAAACAGCC CTAGGCCTAA TTGATTTCTA TGAAAAAAT TATGAAAAAT TTGAAGATTA	240
A	241

(2) INFORMATION FOR SEQ ID NO:2334:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2334:

CACAAACCTG TGTTTTTGAT AAACAGTTGC TTGGGCCTAT TCTCTGCGAC CTACTCTCGT	60
AGGCACCCCT TCTCCCGAAG TTACGGGGTC AATTTGCCGA GTTCCTTAAC AGCAATTCTT	120
CCGATGGTCT TAGGATTCTC TCCTCACCTA CCTGTGTCGG TTTGCGGTAC GGGCACAGAG	180
CTCCTGGATA GAGACTTTTC TTGGCAGCAT GAAATCAGAT ATTTTCGGTAG TAAACTACCT	240
CACCATTACA CCCCAGACTT AACGAAAGAC GGATTTTCCT ATCTTTCATC CTCAGTGCTT	300
AGACGTACTT CCAATAACGT ACGCATATCC TATCCTCCTG CGTCATCCCA TTTCTCATAA	360

(2) INFORMATION FOR SEQ ID NO:2335:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 783 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2335:

CTATTTACTG	TAGAATTGCG	GAAGATGCAA	AAGACTATCT	CAAGGATGGT	GGTAAGATTT	60
ACCTTGAAAAT	TGGATACAAAG	CAAGGTCAAA	GTGTTCCCGA	ACTTTTTTAGA	AAACATCTTC	120
CTGAAAAAAA	AGTTCGAACA	CTCAAAGACC	AATTTGGTCA	AGATAGGATG	GTCGTGGTTG	180
ATGATGGACA	GGATTAGACA	AGAGTTGGAA	AAGGGTGGAG	CTGTCATTCT	GCCTACAGAG	240
ACGGTTTATG	GTCTTTTTCG	CAAGGCCCTTA	GACGAAAAAG	CAGTTGACCA	TGTTTACCAG	300
CTCAAACGTC	GTCCTAGAGA	CAAGGCGCTC	AATCTCAATG	TTGCCTCTTT	AGAGGATATC	360
TTGCACTTTT	CTAAGAATCA	GCCAGCTTAT	CTACAAAAAC	TTGTAGAGAC	CTTTTTGCCA	420
GGTCCCTTGA	CCATTATTCT	CGAAGCCAAT	GACCGAGTTC	CCTATTGGGT	AAATTC TGAC	480
CTTGCAACTA	TTGGATTTCG	GATGCCCAGT	CACCCATCA	CAC TGGATT	AATTCGAGAG	540
ACAGGTCCCT	TGATTGGGCC	GTCTGCCAAT	ATCTCAGGTC	AGGCAAGTGG	TGTAACCTTT	600
GAACAAATTC	TGAAGGATTT	TGACCAAGAG	GTCTGGGTC	TGGAAGACGA	TGCTTTTCTA	660
ACTGGACAGG	ATTCAACTAT	TGTGGATTTG	TCTGGAGACA	AGGTGAAAAT	CTTACGCCAA	720
GGCGCAATTA	AACGAGAAGA	TATTCCTTGCT	CGGTTGCCAG	AGATTTCTTT	TGAGGAGGCT	780
TGA						783

(2) INFORMATION FOR SEQ ID NO:2336:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...297
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2336:

GCACTCGACT	TGACTAATGT	TCAACTTTAC	TACCACATCA	TCATCCCACA	AGTCTTAAGA	60
AGACTGCTAC	CGCAGGCTAT	CAATCTTGTC	ACTCGGATGA	TTAAAACCAC	TTCATTAGTT	120
GTTTTGATTG	GGGTTGTGGA	AGTGACCAAA	GTTGGACAAC	AAATCATCGA	TAGCAATCGC	180
CTGACCATCC	CAACTGCTTC	ATTTTGGATT	TATGGAACCA	TTCTAGTCTT	ATATTTTCGCA	240
GTTTGCTACC	CTATTTCCAA	ACTATCCACT	CAC TTAGAAA	AACATTGGAG	AAACTAA	297

(2) INFORMATION FOR SEQ ID NO:2337:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2337:

GTATGTACTG TTAAGGAGAG AATCATGCCC GTAAGAAAAT TACAATCCTA TGAGGTAGAC	60
TATCAAGAAG AATTAAACCA GCAGCTTCCT CATTACCAAG CTTATACACC TGAAGCGCAA	120
TCTGATGCCA ATCTCAAGGA AATCCTATTT TTTATTAATA TCGCTGTTTT TTGTATCTGT	180
ATTGCTATCT TTAGTTTTAT CTTTTTAGCA TTAAAATTAT CAACTGCTCT TGCCTTTGCC	240
GCAGCAATCG GATTCAGCTT ACTTGTTTTA AAAGTTCAAC GGTCTATTAT CAAACGAAAA	300
CGTAGAAGAT AA	312

(2) INFORMATION FOR SEQ ID NO:2338:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2338:

GAAAGAACTG TTGGTTTCAT CGCTGCGATG TGCATTGACA ATTGTTTAGC AAGTGCTTCG	60
TCTCCACCTT CAACAACTGA AATAACACCG ATACGTCCAC CGTTATGTTG GTATGCTCCA	120
AAGTGTTGTG CGTCTGTTTT TTCAATCAAT GCAAAGCGAC GGAATGAGAT TTTCTCTCCG	180
ATAGTTGCTG TTGCAGATAC GTATGCAGCT TCAAGAGTTT CACCTGAAGG CATTATCAAA	240
GCAAGAGCTT CTTCAATTGTT AGCAGGTTTT CCTTCAGCAA TGACTTTAGC TGTAGTATTT	300
ACCAATTCAA CGAATTGA	318

(2) INFORMATION FOR SEQ ID NO:2339:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 858 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...858

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2339:

AGACCGACTG	TCTTTGCTGG	GGTCATTTTA	CACGTAATGC	TGGGTTCGAC	TTATGCTTGG	60
AGTGTTTTATC	GTAACCCTAT	TATTGAAAAA	ACGGGATGGG	ATCAGGCTTC	TGTTGCCTTC	120
GCCTTTTAGTC	TAGCAATCTT	TTGTTTGGGC	TTATCGGCTG	CATTTATGGG	GCGTTTGGTA	180
GAAAAATTTG	GTCCGAAAGT	CATGGGGAGT	CTATCTGCTT	TTCTATACGC	AGGTGGAAAT	240
ATCTTAACAG	GATTTGCAAT	AGACCGTCAG	GAACGTGTGGT	TGTTGTATCT	AGCTTATGGC	300
ATTTTAGGTG	GGCTTGGTTT	GGGAGCAGGT	TATATTACCC	CTGTGTCAAC	GATTATAAAA	360
TGGTTTCCTG	ATAAACGTGG	TCTCGCAACA	GGTTTAGCGA	TTATGGGGTT	TGGTTTTGCT	420
TCTTTATTGA	CTAGTCCCAT	AGCGCAACAC	CTCATCGCAG	GGGTATGGAT	TGTAGAAACT	480
TTTTATATTT	TAGGAGCAAG	TTACTTTATT	ATCATGCTCC	TAGCTTCACA	ATTCATTAAG	540
CGTCCAAATG	AGCAAGAGCT	TGCAATTTTA	TCTTCTTCAG	GGAAAGAAAA	AACAGCCTCT	600
TTGACGCAAG	GAATGGCTGC	AAATCAGGCT	CTAAAAAGCA	ATCGGTTTTA	TATGCTTTGG	660
ATTATTTTCT	TTATCAACAT	ANCTTGTGGT	TTAGGCTTAA	TTTCAGCGGC	ATCGCCAATG	720
GCACAGGAAA	TGGCTGGCTT	GTCTACAAGT	CATGCAGCAG	TAATGGTGGG	TGTTTTGGGG	780
ATTTTCAATG	GATTTGGTCG	CTTGCTCTGG	GCGAGTTTGT	CTGACTATAT	CGGTCCGCCT	840
CTAACCTTTA	ATATATGA					858

(2) INFORMATION FOR SEQ ID NO:2340:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2340:

TTCCTTGCTG	TTAACTTGCC	CCTTTATACC	TTTCTTATAA	GCCCAGTGAG	CCGCAACCCC	60
GTA CT CAGCC	ACCTCGTGCA	TTTCCTTGGT	TCGAATCTGG	AATTCAATCG	GCCCTTTTGG	120
TCCATAAACA	GTCGTATGGA	TAGACTGATA	ACCATTTGGC	TTGCGGTTGG	CAATATAGTC	180
TTTGAAGCGA	CCTGGCATCG	GTTTCCAAAA	TTCATGCACG	TAACCAAGCA	TGGCATAAAC	240

(2) INFORMATION FOR SEQ ID NO:2341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1929 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2341:

AAGGCAGCTG	TCTTAGCTAA	GATTCAAGAA	CAAGGTAAGT	TGACCAAGGA	ATTGGAAGAA	60
GCTATCTTAG	TTGCCGAAAA	ATTAGCAGAC	GTTGAAGAAC	TCTATCTTCC	TTATAAGGAA	120
AAGCGTCGTA	CCAAGGCAAC	CATTGCCCGT	GAAGCTGGAC	TCTTTCCTCT	TGCTCGCTTG	180
ATTTTGCAGA	ATATAGTTGA	CTTAGAGAAA	GAAGCTGAAA	AGTTCGTCTG	TGAAGGATTT	240
GCGACTGGCA	AGGAAGCCTT	GACCGGTGCA	GTTGATATTT	TGGTCGAAGC	CTTATCGGAA	300
GATGTGACCT	TGCGTTCTAT	GACTTATCAG	GAAGTGCTGA	GACACTCTAA	ACTCACTTCT	360
CAAGCCAAGG	ATGAAAGTCT	TGATGAAAAG	CAGGTTTTTC	AGATTTATTA	TGATTTTTTCA	420
GAGACAGTTG	GAACATGCA	AGGCTATCGT	ACCTTGGCTC	TCAATCGTGG	GGAGAAACTT	480
GGTGTCTTGA	AGATCGGTTT	TGAACATGCG	ACGGACCGTA	TTCTTGCCCT	CTTTGCTACT	540
CGTTTCAAGG	TGAAAAATGC	TTATATTGAT	GAAGTTGTTT	AGCAATCCGT	TAAGAAAAAG	600
GTCTTGCCTG	CTATTGAGCG	TCGTATTCCG	ACAGAAATTA	CTGAGAAAGC	TGAAGAGGGA	660
GCTATCCAAC	TTTTTTCTGA	CAATCTGCGC	AATCTCCTCT	TGGTTGCTCC	ACTGAAAGGG	720
CGCGTGGTTC	TTGGGTTTGA	CCCAGCCTTT	CGTACAGGTG	CCAAGCTAGC	TGTCGTGGAT	780
GCAACAGGAA	AAATGCTGAC	AACTCAGGTT	ATTTATCCTG	TTAAACCAGC	ATCAGCTCGT	840
CAAATCGAAG	AAGCCAAGAA	AGATTTAGCA	GATTTAATTG	GTCAATACGG	TGTAGAGATT	900
ATTGCCATTG	GAAATGGAAC	GGCCAGTCGT	GAAAGTGAAG	CTTTTGTAGC	GGAAGTTCTG	960
AAAGATTTCC	CTGAAGTCAG	CTATGTTATC	GTTAATGAAA	GTGGTGCTTC	TGTCTATTCT	1020
GCCAGCGAAC	TTGCTCGTCA	GGAGTTTCCA	GCTTGACCG	TTGAAAAACG	CTCTGCCATT	1080
TCTATCGCCC	GTCGTTTGCA	AGATCCTCTT	GCCGAATTGG	TCAAAATCGA	TCCTAAGTCA	1140
ATTGGTGTCG	GTCAATACCA	ACACGATGTC	AGTCAGAAGA	AACTCTCTGA	GAGTCTGGAC	1200
TTTGTGTGTCG	ATACAGTGGT	TAACCAAGTT	GGTGTCATG	TCAATACAGC	TAGCCCAGCT	1260
CTTCTTTTAC	ACGTAGCTGG	ACTCAATAAA	ACCATTTCTG	AAAATATCGT	CAAATACCGT	1320
GAGGAAGAGG	GAAAAATCAC	TTCACGCTCC	CAAAATCAAGA	AAGTTCCTCG	TCTGGGAGCC	1380
AAGGCCTTTG	AGCAGGCTGC	TGGTTTCCTT	CGTATCCCTG	AAAGTAGCAA	TATCCTTGAT	1440
AATACAGGAG	TTCACCCAGA	GAATTACACT	GCAGTTAAGG	AACTCTTCAA	ACGTTTAGAT	1500
ATTAAAGACC	TAAACGAAGA	AGCCCAAAGC	AAACTCAAGT	CCCTTTCAGT	CAAGGAAATG	1560
GCTCAAGAGC	TAGACCTCGG	TCCAGAAACC	CTTAAAGATA	TCATTGCAGA	TCTTCTCAAA	1620
CCAGGTTCGAG	ATTTCCGTGA	TTCCTTTGAC	GCACCTGTGC	TTCCGCAAGA	TGTCCTAGAT	1680
ATCAAAGACC	TAGTGGTAGG	TCAGAAGCTA	GAAGGTGTTG	TGCGTAACGT	TGTTGACTTC	1740
GGTGCCTTCG	TTGATATCGG	GATTACAGAG	GACGGCTTGA	TTCATATTTT	TCATATGAGT	1800
CGCAAGTTTA	TCAAACACCC	TAGTCAAGTG	GTGTCAGTTG	GAGATTTGGT	GAGCGTTTGG	1860
GTTAAGCAAA	TTGATACTGA	ACGTGAAAAA	GTTAATCTGT	CTCTCCTAGC	TCCAAATGAA	1920

(2) INFORMATION FOR SEQ ID NO:2342:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 207 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...207
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2342:

CCGCAAGCTG TACTTGAGTA CGGTAAGACG ACGCTGACGT GGTTCGAAGA GATTTTCGAA	60
GAGTATAAGT CTCTACGGAC CAACCATTAT CCTGTAGTAA CAAAAAAGAA GTTGAGACAG	120
ACTGAACTCA ACTTCTTTTT TAGTGTCGTA TCAGCAATGT TAGTCCTGCA TCTGACGTTT	180
TACCTGATAA GGCAAATACA AGACTAG	207

(2) INFORMATION FOR SEQ ID NO:2343:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...195
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2343:

CAGAGAGCTG TGTTTTTGAT AAACAGTTGC TTGGGCCTAT TCACTGCGGC TGACTTTAAG	60
TCAGCACCCC TTCTCCCGAA GTTACGGGGT CATTTCGCCG AGTTCCTTAA CGAGAGTTCT	120
CTCGCTCACC TGAGGCTACT CGCCTCGACT ACCTGTGTCT GTTTGCGGTA CGGGTACAGT	180
ATGTTTAAAC GCTAG	195

(2) INFORMATION FOR SEQ ID NO:2344:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...198
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2344:

CAGAGAGCTG	TGTTTTTGAT	AAACAGTTGC	TTGGGCCTAT	TCACTGCGGC	TGACTTTAAG	60
TCAGCACCCC	TTCTCCCGAA	GTTACGGGGT	CATTTTGCCG	ATGTTTCCTTA	CATCGAGAGT	120
TCTCTCGCTC	ACCTGAGCTA	CTCGCCTCGA	CTACCTGTGT	CGGTTTGCCG	TACGGGTTAG	180
GTATGTTTAA	TACGCTAG					198

(2) INFORMATION FOR SEQ ID NO:2345:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 222 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...222
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2345:

AACTTTTATG	TGAAGAGTTT	GGGCATAAAC	TTTTACCTCT	TCTTCCCTAC	TCACCTGAGT	60
ACAATCCTAT	TGAGAAAACA	TGGGCTCATA	TCAAAAAGAA	CCTCAAAAAG	GTATTACCAC	120
GTTGCCATAC	CTTTTACGAG	GCTCTTTTGT	CCTGCTCTTG	TTTCAATTGA	CTATATTAGA	180
GGCGAGACAT	TTTTCGGTTC	TTTGTCAACT	GTAGTGGGTT	GA		222

(2) INFORMATION FOR SEQ ID NO:2346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2346:

ATTGAAGACT	TAAAAAATCA	AACCTATCCT	AAAGAGAATA	TTGAAATTCT	ATTTATAAAAT	60
GCTATGTCCA	CAGATGGGAC	CACAGCTATC	ATTCAGCAAT	TTATAAAGGA	AGATACAGAG	120
TTTAACTCAA	TTAGATTGTA	TAACAAATCCT	AAGAAAAATC	AAGCTAGTGG	TTTTAACCTG	180
GGAGTTAAAC	ATTCCTGTAGG	GGACCTTATT	TTAAAAATTG	ATGCTCATTTC	AAAAGTTACT	240
GAGAGTTTTG	TAATGAACAA	TGTGGCTATT	ATTCACAACAG	GTGAATTTGT	CTGTGGGGGG	300
CCTAGACCGA	CGATTGTCTGA	AGGAAAAGGA	AAATGGGCAG	AGACCTTGCA	TCTTGTTGAG	360
GAAAATATGT	TTGGAAAGTAG	TATTGCCAAT	TATCGAAATA	GTTCCGAGGA	TAGATATGTT	420
TCTTCTATTT	TTTCATGGGAT	GTATAAACGA	GAGGTTTTCC	AGAAGGTTGG	TTTAGTAAAT	480
GAGCAACTTG	GCCGAACTGA	AGATAATGAT	ATTCATTATA	GAATTCGAGA	ACATGGTTAT	540
AAAATCCGCT	ATAGCCCAAG	TATTCTATCT	TATCAGTATA	TTCGACCAAC	ATTCAAGAAA	600
ATGCTGCATC	AAAAGTATTC	AAATGGTTTG	TGGATTGGCT	TGACAAGTCA	TGTTTCAGTTT	660
AAGTGTTTAT	CATTATTTCA	CTATGTTCCCT	TGTTTATTTG	TTTTGAGTCT	TGTGTTTAGT	720
CTAGCATTGT	TACCGATCAC	ATTCGTATTC	ATAACTTTAC	TATTAGGTGC	CTATTTTCTA	780
CTTTTGTTCAT	TACTCACTTT	GCTGACTTTA	TTAAAAACATA	AAAATGGATT	TCTAATTGTG	840
ATGCCCTTTC	TTTTATTTTC	CATTCACTTT	GCTTATGGCC	TTGGGACGAT	TGTAGGTTTA	900
ATTAGAGGAT	TTAAATGGAA	GAAGGAGTAC	AAGAGAACAA	TAATTTATTT	GGATAAAATA	960
AGCCAAATAA	ATCAAAATAT	GCTACAATAA				990

(2) INFORMATION FOR SEQ ID NO:2347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2347:

GAGTATTATG	TTATGCTAAG	TAAAGAGGAT	TATACTGAAG	AAATCGGGCT	AATAAAGAAA	60
CAAAATTATG	TAGAGGCTGA	ATTGTATCCT	ATAGTTGCTG	ATATAATTAA	GCCAACTTTA	120
AAAGATAGTT	TATCAAAAAG	ATATGTCTTC	GGAAGACAAA	GAAGGGGTTT	GGGACAAATT	180
TATTATGGTC	TAAGTAATTT	TCCTGATATA	GTTATTTTAG	ATAAGACTTA	TGAAAACAAA	240
TCTAGGAAAA	GTATAAAAAT	TGAAGAATGG	AAGAACTTC	GAGGATGCGT	GGAAGTTAAG	300
AATTTAAATT	ATAGTTTAAT	TACAGAGGAA	AAAATCAAAT	CAACCATATC	GAACAGTTTT	360
GAACATATAA	CTGGAGAGAT	GGAACAAC TA	ACTGGAGAGA	TGGGACAAC T	TATTGGAGAC	420
CTTTTATGGT	ATAAAAAAGT	AATTTATACA	AATGGAATTG	AATGGAGATT	TCTAAGTTTA	480
GATGACAAGG	AAGAGATAGA	TAATACAATT	GTTGAAGTAG	TTAACAAAAG	AATAGAAAACA	540
GAAGAAGCGG	GAAATTCCTT	TGATTGGTGG	AAGAATATTA	AAGATTTATC	GTTCAATTAT	600
ACGGATATAT	GCCTATCTAA	AGATTGTAGA	CAAGAGTGGA	ATGAATTTGT	AAAAAGGGTA	660
AAGGAAATAG	AATGGTAG					678

(2) INFORMATION FOR SEQ ID NO:2348:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1131 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2348:

GGAAGAGACT	TTAGAGCATT	TTTTCATTCA	AGAGTGCGGA	ATGATTTGAA	ATATGGTATA	60
ATAAAAGGGA	ATTTCTACAG	AAAAGAGAAG	ATTATGTCAA	ATTTTGCCAT	TATTTTAGCA	120
GCGGGTAAAG	GGACTCGCAT	GAAATCTGAT	TTGCCAAAAG	TTTTCACAA	GGTTGCGGGT	180
ATTTCTATGT	TGGAACATGT	TTTCCGTAGT	GTGGGAGCTA	TCCAACCTGA	AAAGACAGTA	240
ACAGTTGTAG	GACACAAGGC	AGAATTGGTT	GAGGAGGTCT	TGGCTGGACA	GACAGAATTT	300
GTGACTCAAT	CTGAACAGTT	GGAACCTGGT	CATGCAGTTA	TGATGACAGA	ACCTATCTTA	360
GAAGGTGTGT	CAGGACACAC	CTTGGTCATT	GCAGGAGATA	CTCCTTTAAT	CACTGGTGAA	420
AGCTTGAAAA	ACTTGATTGA	TTTCCATATC	AATCATAAAA	ATGTGGCCAC	TATCTTGACT	480
GCTGAAACGG	ATAATCCTTT	TGGCTATGGA	CGAATTGTTC	GTAATGACAA	TGCTGAGGTT	540
CTTCGGTCAT	TGTTGAGCAG	AAGGATGCTA	CAGATTTTGA	AAAGCAAATC	AAGGAAATCA	600
ACACTGGTAA	CATACGTCTT	TGACAACGAG	CGTTTGTGTT	AGGCTTTGAA	AAATATCAAT	660
ACCAATAACG	CTCAAGGCGA	ATACTATATT	ACAGACGTCA	TTGGTATTTT	CCGTGAAACT	720

GGTGAAAAAG TTGGCGCTTA TACTTTGAAA GATTTTGATG AAAGTCTTGG GGTAATGAC	780
CGTGTGGCGC TTGCGACAGC TGAGTCAGTT ATGCGTCGTC GCATCAATCA TAAACACATG	840
GTCAACGGTG TTAGCTTTGT CAATCCAGAA GCAACTTATA TCGATATTGA TGTGAGATT	900
GCTCCGGAAG TTCAAATCGA AGCCAATGTT ATCTTGAAAG GGCAAACGAA AATTGGTGCT	960
GAGACTGTTT TGACAAACGG TACTTATGTA GTGGACAGCA CTATCGGAGC AGGAGCGGTC	1020
ATTACCAATT CTATGATTGA GGAAAGTAGT GTTGCAGACG GTGTGACAGT CGGTCCTTAT	1080
GCTCACATTC GTCCAAATTC AAGTCTGGGT GCCCAAGTT CATATTGGTA A	1131

(2) INFORMATION FOR SEQ ID NO:2349:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...237
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2349:

TATTCATATG TATGTGTCGT TCTAATTGTC ACTGCCTTCT TGATGATAGA GAGTATTTTA	60
GAATCCAGTT CTGGGGGGTA CAATTTATTT AGAGGAAACA GTAGTCCAGC TATTCCGTGT	120
TGGAATGATA AATTACTTAC GAAATTTCCA AATTCTGTTG AAGAAGTGAT CCTTCCTTCA	180
GAATTTACAG TTTTATCTAG TAAAATTGT AGAACACTAT TACATTCTGT TTTGTAA	237

(2) INFORMATION FOR SEQ ID NO:2350:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1488 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...1488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2350:

AAGGAGTATG	TTTTGAAAGA	GTTAGATCAA	AACCAAGCCC	CAATTTATGA	AGCCTTGGTG	60
AAGTTACGCA	AGAAAAGGAT	TGTTCCCTTT	GATGTTCCAG	GTCACAAGCG	TGGACGGGGA	120
AATCCAGAAC	TTGTCGAACT	CTTAGGAGAA	AAATGTGTAG	GCATTGATGT	CAATTCGATG	180
AAACCCTTGG	ATAATTTAGG	CCATCCTATT	TCGATTATTTC	GTGATGCAGA	GGAGCTGGCT	240
GCAGATGCTT	TTGGAGCTAG	CCATGCCTTT	CTAATGATTG	GTGGAACAAC	TTCATCGGTG	300
CAGACTATGA	TTCTGGCAAC	CTGCAAGGCA	GGAGATAAGA	TTATTCTGCC	ACGAAATGTC	360
CATAAATCTG	CTATCAATGC	GTTGGTTCTA	TGTGGTGCCA	TTCCCATCTA	TATCGAGATG	420
AGTGTAGATC	CTAAGATTGG	TATCGCTTTA	GGTCTTGAAA	ATGACCGAGT	AGCACAGGCC	480
ATAAAGGACC	ATCCAGATGC	TAAGGCTATC	CTAATCAACA	ATCCTACTTA	CTACGGCATC	540
TGTTTCAGACC	TAAAGGGGTT	GACAGAAATG	GCTCATGAAG	CTGGCATGAT	GGTTTTAGTA	600
GATGAAGCCC	ATGGAGCGCA	TTTGCATTTT	ACTGGTAAAC	TTCCAATTTT	TGCTATGGAT	660
GCAGGAGCTG	ATATGGCAGC	AGTTTCCATG	CATAAGTCTG	GTGGGAGTTT	GACACAAAGT	720
TCGCTTCTTT	TAATCGGGGA	GCAGATGAAT	CCCAGTACG	TTCGTCAGAT	TATAAACCTG	780
ACCCAGTCTA	CATCTGCCTC	TTACTTATTG	ATGGCTAGTT	TGGATATTTT	ACGTCGCAAC	840
TTGGCCCTTC	GTGGTAAAGA	GTCGTTTGAG	GAAGTCATTG	AGCTATCCGA	GTACGCTCGT	900
CATGAAATCA	ATGCCATTGG	CGGTTACTAT	GCTTACTCAA	AAGAGTTAAT	AGATGGTGTG	960
TCGGTCTGTG	ATTTTGATGT	AACCAAGTTG	TCAGTTTACA	CTCAGGGAAT	AGGCTTAACA	1020
GGTATCGAGG	TTTATGACCT	CTTGCGAGAC	GAATACGACA	TTCAGATCGA	GTTTGGTGAT	1080
ATCGGCAATA	TCTTGGCCCTA	TATTTCCATC	GGCGACCGCA	TCCAAGACAT	CGAGCGCTTG	1140
GTTGGTGCTC	TGGCTGATAT	TAAGAGACTC	TATTCACGAG	ATGGGAAGGA	CTTAATAGCT	1200
GGAGAATATA	TTCAGCCCGA	GTTGGTGCTG	TCTCCACAAG	AAGCCTTCTA	TTCAGAGAGA	1260
AAAAGTTTGA	CCTTAGATGA	GTCTGTTGGA	CAGGTCTGTG	GAGAATTTGT	CATGTGCTAT	1320
CCTCCAGGGA	TTCTATCTT	GGCTCCTGGT	GAACGCATTA	CACGAGAAAT	TGTAGACTAT	1380
ATCCAATTCTG	CCAAGGAACG	TGGTTGCTCC	CTCCAAGGGA	CGGAAGATCC	AGAGGTCAAT	1440
CATATCAACG	TTATTAAGAG	AAAGACAAAC	TATAAGAAAA	GTCAATAG		1488

(2) INFORMATION FOR SEQ ID NO:2351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2351:

AAGACGGACT	TTGCGCGCAT	TAAAATGACC	CTGTCCAATT	ATTTTTACAA	GGTCAAACAG	60
CAGTATCCTT	TGACAGAAAA	ACAGCAGGAG	CTCTATGACA	TTTTAGGAGA	TGTTAATCCT	120
GAGTATGCC	TCAAGTATAT	GACGGCTTTT	TTGTTGAAAT	TTCTCAAAAA	AGACCAGCTT	180

ATGCAGAAAT GCCGTGATAT CTTTGTGGAC AGTTTGGTTG TCTTAGGCTA TATTGTGCAA	240
AATGAAGATA GAAAGTATGA GTTGGCTATC GATTTTGATA AGGAGAGATT AACTTTCTAC	300
TTAGCGTGA	309

(2) INFORMATION FOR SEQ ID NO:2352:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...267
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2352:

TTGTATAATG TAATTACACC GTCGGTAATA GTGCTAGCAG ACCAAAATAA AGCAGATTGG	60
TCGTATGATG AAAATACTGT AATTAACATT TATGATGATG CTAATTTTGA AGATGGTAGG	120
TTGCATATGA CCTTTGAACA ATTCTTCAAA TTGGCACAAA TAGCTAGAGA AGAAGGTCTT	180
GAAATTCATT CTCCGTTTGA GAGAGCTGGT GCGACTAAAT CTGCTCGTTA TATAGCGAAA	240
TGGATTTTGA GAAATAAAAA ACATTAA	267

(2) INFORMATION FOR SEQ ID NO:2353:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1026 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1026
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2353:

AAAAATAATG	TTACATTTAT	ATCCGCAGAT	ATCTTTTCGAT	ACCAAATCTA	CATGAAAGGA	60
CGGGGTATGA	AACTTTCTCA	TTATTTAATT	GGCTTACTTC	TACTCCTAGT	CTTTCTCTCT	120
ATTAGCATTG	GGACCAGTGA	TTTTTCATGG	GGAAAGCTAT	TTGATTTCTGA	CCAGCAGACC	180
TGGCTCCTCT	TTCAAGAGTC	CCGTCTCCCA	AGAACTATCA	GTATTCTCCT	GA CTGCCCTCT	240
AGTATGAGTA	TGGCAGGCCT	TCTCATGCAG	ACTATTACCC	AAAATCAGTT	TGCTGCACCG	300
AGTACAGTTG	GAACGACTGA	AGCCGCCAAA	CTGGGAATGG	TGCTGAGCCT	TTTTGTCTTT	360
CCATCGGCTA	GTCTGACCCA	AAAGATGCTC	TTCGCTTTTG	TTTCATCCAT	CGTATTCCAC	420
CTCTTCTTCC	TAGCCTTTAT	GACCATTTTT	ACTGTAAAGG	AAAGGTGGAT	GTTGCCTCTG	480
ATTGGGATCA	TCTATAGCGG	GATTATCGGC	TCAGTCACAG	AAGTTATCGC	CTATCGTTTC	540
AATCTGGTTC	AGAGTATGAC	TGCCTGGACC	CAGGGCTCCT	TCTCCATGAT	TCAGACCCAT	600
CAGTATGAGT	GGCTCTTCTT	AGGCCTCATC	ATCCTGATAA	CCGTTTGGAA	ATTATCCCAA	660
ACCTTCACCA	TCATGAATCT	AGGGAAAGAA	ACCAGCGAGA	GTTTGGGGAT	TTCTACTTCC	720
CTACTTGAAA	AACTGGCCCT	CTTTCTGGTG	GCGCTAACGA	CAAGCGTCAC	CATGATTACC	780
GTGGGTGGCC	TACCATTCTT	CGGAGTTATC	GTTCCCAATC	TTGTTTCGCA	GTGCTATGGA	840
GATAATCTAA	GTCAAACCAA	ACTCATGGTC	GCACTGGTTG	GTGCCAATCT	AGTTCTGGCT	900
TGCGATATCC	TATCCCGAGT	TCTGATTAGG	CCCTATGAGT	TGTCTGTCAG	TCTCTTGCTA	960
GGAATCATCG	GTAGTCTCGT	CTTTATCCTA	CTTCTCTGGA	GAGGGGGACG	AAAAGATGCA	1020
GA CTAA						1026

(2) INFORMATION FOR SEQ ID NO:2354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2354:

GTTATAAATG	TAAGTAAGCA	TTATGGTCAT	TCAATCATTC	TCAAAGATAT	AAATTTTGCA	60
CTTAACAAGG	GTGAAATTGT	TGGTCTAGTA	GGGAGAAATG	GAGTTGGTAA	GAGTACGTTG	120
ATGAAAAATC	TTGTTTCAGAA	TAATCAACCG	ACTTCAGGTA	ATATTATAAG	CAGTGATAAT	180
ATTGGGTATT	TAATCGAAGA	ACCAAAATTA	TTTTTATCTA	AAACAGGTTT	AGAGAATTTA	240
AAATATTTGT	CAAAATTTATA	TGGTGTTGAC	TACAATCAAG	AAAGATTTAG	AAGTTTGATC	300
CAAGAGTTAG	ATTTGACTCA	GTCTATTAAT	AAAAAAGTAA	AGACCTATTC	TTTGGGTACA	360
AAACAAAAAT	TAGCTTTGCT	TCTAACTCTC	GTTACGAAAC	CTGATATATT	GATTTTAGAT	420
GAACCGACTA	ATGGTTTAGA	TATTGAATCA	TCACAAATAG	TTTTAGCGGT	TCTAAAAAAA	480
TTAGCTTTAA	ATGAAAACGT	GGGAATTTTA	ATATCGAGTC	ATAAATTAGA	AGACATTGAA	540
GAAATTTGTG	AGAGGGTTCT	TTTCTTGAG	AGCGGGCTTT	TGACATTTCA	AAAAGTAGGA	600
AAAGATAGTC	ATAATTTCTT	GTTTGAGATA	GCTTTTTTCAT	CAGCTACAGA	TAGAGACATT	660
TTCAATTACCA	AACAAGAATT	TGGGGATATT	GTTTCAGGAAG	AGGGACTGAG	AATTACTATG	720
TCTGGGAATA	TTCAAAGTAG	TGAGCTTTTT	AAATTTTTTTA	ACGAAAACTC	TATTAAAGTA	780
GTTGATTTTG	AAACTAAAAA	AGAGACGCTT	AAAGATATTT	ACTTAAATCG	TTCAAAATAA	840

(2) INFORMATION FOR SEQ ID NO:2355:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2355:

TTGACAAATG TAGATTTTGG AGGTATGGTA ATGCAGATTT CAGATGCAGA ATGGCAGGTC	60
ATGAAGATTA TTTGGATGCA GGGGGAGCAG ACCAGTACAG ATTTGATTAG GGTTTTGGCA	120
GAGCGGTTTCG ACTGGTCCAA GTCAACCATT CAAACTCTTT TGGCTCGTTT GGTTGAGAAA	180
GAGTGTCTGA CTCGGAAAAA AGAAGGCAAG TTCTTTGTTT ATTCAGCCCT TTTAACCTCTA	240
GACCAAAGTC GGGATTTACT TGTCCAAGAT ATCAAAGACA AGGTTTGTTT CCGTAGGATT	300
AGGAATTTGT TGGCTGACTT GATTGTAGAA TGTGAATTTA CTCAGACTGA CTTGGAAGAC	360
TTGGAAGCTG TGATTTTCTA GAAGAAATCA AGTGCTGTAA CAGAAGTAAG ATGTAATTGT	420
ATGTAA	426

(2) INFORMATION FOR SEQ ID NO:2356:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2356:

AAAGAAAATG TTATGTCTGA ACGTAGAATC TCTGAAAAGT CTCTTGAAAA TCTCAGAAAA	60
TCAAACCAAG AATCCAATTT ATTAACCAGA GAAGCCATTG AAACAGCCCT CTTGCAACTC	120

TTGGAAAAAA AGGAACTGAC CAAGATTAGT ATTTCTGAAT TGGTCAAACG TGCAGGTGTT	180
TCGCGTGCGG CCTTTTATCG CAATTATGAC TCCAAAGGAG GAATTTTAGA GAGGTCTTTA	240
AAAGAACTGT CCACAATATT ATGA	264

(2) INFORMATION FOR SEQ ID NO:2357:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...267
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2357:

ATGAAGAATG TAGAATTAAA GGAGAAAAAC ATGACATTTG AAGAGATCCT GCCTGGGTTA	60
AAGGCTAAGA GAAAATATGT ACGAACTGGT TGGGGAGGTG CGGAAAACTA TGTCCAACTC	120
TTTGATACCA TCGAGCAAAA TGGGCTTGCA CTTGAAATGA CACCTTATTT CCTAATCAAC	180
GTTTCTGGCG AAGGAGAAAG TTTTTCATG TGGAGCCCGA CAGTTTGTGA TGTTTTGGCA	240
ACGGATTGGG TAGAAGTGCA TGAATAA	267

(2) INFORMATION FOR SEQ ID NO:2358:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...282
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2358:

AACCGTGATG TGACGAGCAC CGATAGCCAT TCCTTTATCA TCATTGATAG TACGAAAGAA	60
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ATTCAAGACA TTGTTGTAAT TATCAAAGGG CTCACCGATT CCCATGACAA CGATATGGCT	120
GACGCGTTCA TCCTGACCAC GCTCAGCAAA GTATTTCTGA ACCAGCATGA TTTGCGCTAC	180
GATTTACCG TTATTGAGGT CACGTTGCTT CTTAATCAAA CCAGAGGCAC AGAAGGTACA	240
ACCGATATTA CAGCCGACCT GAGTGGTCAC ACAGACAGAT AA	282

(2) INFORMATION FOR SEQ ID NO:2359:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...357
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2359:

ACAAGAGATG TTGACTTAAT GAATACCATA GAGCGGACTA GGCGGCTGGT TAAAGGCTGT	60
GCAACACACT GTTTTGAGGT TGCAGATAGA ACTGACGAAG TCAGCTCAAA GCACTGCTTT	120
GAGGTTGTAG ATAGAACTGA CGAAGTCAGC TCAAAGCACT GCTTTGAGGT TGCAGATGAA	180
ACTGACGAAG TCAGCTCAAA ACATGTTTTT GAGGTTGTGG ATGAAACTGA CGAAGTCAGC	240
TCAAAACATG TTTTGAGGT TGTGGATGAA ACTGACGAAG TCAGCTCAAA ACATGTTTTT	300
GAGGTTGTGG ATGAAACTGA CGAAGTCAGT AACCATACAT ACGGTAAGGC GACGTGA	357

(2) INFORMATION FOR SEQ ID NO:2360:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 516 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...516
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2360:

AACTCTTG	TGAAGAGTTT	GGGTATAAAC	TTTTACCTCT	TCCTCCCTAC	TCACCTGAGT	60
ACAATCCTAT	TGAGAAAAACA	TGGGCTCATA	TCAAAAAGCA	CCTCAAAAGG	GTATTACCAA	120
GTTGCAATAC	CTTTTATGAG	GCTCTTTTGT	CTTGTTCTTG	TTTCAATTGA	CTATATAAAT	180
TGTCTAAGCG	AAACAACCGA	TAAGAATTGG	CACAAAAGCG	ACCGTGTTTT	TGTTACCAAT	240
ACAGGAAAAA	CAGTTCATAG	TTCTATCTTG	AGCAAGTCTC	TCCAGCGAGC	AAACGAACGC	300
CTTAAAAAAC	CAATTCCCAA	ACATCTGTCC	CCTCACATCT	TCAGACACAC	CACTATTAGC	360
ATCTTATCAG	AAAATAAAAT	TCCTTTAAAA	ACAATCACGG	ACAGGGTTGG	TCATTCCGAC	420
TCTGAAGTCA	CTACTTCCAT	CTACACCCAC	GTCACAAAGA	ACATGAAAGA	TGAAGCAATC	480
AATGTACTGG	ATAAAGTTAT	GAAAAAGATT	TTTTTAA			516

(2) INFORMATION FOR SEQ ID NO:2361:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...303
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2361:

GGAAGNCGTG	TCCTTTTCTA	CAATCCTGCC	AAGTCAACAG	TCAATGAGGA	AGACTATTTG	60
ACTGTTATTC	CTCACCTGCC	TAAAAAAGGA	TTTTCCCGTG	ATTTTTTTAGC	TTATTTTTCG	120
CTTTTCCTTA	AAGATACTGC	TGAGGTTGGG	CTAGATGTCC	TCATGGACTT	TTTGGAAGAC	180
CCAGAAGCAG	AGGAATTTGT	CATGGAATGG	AACCAAGAAG	TCTTAGAAGA	AGGAAAAGTT	240
GGCTTGGAAG	AGGGAGAAAT	TACCCCTTATC	CGAGATACTA	GGAGTTGGTT	GGAGGTGTTA	300
TGA						303

(2) INFORMATION FOR SEQ ID NO:2362:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 897 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2362:

ATGGAAAGTG	TCGGAGATGT	ACTCAAACGT	CAACCAAGTC	GTTTTTCACTA	TCAAGATTTA	60
GTTTCAGAAAA	TCATGAAGGA	TCCTGATGTT	GCGGCCTTTG	TCCAGCAAGA	ATCCCTCAAT	120
CAGGACGAGT	TGAACCGTAG	TATTTCCAAG	TTTAACCAAT	ACATCACTGA	GAGAGATAAA	180
TTCTTCCGAG	GAGATACAGA	TTATATTGCC	AAAGGCTACA	AGCCTATATT	AGTCATGAAC	240
CATGGCTATG	CGGATGTTTC	TTATGAAGAA	ACTCCTGAAC	TAATCGCAGC	TGAAAAAGAA	300
GCGGCTATCA	AGAAACGTCT	CAACTTAATT	AATTTTCCAT	CTAGCCTGAA	AAATGTCAGT	360
TTTTTTAGATG	TTTATCGTGA	TGATGTTTCA	CGCTTAACTG	TTCTAAAAAG	AATGATAGAA	420
TTTGTTAACG	ATTACCCCAA	TAATTTGAAA	GGTCTTTACT	TGTATGGAGA	CTTTGGTGTG	480
GGTAAAAGTT	TCATGGTGGC	TGCCCTAGCT	CATGATTTAT	CAGAAAAACG	TGGTGTATCA	540
TCCACTCTCC	TCCACTATCC	TAGCTTTGTC	ATTGATGTCA	AAAATGCTAT	CAGTGATGGC	600
AATGTTAAGA	CCTTAGTGGA	TGAGATTAAG	CTTTCTGAAG	TCCTGATTTT	AGATGATATT	660
GGTGCCGAGC	AATCCACCAC	TTGGGTGCGT	GATGAAATCC	TGCAGGTCAT	TCTCCAATAT	720
CGGATGCAGG	AAAATTTTACC	GACCTTTTTTC	ACCTCTAACT	TCAACTTTGA	AGATTTGGAG	780
AAGCATTTTCG	CTAAAGGGAA	AAATGGAAAT	GACGAAACCT	GGGAAGCCAG	ACGCGTCATG	840
GAACGCATCC	GTTATTTGGC	TGAGGAGACT	CGTTTAGAAG	GAGTAAACCG	TCGATGA	897

(2) INFORMATION FOR SEQ ID NO:2363:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 609 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2363:

GAGCGAGGTG	TGTTCTTAGC	TGTTGACAAT	GAAATCAAAG	GCTTGCTTGC	TTTGCAAGAT	60
ATTCCTAAGG	AAAATGCTAA	GCTAGCCATC	AGTCAGCTAA	AAAAACGTGG	TCTCCGAACA	120
GTCATGCTGA	CAGGAGACAA	TGCTGGTGTG	GCGTGTGCTA	TTGCAGATCA	AATCGGAATT	180
GAAGAGGTCA	TTGCAGGCGT	CTTGCCAGAA	GAAAAAGCCC	ATGAAATCCA	TAAACTGCAA	240
CAGTCAGGGA	AAGTAGCCTT	TGTTGGGGAC	GGTATCAATG	ACGCTCCTGC	CCTTAGTGTA	300
GCAGATGTGG	GGATTGCTAT	GGGAGCTGGA	ACAGATATCG	CCATCGAGTC	AGCAGATTTG	360
GTGTTGACAA	CCAATAATCT	TTTAGGAGTG	GTTTCGTGCCT	TTGATATGAG	TAAGAAAACC	420
TTTCATCGAA	TTCTACTCAA	TCTTTTCTGG	GCTTTTATCT	ACAATGTTGT	CGGAATTCCG	480
ATTGCAGCAG	GAGTCTTTTC	AGGTGTTGGA	CTGGCTCTCA	ACCCAGAATT	GGCAGGTCTA	540
GCCATGGCCT	TTAGTTCTGT	ATCTGTTCTG	ACCAGTTCCT	TTCTGTTAAA	TTTTAGTAAA	600
ATAGACTAA						609

(2) INFORMATION FOR SEQ ID NO:2364:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 456 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...456
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2364:

ATTGGAGGTG	TTATGAAAGA	TAGTCATTTG	CTAGCCCATC	ATATTCGTTT	GTTGAATGGG	60
CGGATTTTTC	AAAAGTTACT	GAGTCAAGAT	CCTGAGGCTC	TTTATAGGGG	TGAACAGGGC	120
AAGATTTTAT	CGGTTTATG	GAATAGTGAA	ACTGGCTGCG	CAACTGCGAC	AGATATCGCG	180
CTTGCGACTG	GGCTTGCGAA	TAATACGCTG	ACGACTATGA	TAAAAAAGCT	AGAGGAACAA	240
AAGCTTGTA	TTGTTAGTCC	GTGTGGAAAA	GACAAGCGTA	AGAAGTATTT	AGTTTTAACG	300
GAGTTAGGCA	AGTCCCAGAA	AGAAGTGGGG	CATCGTGTCA	GTCAGAAATT	GGATACTATC	360
TTTTACAAAG	GATTTTCAGA	GGAAGAAATT	CACCAATTTG	AAGGTTTTC	AGAAAGAATT	420
TTGGCGAATC	TGAAAGAGAA	GGGAAATGAG	GTTTAG			456

(2) INFORMATION FOR SEQ ID NO:2365:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...201
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2365:

TTGGATTTCG TCAATCAAGT CTTGTGTTTG TTCCCTCATA TTGCTATAAC TTCTGAGGAC	60
TCGTTTGGTC AGTGGACTAT GCTTGGAGAC TTGGTTGGCT TGATTTTCTG CCTGATGTTG	120
GTATTGGAAA ATAAATTCTC GGTAGCCAGT AAAGCCACAC TTTT TAGCAA AGCGGGTCAA	180
AGCAGCTTGA GAAATATGTA A	201

(2) INFORMATION FOR SEQ ID NO:2366:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...228
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2366:

GCTGACTTCG TCAGTTTTAT CGACAACCTC AAACACTGCT TTGAGCAACC TGCGGCTAAC	60
TTCTAGTTT GCTCTTTGAT TTTCATTGAG TATGACTTTA GCGGTTGTCA ATTTTCTCTG	120
GATAAACGTC GTGTTGGAAA ACGCGTTGTT CTGCCAAGNC CTCATACTTA TTTCCTTGCT	180
TACCGTAATT GTAATAGGGG TCGATTGACA TGCCACCGCG CGGAATAA	228

(2) INFORMATION FOR SEQ ID NO:2367:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 786 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...786
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2367:

AGGAGATTCG TTATGAAGAA TAATCGTATT TTAGCACTTT CTGGAAATGA TATTTTTAGT	60
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GGTGGTGGAC	TGTCAGCTGA	TTTGGCTACC	TATACCTTGA	ACGGCTTGCA	TGGGTTTGTA	120
GCAGTGACTT	GTTTGACAGC	CTTGACAGAA	AAAGGATTTG	AAGTCTTTCC	AACTGATGAT	180
ACCATTTTTT	AACATGAATT	AGATAGCTTG	CGTGATGTGG	AATTTGGGGG	AATTAAGATT	240
GGTCTTCTCC	CTACTGTCAG	TGTGGCTGAG	AAGGCCTTGG	ACTTTATCAA	ACAACGCCCA	300
GGAGTACCTG	TGGTGTGGA	TCCTGTCTTG	GTCTGCAAGG	AAACGCATGA	TGTAGCTGTC	360
AGTGAGCTCT	GCCAAGAGTT	GATTCGCTTC	TTCCCTTATG	TCAGTGTGAT	TACGCCTAAT	420
CTCCCAGAAG	CAGAATTATT	ATCCGGTCAG	GAAATTAAAA	CCTTGGAAGA	CATGAAAAC	480
GCAGCGCAGA	AATGTCATGA	TTTAGGAGCG	CCAGCAGTCA	TTATCAAGGG	AGGCAATCGT	540
CTTAGTCAGG	ACAAGGCTGT	GGATGTCCTT	TATGATGGAC	AGACCTTTAC	TATCCTAGAA	600
AATCCAGTTA	TCCAAGGCCA	AAATGCTGGT	GCAGGTTGTA	CCTTTGCCCT	TAGCATTGCC	660
AGTCACCTGG	TTAAAGGTGA	TAAATTTTTG	CCAGCAGTAG	AAAGCTCTAA	GGCTTTCGTT	720
TATCGTGCTA	TTGCACAAAG	AGATCAGTAT	GGAGTAAGAC	AATATGAAGC	AAACAAAAAC	780
AACTAA						786

(2) INFORMATION FOR SEQ ID NO:2368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2368:

TTTAAGTTCG	TCCTATTTGT	AAAACAAATG	AAACAATTTT	AACTAAGGAG	GAGAAAACAA	60
ATGGAACCTG	TATTACCAAA	TAATTATGTT	GTGATTGATG	AAGAAGAAAT	GATGTATCTT	120
GATGGGGGAG	CTTATTTAAG	CAAGCGTGCT	TGTCAAGGAA	TTTGCGTAGC	TTTAGCTATG	180
AGTTCAGGAA	CTTTTATAGC	ATTAGCTGGA	GCTGCAGTTT	TAACCAAAAA	ACTAATAAAC	240
TATATTAAGG	TTGGAAGCTT	TGGAGGCTGG	CTTATTGGTG	CAGCAGCAGG	TGTATTGGCT	300
GGGGCGGCAG	GAAGAATAGC	TTACTGTATT	GGATATGGTA	CTCTTAATAG	AGATTGTGAT	360
ATTAGCGGGA	ACCCTTATCC	TTGGGATGGA	TTCATATCTG	CGACAGTAAG	ATGA	414

(2) INFORMATION FOR SEQ ID NO:2369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2369:

ATATTTCTCG	TAAGGAACAG	GTGTTACCAA	TGGTACCGGC	TGGTAAGAGT	AATCATGAGA	60
TGTTGGGGGT	GCA GTTCCAT	GCGTAGAATG	TTAACAGCAA	AACTACAAAA	TCGTT CAGGA	120
GTCCTCAATC	GCTTTACAGG	TGTCCTATCT	CGTCGTCAGG	TTAATATTGA	AAGCATCTCT	180
GTTGGAGCAA	CAGAAGATCC	GAATGTATCG	CGTATCACTA	TTATTATTGA	TGTTGCTTCT	240
CATGATGAAG	TGGAGCAAAT	CATCAAACAG	CTCAATCGTC	AGATTGATGT	GATTTCGCATT	300
CGAGATATTA	CAGACAAGCC	TCATTTGGAG	CGCGAGGTGA	TTTTGGTTAA	GATGTCAGCG	360
CCAGCTGAGA	AGAGAGCTGA	GATTTTAGCG	ATTATTCAAC	CTTTCCGTGC	AACAGTGGTA	420
GACGTAGCGC	CAAGCTCGAT	TACCATT CAG	ATGACGGGAA	ATGCAGAAAA	GAGCGAAGCC	480
CTATTGCGAG	TCATT CGCCC	ATACGGTATT	CGCAATATTG	CTCGAACGGG	TGCAACTGGA	540
TTTACCCGCG	ATTAA					555

(2) INFORMATION FOR SEQ ID NO:2370:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2370:

AATCCACTCG	TTGCCCCTGT	TACTCCTGCC	CAAAGAGCCA	CACCAAATTT	AGCTCCTATG	60
TATCCACATG	CTCCCATAAA	TGGCGCTCCA	ACACCACTCG	CAGCACAAAT	AGCTGTCCCT	120
AACCCCCAGC	CACCAAAAAGC	AGCACCACCA	CCTTCTAAGA	CATTAGTTTG	CCAATTATTC	180
TTGCCTCCTT	CAATACTAGA	TAACATAGTT	ATATCCATTT	CATGA		225

(2) INFORMATION FOR SEQ ID NO:2371:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 699 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...699

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2371:

CAACCACTCG	TCTGGTTAAG	GAGCAAGGGC	ATTTTGCAGG	GCATAATTTG	TTTGCGGATG	60
GAGCCATTAC	CATCCAAGAC	GAGTCCAGTC	AGCTGGTTGC	TCCGACGCTT	GATTTACAAG	120
GTGATGAGCG	AGTGCTTGAT	CCTGTGCGGC	TCCAGGTGGA	AAACAGCCCA	TATAGCCTCT	180
TATCTTACGA	CAGGTCAGGT	TACTGCTCTG	GACTTGACG	ACCACAAGTT	GGATTTAATT	240
CAAGAAAATG	CCCAACGTC	GGGAGTTGCA	GATCGGGTTC	AAACTCAAAA	ATTGGATGCC	300
AGAAAGGTGC	ATGAGTTTTT	TGACCAGGAT	TCCTTTGATA	AGATTTTGTT	GGATGCTCCT	360
TGTTTCAGGAA	TCGGTCTTTT	GCGCCGAAAA	CCAGATATCA	AATACAATAA	AGAAACGGCA	420
GATTTTCGCGT	CCTTGCAGGA	AATTCAGTTA	GAAATATTAG	GTAGTGTTTG	TCAAATACTA	480
GGCAAAGGTG	GTATAATAAC	TTATAGCACC	TGCACTATCG	TCTCAGAGGA	GAATTTTCAA	540
GTCGTTAAGG	CCTTTTTAGA	GAGTCATCCC	GAGTTCGAGC	AGGTAAACT	AGAACATGAA	600
TGTAAGGATA	TCATGAAAGA	CGGCTGTATC	CTCATTACAC	CTGAATTGTA	TGGAAGTGAT	660
GGATTCTTCA	TCAGTCAATT	TCGCAAGATA	TCGGATTAG			699

(2) INFORMATION FOR SEQ ID NO:2372:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 435 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2372:

GGGGCACTCG	TGGTGACGAG	GCATGGACAT	TTTGCTACAG	GGATTTATAG	TTCTTTACAA	60
TTGATTGCAG	GCAATCAAGA	AAATGTGGAG	GCGATTGACT	TTGTGGAAGG	AATGTCAGCA	120

GATGAACTCA	AGCAAAAAAT	CTTACTTGCA	ATTTCAAATG	AAGAAGAAGT	TTTAATCCTA	180
AGTGATCTCT	TGGGAGGATC	GCCATTCAAG	GTTTCTTCTA	CCATAATGGG	AGAAAAATCCA	240
GCCAAAACAA	TGAATGTTCT	CTCGGGTTTG	AACTTAGCCA	TGTTAATGGA	AGCAGTCTTT	300
GCTAGAATGG	CTCATAGCTT	TGATGAAGTT	GTTAATAAAT	CAGTAGTGGC	GGCCCAGGGC	360
GGAGTCGTAA	ATGGTAAAGA	ATTGTTTTCA	ACGGATGCAG	AGGAAGAGGA	AGAAGATTTC	420
GAATCGGGTA	TTTAA					435

(2) INFORMATION FOR SEQ ID NO:2373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2013 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2373:

GCGCAACTCG	TGGTGAAGAC	GCGATGGCTA	AAAAGATCTT	CTAATGCAAT	TACTAATGAT	60
TTAGATAATT	CACCAACTGT	TAATCAGAAT	CGTTCTGCTG	AAATGATTGC	CTCTAATTCA	120
ACCACTAATG	GTTTAGATAA	TTCGTTAAGT	GTTAATAGTA	TCAGCTCTAA	TGGTACTATT	180
CGTTCCAAAT	CACAAATTAGA	CAACAGAACA	GTTGAATCTA	CAGTAACATC	TACTAATGAA	240
AATAAGAGTT	ATAAGGAAGA	TGTTATAAGT	GACAGAAATTA	TCAAAAAAGA	ATTTGAAGAT	300
ACTGCTTTTAA	GTGTAAAAGA	TTATGGTGCG	GTAGGTGATG	GGATTTCATGA	TGATCGACAA	360
GCAATTCAAG	ATGCAATAGA	TGCTGCAGCT	CAAGGGCTAG	GTGGAGGAAA	TGTATATTTT	420
CCTGAAGGAA	CTTATTTAGT	AAAAGAAAT	GTTTTTTTAA	AAAGTCATAC	ACACTTAGAA	480
TTGAATGAGA	AAGCTACAAT	TCTAAATGGT	ATAAATATTA	AGAATCACCC	TTCCATTGTT	540
TTTATGACAG	GTTTATTTAC	GGATGATGGT	GCGCAAGTAG	AATGGGGCCC	AACAGAAGAT	600
ATTAGTTATT	CTGGTGGTAC	GATTGATATG	AACGGTGCTT	TGAATGAAGA	AGGAACATAA	660
GCAAAAAATC	TACCACTTAT	AAATCTTCA	GGTGCAATTTG	CTATTGGGAA	TTCAAATAAC	720
GTAACATAAA	AAAATGTAAC	ATTCAAGGAT	AGTTATCAAG	GGCATGCTAT	TCAAATTGCA	780
GGTTCGAAAA	ATGTATTAGT	TGATAATTCT	CGTTTTCTTG	GGCAAGCCTT	ACCCAAAACG	840
ATGAAGGATG	GGCAAATCAT	AAGTAAGGAG	AGCATTTCAGA	TTGAACCATT	AACTAGAAAA	900
GGTTTTCCCT	ATGCCCTTGA	TGATGATGGG	AAAAAATCTG	AAAATGTGAC	TATTCAAAAAT	960
TCCTATTTTG	GCAAAAGTGA	TAAATCTGGG	GAATTAGTAA	CAGCAATTGG	CACACACTAT	1020
CAAACATTGT	CGACACAGAA	CCCCTCTAAT	ATTAAAAATTT	TAAATAATCA	TTTTTGATAAC	1080
ATGATGTATG	CAGGTGTACG	TTTTACAGGA	TTCCTGATG	TATTAATCAA	AGGAAATCGC	1140
TTTGATAAGA	AAGTTAAAGG	AGAGAGTGTA	CATTATCGAG	AAAGCGGAGC	AGCTTTAGTA	1200
AATGCTTATA	GCTATAAAAA	CACTAAAGAC	CTATTAGATT	TAAATAAACA	GGTGGTTATC	1260
GCCGAAAATA	TATTTAATAT	TGCCGATCCT	AAAACAAAAG	CGATACGAGT	TGCAAAAGAT	1320
AGTGCAGAAAT	ATTTAGGAAA	AGTATCAGAT	ATTACTGTAA	CAAAAAATGT	AATTAATAAT	1380
AATTCCTAAGG	AAACAGAACA	ACCAAATATT	GAATTAATTAC	GAGTTAGTGA	TAATTTAGTA	1440
GTCTCAGAGA	ATAGTATATT	CGGGGGTAAA	GAAGGAATTG	TTATTGAGGA	TTCAAAGGGT	1500
AAAATAACCG	TTTTAAATAA	CCAATTTTAT	AATTTATCCG	GTAAGTATAT	ATCATTCATC	1560
AAATCTAATG	CAAAATGGGAA	AGAACCTGTT	ATACGTGATA	GCGATGGTAA	TTTCAATATT	1620

GTAACGGAGA	ATGGGCTTTA	CAAAATTGTA	ACAAATAATT	TAAGTGATAA	AAACGAAAAA	1680
GAAAAAACA	AAGAGGAAAA	ACAATATAAT	TCAAATAATG	TAATTGATAG	TAACCAGAAG	1740
AACGGAGAGT	TTAACTCAAG	TAAAGATAAT	AGACAAATGA	ATGACAAGAT	CGACAATAAA	1800
CAAGATAATA	AGACAGAAGA	AGTAACTAT	AAAATAGTTG	GAGATGGCAG	AGAAACTGAA	1860
AATCATATTA	ATAAATCTAA	AGAAATAGTA	GATGTAAAC	AAAAATTACC	AAAGAGAGGT	1920
TCGTACAAGA	TTATGGAACT	ATTTTAAACA	GTGACAGGAA	TTGGTTTACT	TTTGACACTA	1980
AAAGGGTTGA	AGTATTATGG	TAAAGATAAA	TAA			2013

(2) INFORMATION FOR SEQ ID NO:2374:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...375
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2374:

ATGGAAC	TCG	TATTAC	CAAA	TAATTAT	GTT	GTTCTTG	GAGC	AAGAAG	GAT	GATATCTT	60
GATGGGG	GAT	TTTCTAT	TCC	GAGATGG	CCT	GTTGCA	CAG	CCATTAA	TAT	AGCTTTTAAT	120
GGTGTTTT	AG	GTGGAGG	AGC	AATCAGT	CTA	GTTAGAA	ATT	ATATTCG	TAA	TTATGGTTTG	180
CGGCGAG	TTA	CAAGCG	CAAT	TGCTGG	GAGCA	GCTGCA	AGAT	ATGTTGG	GGGT	ACGAGTTGCA	240
AATAGAG	TGG	CAGGAT	TTTGC	ACTGTCT	GTCT	ATTAAT	GGAT	TTGCAG	CTTG	GATGTCAATT	300
GGCGATG	CTA	TTACAACA	AT	CTGGG	CCAAC	AATGAT	GTA	ATAGGAG	GAGA	CCCAAATTTA	360
AACGCCT	TGT	GGTAA									375

(2) INFORMATION FOR SEQ ID NO:2375:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2375:

AGGGAAC	TCG	TATTACCAAA	TAATTATGTT	GCTCTTGAGC	AAGAGGAGAT	GATGTATCTT	60
GATGGGG	GGGG	GTTATTTAAG	CAAGAGTGCT	TGTCAAGGAA	TTTGCGCAGC	TTTAGCTATG	120
AGTCCAG	GAA	CTTTTATAGC	ATTGACTGGA	GCTGCAGTTT	TAACAAAAAA	ACTAATAAAC	180
TATATTA	AAG	TTGGAGGCC	CTTGAGGTTG	CTTATTGGTG	CAGCAGCAGG	TGTATTGGCT	240
CTTATCT	TTTT	TGATAAAAA	TTGTGTAGAT	ACTACGATAA	AGGTTCTATT	AAACAGAATC	300
TTTAAGG	CAA	GTAAGGTAAT	GAAAAGGAGG	ATATTTTCTC	TTTTTTGTACT	AGATTTGATG	360
GTCTATA	TAT	TTTTAGGTTA	TGTTTTAGTG	ATACAAAAAG	ACGTATATCT	GTTTTCAATT	420
CTGATAA	TTT	TTTCTAATTT	TTCAGTTCCC	TTTATCAGAG	AAAAAGAGTA	TGAATTATTT	480
AAAAATA	AAGA	AATGA					495

(2) INFORMATION FOR SEQ ID NO:2376:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 592 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2376:

CGCGCTC	GTG	AAGCTAG	TAAAAGCCTC	NNTGGATGGA	CAGTTGGAAG	AAAAAGGAAA	60
TTTGACAG	AT	AAAATCAAGA	GTCTGTCAAA	AGGAGGTCAG	CAGAAGATTC	AGCTCATTAT	120
TACTCTGA	TT	CATGAACCAG	ACCTGATTAT	CTTGGATGAG	CCTTTTAGTG	GATTGGACCC	180
AGTTAATA	CA	GAATTGCTCA	AACAAGTCAT	TTTTCAGGAA	AAAGAGCGCG	GAGCAACCAT	240
TATCTTTT	CT	GACCATGTCA	TGACCAATGT	TGAGGAACCT	TGTGACGATA	TTCTGATGAT	300
CCGAGATG	GC	CGTGTGGTCT	TGCACGGACC	AGTTCAGGAT	GTCCGCAATC	AATACGGGAA	360
AACGCGTC	CTC	TTTGTTTCAA	GTGAACGAAG	CAAGGAAGAA	TTGGAAAATC	TTCTCATGT	420
CAAACAGG	TG	AGCTTGACCA	AACAAGGTAG	TTGGAAATTG	ATTTTGGAGG	ATGAGAGCGC	480
TGGAAGGG	AA	CTCTTCCCAA	TCTTGACTCA	AGGTCAATAT	ATCGCAACAT	TTGACCAACA	540
AGCGCCAA	CT	ATCGATGAAA	TCTTTAAACT	AGAATCAGGA	GTGGAAGTAT	GA	592

(2) INFORMATION FOR SEQ ID NO:2377:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 750 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...750
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2377:

TCTACCTGCT TTTCTTTTTA TTGCTTCAAA CCAGTCTATT TTTATAAAGG AGTTATTATG	60
GAATTTACAG ATATTGCGAT GGAATTATCC AAGAAAGCTT GGCAGGCTTC CTTTCATCAT	120
CCCTTTATTT TACAATTACA AGAGGGGAAT TTAGAACCTG CCATTTTCCG CTATTACCTG	180
ATTCAGGATG CCTACTATCT GAAGGCCCTT TCAGAAATCT ATCATCTTTT GGCTGATAAG	240
ACTTCAAACC AAGAGATGAA AAGACTCTTG AAACAAAATG CTCAGGGTTT AGTGGAGGGT	300
GAGTTATTTA TTCGCCAACA ATTTTTC AAG GAAATGGAAA TCAGCGACCA GGAAATGGAG	360
CAACATCCAA TTGCTCCAAC CTGTTATCAT TACATTTCTC ATATTTATAG GCAATTTGCA	420
GAACCGAACT TAGCCATCGC TTTTGCAAGC TTGCTTCCTT GTCCTTGGTT ATACCATGAT	480
ATAGGCAAAT CACTTAATCT TAAACCATCA CCAAATCCTC TCTATCAACA ATGGATTGAA	540
ACTTATATTA CGGATGAGTT AGAGCAACAG ATCAGAGAGG AGGGAGCACT GGTCAATCAG	600
CTCTATCGAG AAAGTGATGA GACAGATAAG CAAAAAATGC TAGATGCCTT CCACATCAGT	660
GTTCATATGG AAGCCAAGTT TTGGGAGATG GCTTACCAAC ACCAGACATG GAAGAGCGAT	720
TTACAGTCTT TAGAAAAAAG AGAAGAATAG	750

(2) INFORMATION FOR SEQ ID NO:2378:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1128 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1128
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2378:

ATTCTATGCT TCTATCTATT TATTCGGAAA AGAAGGCTTT TCTTCAGAAG AAAGCTAATA	60
GCTTATTTGA AATTTTCTCC TCTCTGTTGG ATAGTCCCGT CTATCTATGT TATAATGAAA	120
GAAGGATTTA AAATCGGAAA AGGAGTATTT ATGCTAAAAT TAGGTGTCAT CGGAACTGGC	180
GCTATCAGCC ATCATTTTCAT AGAAGCAGCC CATACCAGTG GAGAATACCA ACTGGTCGCA	240

ATCTATTCTA	GAAAACTAGA	AACTGCAGCA	ACCTTTGCTT	CTCGCTATCA	GAATATCCAA	300
CTATTTCGATC	AATTAGAAGT	CTTCTTCAAA	TCTTCTTTTG	ATTTAGTCTA	TATCGCCAGT	360
CCAAACTCCT	TACATTTTGC	TCAGGCAAAA	GCTGCCCTGT	CTGCTGGTAA	ACATGTTATT	420
CTCGAAAAAC	CAGCTGTCAC	TCAACCACAA	GAATGGTTTG	ATTTGATTCA	AACAGCTGAA	480
AAAAATAACT	GTTTTATCTT	TGAAGCAGCT	CGTAATTACC	ACGAGAAAGC	CTTTACTACT	540
ATCAAAAAC	TTTTAGCAGA	TAAGCAAGTG	TTAGGAGCAG	ATTTCAACTA	TGCCAAATAC	600
TCTTCCAAGA	TGCCTGACTT	GTTGACTGGA	CAAACACCAA	ATGCTCTTTC	AGACCGTTTT	660
GCTGGTGGAG	CCCTCATGGA	TTTGGGGATT	TATCCCCTCT	ATGCTGCTGT	TCGTCTTTTT	720
GGAAAAGCCA	ATGACGCGAC	TTACCATGCT	CAACAGCTTG	ACAATAGCAT	TGACCTAAAT	780
GGAGATGGTA	TCCTCTTCTA	CCCAGACTAT	CAAGTTCACA	TCAAGGCTGG	AAAAAACATC	840
ACTTCCAATC	TTCTTTGCGA	GATTTATACA	ACAGATGGAA	CCTTGACTCT	CAACACGATT	900
GAGCATATTC	GCTCAGCTAT	TTTTACCGAC	CACCAAGGAA	ATCAAGTCCA	GCTTCCTATC	960
CAACAGACTC	ATCATACGAT	GACTGAGGAA	GTCGCTGCAT	TTGCACACAT	GATCCAGCAA	1020
CCAGATCTGA	ATCTCTACCA	AACTTGGCTG	GATGATGCAG	GCTCTGTTCA	TGAGCTACTA	1080
TATACCATGC	GCCAGACTGC	TGGTATTAGA	TTTGAGGCAG	AAAAATGA		1128

(2) INFORMATION FOR SEQ ID NO:2379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1110 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2379:

GGAGAATGCT	TAATGCTTGA	AAGACTGAAA	AGCATACATT	ATATGTTTTG	GATCAGTTTA	60
ATTTTTATGG	TTTTCCCCAT	CCTAACTGTA	GTGACTGGGT	GGCTTTCGTC	CTGGCATTTA	120
TTGATTGATA	TTCTATTTGT	AGTGGCGTAT	TTGGGTGTTT	TAACAACTAA	GAGCCAGCGT	180
CTATCTTGGC	TATATTGGGG	CATCCTGCTG	ACTTATGTAG	TTGGGAATAC	TGCCCTTTGTG	240
GCTGTTAATT	ATATCTGGTT	TTTCTTTTTT	CTATCCAATC	TCTTAAGCTA	TCATTTTCAGC	300
GTAGGTGGTT	TAAAGTCTTT	ACATGTCTGG	ACTTTTCTTC	TTGCTCAAGT	CCTTGTTGTG	360
GGTCAACTGT	TGATTTTTCA	GAGAATCGAA	GTTGAGTTTC	TATTCTATCT	ACTTGTAATT	420
CTTGCTTTTG	TCGATTTAAT	GACTTTTGGC	TTGGTTTCGA	TTTCAATTGT	GGAGGATTTG	480
AAAGAAGCAC	AGGCTAAGCA	AAATGCCAG	ATAAATCTAT	TGCTTGCTGA	AAATGAACGC	540
AATCGTATCG	GTCAAGATTT	GCATGATAGT	CTGGGGCATA	CCTTTGCTAT	GCTTAGTGTT	600
AAAACGATC	TAGCCTTGCA	GTTATTTTCA	ATGGAGGCTT	ATCCACAGGT	GGAAAAGGAA	660
TTAAAAGAAA	TTCAACGAT	CAGCAAGGAT	TCCATGAATG	AAGTTCGAAC	TATCGTGGAA	720
AATCTTAAGT	CTAGAACTTT	GACATCCGAA	CTAGAGACTG	TGAAAAAGAT	GTTAGAAATT	780
GCTGGAAATG	AGGTGGAAAC	GGATAACCAA	CTAGATACTG	CTAGCCTTAC	TCAAGAATTG	840
GAGTCAATGG	CTTCTATGAT	TTTGCTTGAG	TTGGTGACCA	ATATCATCAA	ACATGCCAAA	900
GCGTCTAAAG	CTTACTTAAA	ATTAGAACGG	ACAGAGAAGG	AACTCATTTT	AACAGTAAGT	960
GATGATGGCT	GCGGCTTTGC	TTTTCTAAAA	GGAGATGAGC	TCCATACAGT	CCGAGATCGT	1020
GTTTTTCCAT	TTTCAGGAGA	AGTAAGTGTA	ATCAGTCAGA	AACATCCAAC	GGAAGTGCAA	1080

GTTCGACTAC CTTATAAGGA GAGAACTAA

1110

(2) INFORMATION FOR SEQ ID NO:2380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2380:

GCCCCATCCG	TGGTGAAGAC	AGATTGCCTT	TTTCGCGAAA	TTATTGACCA	AGGTCATTAC	60
CACTACAAC	ACAGCAAAGT	TATTTTGTGAT	AGCATCAGCT	ACGACAGCCG	AAAAGTAACA	120
GAAGACACTC	TTTTTTTTCG	AAAAGGCGCT	GCCTTTAAAA	AAGAATACCT	TCTTTCTGCT	180
ATAACACAAG	GTTTAGCTTG	GTATGTAGCT	GAAAAGGACT	ACGAAGTCGA	TATCCCTGTC	240
ATCATTTGTGA	ACGATATAAA	GAAAGCCATG	AGTTTGATTG	CCATGGAGTT	CTATGGTAAT	300
CCACAAGAGA	AACTCAAAC	CCTTGCCTTT	ACTGGTACTA	AGGGTAAGAC	AACAGCAACC	360
TATTTTCGCCT	ATAACATCTT	ATCTCAGGGG	CATAGACCTG	CTATGTTGTC	GACCATGAAC	420
ACAACTCTTG	ATGGCGAGAC	TTTCTTTAAG	TCAGCGTTGA	CAACCCCTGA	GAGTATTGAC	480
CTCTTTGACA	TGATGAATCA	GGCTGTGCTA	AATGACCGTA	CCCACCTCAT	CATGGAAGTC	540
TCCAGTCAAG	CCTATCTAGT	CCATCGAGTC	TATGGACTGA	CCTTTGATGT	AGGAGTCTTT	600
CTTAACATCA	CTCCTGACCA	TATCGGCCCG	ATTGAACACC	CTAGCTTTGA	AGACTATTTT	660
TACCACAAGC	GTCTCTTGAT	GGAAAATAGC	CGAGCAGTCA	TCATTAACAG	TGACATGGAC	720
CACTTCTCAG	TCTTGAAAGA	ACAGGTTGAA	GATCAAGACC	ATGATTTCTA	TGGTAGCCAA	780
TTTGATAACC	AAATCGAGAA	TTCCAAAGCC	TTTAGCTTTT	CAGCTACGGG	TAAACTCGCT	840
GGAGATTATG	ATATCCAAC	CATTGGCAAC	TTCAACCAAG	AAAATGCAGT	TGCTGCTGGA	900
CTTGCTTGTC	TCCGTCTCGG	AGCAAGTCTT	GAGGACATCA	AAAAAGGCAT	CGCTGCAACC	960
CGCGTTCCTG	GTCTGATGGA	AGTCCTCACT	CAGAAAAATG	GAGCCAAGGT	CTTCATCGAC	1020
TATGCCCCACA	ATGGGGATAG	TCTGAAAAAA	CTCATCAATG	TGGTTGAAAC	TCATCAAACC	1080
GGAAAGATTG	CTCTGGTTCT	GGGATCAACA	GGAAACAAGG	GAGAAAGTCG	TCGTAAGGAC	1140
TTTGCGCTCC	TCCTCAATCA	ACACCGTGAG	ATTCAAGTCT	TTCTGACTGC	TGATGACCCCT	1200
AACTATGAAG	ACCCAATGGC	CATTGCAGAT	GAAATTAGTA	GCTACATCAA	TCATCCTGTT	1260
GAAAAGATTG	CGGATCGCCA	AGAAGCCATC	AAGGCGGCAA	TGGCTATCAC	AAATCACGAA	1320
TTAGATGCAG	TTATTATTGC	GGGTAAGGGA	GCCGATTGTT	ACCAAATCAT	CCAGGGCAAG	1380
AAAGAATCCT	ACCCAGGAGA	TACAGCCGTC	GCAGAAAATT	ATTTATAA		1428

(2) INFORMATION FOR SEQ ID NO:2381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2381:

GCGCAGCCCG	TCCAGGTGCT	CGTAGTGAGT	CTCTTGAAAG	CTACATCAAG	CGTCTCCATG	60
ATTTGGAAGA	AATTGCTAAC	GGCTTTGAAG	GAGTGCAAAC	TAGCTTTGCC	CTTCAAGCAG	120
GACGTGAAAT	TCGTATCATG	GTCAATCCAG	GAAAAATCAA	GGACGACAAA	GTCACAATCT	180
TGGCTCACAA	AGTTCGTAAG	AAAATTGAAA	ACAATCTCGA	TTATCCAGGA	AATATCAAGG	240
TAA						243

(2) INFORMATION FOR SEQ ID NO:2382:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1245 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2382:

AATTCTACCG	TTAGTAACAA	TTACATACAC	AATCAAGTGC	ACACCTGTGA	AGTTGGATGG	60
AACCGTGGCC	CTGCCACTCC	AACGTTTTGT	CAGGTGTGCT	TTTTTCATAA	AGGAGTTCTT	120
ATGTTAGATA	TCAAACGTAT	TCGTACAGAT	TTTGAAGCTG	TCGCAGAAAA	ATTAGCTACA	180
CGTGGTGTAG	ATGCTGCTGT	CTTGAATGAA	ATGAAAGAAA	TCGATGCTAA	ACGTCGTAAC	240
ATCTTGGTCA	AGGTTGAAAC	TCTCAAAGCA	GAACGTAACA	CAGTTTCTGC	TGAGATTGCC	300
CAAGCTAAGC	GCAACAAGGA	AAATACAGAT	GACAAGATTG	CTGCCATGCA	AAATCTATCT	360
GCTGAGGTTA	AAGCCTTGGA	TGCTGAATTG	GCAGAAATCG	ATGCTAAATT	GACAGAATTT	420
ACAACGACTC	TTCCAAATAT	CCCAGCTGAC	AGCGTTCCTG	TTGGGGCTGA	CGAAGACGAC	480
AATGTGGAAG	TTCGCCGTTG	GGGTACTCCA	CGCGAGTTTG	ACTTCGAACC	TAAAGCTCAC	540
TGGGATCTCG	GTGAAGACCT	TGGTATCCTT	GACTGGGAAC	GCGGTGGTAA	GGTAACAGGC	600
GCTCGCTTCC	TCTTCTATAA	AGGCCTCGGT	GCTCGTTTGG	AACGTGCTAT	CTACAACTTT	660

ATGTTGGATG	AACATGGAAA	AGAAGGCTAT	ACTGAAGTCA	TCACACCTTA	CATAGTCAAC	720
CATGATTCTA	TGTTTGGTAC	TGGTCAGTAT	CCAAAATTTA	AGGAAGATAC	TTTTGAACTC	780
AGCGATACCA	ACTTTGTCTT	GATTCCAAC	GCTGAAGTTC	CTCTGGCAAA	CTACTACCGT	840
GATGAAATCT	TAGACGGCAA	AGATCTTCCA	ATCTACTTCA	CTGCTATGAG	TCCGTCATTC	900
CGTTCTGAGG	CTGGTCTGTC	CGGTCGTGAT	ACGCGTGGCT	TGATCCGTTT	GCACCAATTC	960
CACAAGGTTG	AAATGGTCAA	ATTTGCCAAA	CCAGAAGAAT	CTTACGAAGA	ATTGGAAAAA	1020
ATGACAGCCA	ACGCTGAAAA	CATTCTTCAA	AAACTCAACC	TTCCATACCG	TGTCGTTGCT	1080
CTCTCTACTG	GAGATATGGG	CTTCTCAGCT	GCGAAGACTT	ACGACTTGGA	AGTGTGGATT	1140
CCAGCACAAA	ACAATTACGT	GAAATCTCAA	GCTGTTCAAA	CACAGAAGAT	TTCCAAGCCG	1200
TTCGTGCCCCA	AATCCGTTAC	CGTGATGAAG	CAGATGGCAA	GGTGA		1245

(2) INFORMATION FOR SEQ ID NO:2383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2383:

ATCAGGTGCT	TTCGGACGTG	GTATGGTTCC	ATCAAGGAGC	TTTCTACTGG	TGAACACGAA	60
GCAGTTGAAC	TTCGCGACGG	TGACAAATCT	CGTTACGGTG	GTCTTGGTAC	ACAAAAAGCT	120
GTTGACAACG	TAAACAACAT	CATTGCTGAA	GCTATCATTG	GCTACGATGT	ACGTGATCAA	180
CAAGCTATTG	ACCGTGCTAT	GATCGCACTT	GACGGTACTC	CTAACAAAGG	TAAATGGGGT	240
GCGAATGCAA	TCCTCGGTGT	GTCTATCGCT	GTAGCTCGTG	CTGCTGCTGA	CTACCTTGAA	300
ATCCCACTTT	ACAGCTACCT	TGGTGGATTG	AACACTAAAG	TTCTTCCAAC	TCCAATGATG	360
AACATCATCA	ACGGTGGTTC	TCACTCTGAC	GCTCCAATCG	CTTTCCAAGA	GTTTCATGATC	420
TTGCCAGTTG	GTGCGCCAAC	ATTTAAAGAA	GCCCTTCGTT	ACGGTGCTGA	AATCTTCCAC	480
GCCCTTAAGA	AAATCCTTAA	ATCACGTGGT	TTGGAAACTG	CCGTAGGTGA	CGAAGGTGGA	540
TTCGCTCCTC	GTTTCGAAGG	AACTGAAGAT	GGTGTTGAAA	CTATCCTTGC	TGCGATTGAA	600
GCTGCTGGAT	ATGTACCAGG	TAAAGACGTA	TTTATTGGAT	TTGACTGTGC	TTTCATCAGAA	660
TTCTACGATA	AAGAACGTAA	AGTTTACGAC	TACACTAAAT	TTGAAGGTGA	AGGTGCTGCT	720
GTTTCGTACAT	CTGCAGAAAC	AATCGACTAC	CTTGAAGAAT	TGGTTAACAA	ATACCCAATC	780
ATCACTATTG	AAGATGGTAT	GGATGAAAAC	GACTGGGATG	GTTGGAAAGC	TCTTACTGAA	840
CGTCTTGGTA	AGAAAGTACA	ACTTGTGTTG	GACGACTTCT	TCGTAACAAA	CACTGACTAC	900
CTTGCACGTG	GTATCCAAGA	AGGTGCTGCT	AACTCAATCC	TTATCAAAGT	TAACCAAATC	960
GGTACTCTTA	CTGAAACTTT	TGAAGCTATC	GAAATGGCTA	AAGAAGCTGG	TTTACTGCT	1020
GTTGTATCAC	ACCGTTCAGG	TGAAACTGAA	GATTCAACAA	TCGCTGATAT	TGCAGTTGCA	1080
ACTAACGCAG	GACAAATCAA	GACTGGTTCA	CTTTCACGTA	CAGACCGCAT	CGCTAAATAC	1140
AACCAATTGC	TTCTATATCGA	AGACCAACTT	GGTGAAGTAG	CTGAATATCG	TGGATTGAAA	1200
TCATTCTACA	ACCTTAAAAA	ATAA				1224

(2) INFORMATION FOR SEQ ID NO:2384:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2736 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2736
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2384:

GGGGCTCGCT	TTAGCTCAAC	CGATTCTTAT	CAGAATCACA	AGTTTACATT	TAAAACGTTA	60
AAATTTAAAT	TTAGAATGAG	GTTTTACTTC	ATGGAAAATG	TTGTTGTACA	TATTATCTCA	120
CATAGTCACT	GGGACCGTGA	GTGGTACTTG	CCTTTTGAAA	GCCATCGTAT	GCAGTTGGTG	180
GAATTGTTTG	ACAATCTCTT	TGATCTCTTT	GAAAATGACC	CTGAGTTCAA	GAGTTTCCAC	240
TTGGATGGAC	AAACTATTGT	CCTTGATGAC	TACTTACAAA	TTCGCCCTGA	AAATCGTGAC	300
AAGGTCCAAC	GCTACATTGA	CGAGGGCAAA	CTTAAAATTG	GTCCCTTTTA	CATCTTGCAG	360
GATGACTACT	TGATCTCCAG	TGAAGCCAAT	GTCCGCAATA	CCTTGATTGG	TCAACAAGAA	420
GCTGCCAAAT	GGGGTAAATC	AACCCAGATT	GGCTACTTTC	CAGATACCTT	TGGAAATATG	480
GGACAAGCTC	CTCAAAATCCT	TCAAAAATCA	GGTATTACAG	TGGCAGCCTT	TGGTCGTGGT	540
GTGAAGCCGA	TTGGATTTGA	CAACCAAGTC	CTTGAAGATG	AGCGGTTTAC	ATCCCAGTTT	600
TCAGAAATGT	ACTGGCAGGG	TGTGGATGGT	AGTCGTGTTT	TAGGTATTCT	CTTTGCCAAC	660
TGGTACAGTA	ATGGGAATGA	AATCCCAGTT	GACAAAGATG	AGGCCTTGAT	CTTCTGGAAA	720
CAAAAAATTGT	CAGATGTGCG	TGCCTACGCT	TCGACCAACC	AATGGTTGAT	GATGAACGGC	780
TGTGACCACC	AGCCTGTCCA	GAAAAATCTG	AGCGAAGCCA	TTCGTGTGGC	AAATGAACTC	840
TTCCCGGATG	TAATCTTTGT	TCATAGTTCT	TTTGATGAAT	ATGTTCAAGC	TGTAGAAGGT	900
GCGCTTCCTG	AACACTTATC	AACTGTTACA	GGTGAGTTGA	CCAGTCAGGA	AACAGATGGC	960
TGGTACACAC	TTGCCAACAC	TTCTTCATCC	CGCATTTACC	TAAAACAAGC	CTTCCAAGAA	1020
AATAGCAACC	TCCTAGAGCA	AGTGGTAGAA	CCCTTGACTA	TTATCACTGG	TGGACACAAC	1080
CACAAGGACC	AGTTGACCTA	TGCTTGGAAG	ACACTTTTGC	AGAATGCGCC	ACATGATAGT	1140
ATCTGTGGCT	GTAGCGTGGA	CGAAGTTCAC	CGCGAGATGG	AAACGCGTTT	TGCCAAGGTC	1200
AACCAAGTAG	GAAACTTTGT	TAAAAGTAAT	TTGCTCAACG	AGTGGAAGGG	TAAAATTGCT	1260
ACGGATAAGG	CTCAAAGTGA	CTATCTCTTT	ACTGTCATTA	ACACAGGCCT	GCATGATAAG	1320
GTCGATACTG	TCAGCACAGT	GATTGATGTG	GCGACTTGTT	ATTTCAAGGA	ATTGCACCCA	1380
ACAGAAGGCT	ACAAAAAGAT	GGCTGCTCTT	ATCTTGCCAA	GTTACCGTGT	GGAGGACTTG	1440
GATGGTCGTC	CTGTAGAGGC	TACAATCGAA	GACCTCGGAG	CTAATTTTGA	GTATGATTTA	1500
CCAAAAGACA	AGTTCCGCCA	AGCTCGTATT	GCTCGTCAAG	TGCGCGTGAC	CATTCCAGTT	1560
CACCTAGCGC	CGCTTTCTTG	GACAACCTTC	CAATTGCTGG	AAGGAAAACA	AGAACACCGT	1620
GAGGGTATTT	ACCAAAACGG	AGTGATTGAT	ACACCATTCG	TAACGGTGAG	TGTGGATGAC	1680
AACATCACAG	TCTATGACAA	GACAACCTAC	GAAGCCTATG	AAGACTTTAT	CCGCTTTGAA	1740
GACCGTGGGG	ACATCGGAAA	CGAGTATATC	TATTTCCAAC	CAAAAGGAAC	AGAGCCAATC	1800
TTTGCAGAGC	TTAAGGGCCA	CGAGGTCCTG	GAAAACACAG	CTTGCTATGC	TAAAATCTTG	1860
CTCAAACATG	AATTGACCGT	GCCTGTCTAG	GCGGATGAAA	AGCTAGAAGA	AGAGCAACAA	1920
GGTATCATCG	AGTTTATGAA	GCGTGAGGCT	GGACGGTCAG	AAGAATTGAC	AAACATTCCCT	1980
CTGGAAACTG	AGTTGACTGT	CTTCGTTGAC	AATCCACAAA	TCCGCTTCAA	GACTCGCTTT	2040
ACTAACACTG	CCAAGGATCA	CCGTATCCGT	CTCTTGGTCA	AGACTCATAA	CACGCGTCCA	2100

AGCAATGATT	CTGAAAAGTAT	CTATGAGGTG	GTGACACGAC	CAAACAAACC	AGCTGCTTCA	2160
TGGGAAAATC	CTGAAAATCC	TCAACACCAA	CAAGCTTTTG	TCAGTCTGTA	TGACGATGAA	2220
AAAGGGGTGA	CTGTATCCAA	TAAGGGATTG	AATGAATACG	AAATCCTTGG	GGATAACACC	2280
ATTGCCGTGA	CCATTTTGCG	TGCATCAGGT	GAGCTAGGTG	ACTGGGGCTA	CTTCCCAACG	2340
CCAGAAGCAC	AATGCTTGCG	TGAGTTTGAA	GTGCGAGTTG	CAC TTGAATG	CCACCAAGCC	2400
CAAGAACGCT	TCTCAGCCTA	TCGTGCTGCC	AAAGCCTTGC	AGACACCGTT	TACCAGCCTT	2460
CAGCTTGCTA	GACAGGAAGG	AAGCGTGGTT	GCGACTGGTA	GCCTCTTGAG	CCATTCTGTT	2520
CTCAGCATAC	CGCAAGTTTG	TCCAACAGCC	TTTAAAGTGG	CGGAAAATGA	AGAAGGCTAT	2580
GTCCCTCCGTT	ACTATAATAT	GAGTCAAGAA	AATGTGCGCA	TATCAGAACA	TCAACAAACC	2640
ATTCTTGACT	TACTTGAGCG	ACCATATCCA	GTTCAATTCAG	GACTATTGGC	TCCACAAGAG	2700
ATTCTGTACAG	AATTTCATCAA	AAAAGAAGAA	ATTTAA			2736

(2) INFORMATION FOR SEQ ID NO:2385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2385:

TTTTGGTACG	TGGAGTTTTG	GTATTTATTT	TTAGCTCAAA	TCCTTGCAAA	TATGATTGGT	60
TTGACTACGA	TTTATTGGTT	ATTCAATCAA	ATTATTACTT	ATGGGGTTAT	TGCGGCGGTT	120
GTTATCTTCT	CTCCAGAGAT	TCGGACTGGT	TTGGAACGTT	TGGGAAGAGC	GACAGATTTC	180
TTTTCCAATG	CCCCTATTAG	TGCTGAGGAA	CAGATGATTC	GTGCCTTTGT	TAAGTCTGTT	240
GAATACATGA	GTCCTCGTAA	AATCGGGGCC	TTGGTTGCTA	TTCAGCGTGT	ACGTACCTTG	300
CAGGAGTATA	TTTCGACAGG	AATCCCCTTG	GATGCTAAGA	TTTCTGCAGA	ACTTCTCATT	360
AACATTTTTA	TTCCCAACAC	TCCCCTACAT	GACGGTGCGG	TGATTATCAA	AGAAGAACGT	420
ATCGCTGTGA	CGTCTGCCTA	TCTGCCCTTG	ACAAAAACA	CAGGTATTTT	CAAGGAATTT	480
GGGACCAGAC	ACCGGGCGGC	TATCGGTTTA	TCAGAAGTCT	CAGATGCCTT	GACTTTTGTC	540
GTATCAGAGG	AAACGGGAGG	AATTTTCGATA	ACCTATAATG	GAAGGTTTAA	GCACAACCTA	600
ACACTTGATG	AATTTGAAAC	AGAATTACGT	GAAATCTTAC	TTCCAAAAGA	GGAAGTGGGT	660
CTTAGTTTTA	AAGAACGATG	GCTAGGAGGA	TGGAAACATG	AAAAAAAATA	G	711

(2) INFORMATION FOR SEQ ID NO:2386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2386:

AATAGCCACG	TTGGTGCATG	TGCAGTTTTG	GCAGGTGTGA	TTGAGCCAGC	TAGTGCTGAA	60
CCAGTCCGTG	TCGGAGACAA	TGTTCTTATC	GGTGCTAATG	CAGTGGTTAT	CGAAGGAGTC	120
CAAATCGGTA	GTGGTTTCAGT	TGTCGCAGCA	GGAGCTATTG	TTACCCAAGA	TGTCCCAGAA	180
AACGTGGTAG	TAGCAGGTGT	TCCAGCTCGT	ATTATCAAAG	AAATTGATGC	CCAAACTCAA	240
CAAAAAACAG	CGCTAGAGGA	TGCGCTTCGT	ACCTTGTA			279

(2) INFORMATION FOR SEQ ID NO:2387:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 480 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2387:

ATACTATTTT	TAACGAAAAA	ATTAAGAAAT	TGGAGAACTA	ATATGAAACT	TGAAAAACAT	60
TTGATTAAAGC	TTAATAAACA	ATTTTCTAAC	AAGGAGGAAG	CTATTTGTTA	TTGTGGGCAA	120
GTTCTTTATG	AGGGTGGATA	TGTTAATGAA	GACTATATTG	AAGCCATGAT	TGAGCGAGAT	180
AAAGAGCTAT	CTGTTTACAT	GGGTAACTTT	ATCGCCATAC	CGCATGGAAC	AGATGCAGCA	240
AAAAAGGATG	TCCTCAAGTC	TGGTATTACA	GTCGTTCAAG	TCCCTAGAGG	GGTTGATTTT	300
GGGAATGTAT	CTAACCTCA	AGTGGCAACG	GTTCTTTTTG	GTATTGCTGG	TATTGGTAAT	360
GAACACTTAG	AAATTATTCA	GAAAATTTCT	ATCTTCTGTG	CAGATGTAGA	TAATGTTCTT	420
AAACTAGCAG	ATGCTCAGTC	AAAAGAGGAA	GTATTGCGCT	TATTTGATGC	TGTTGAATAA	480

(2) INFORMATION FOR SEQ ID NO:2388:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 396 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2388:

GGTGGACACG	TGATTGATGT	CAATCTCATT	AACGGGATTG	CGCTAGCCTT	TGAGGGGGAT	60
GCGGTGTATT	CTATGTATAT	TCGCCGTCAC	CTCATCCTCA	AAGGTATGAC	CAAACCCAAT	120
AAACTCCATC	AAGAAGCAAC	TAAGTACGTG	TCAGCCAAGG	CTCAGGCTCG	CCTGATTGCT	180
CTCATGTTGG	AGGAGCAGGT	CCTAACGGAA	AAAGAAGAAG	AAATCTACAA	ACGTGGCCGC	240
AATACCAATA	GCCACACAAA	GGCTAAAAAT	GCAGATGTCG	TGACTTATCG	TATGTCCACG	300
GGATTTGAAG	CGGTTATGGG	CTATCTCCAT	ATGACTGAGA	ATCTGGAACG	TCTTGAGAGT	360
TTGGTTTCAT	GGTGCATCCA	AAAAGTGGAG	GGCTAG			396

(2) INFORMATION FOR SEQ ID NO:2389:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2037 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2389:

CCTTTGCACG	TTCACAGGGA	CGCTACACCA	CAGATGATGG	TTATATCTTC	AATGCATCTG	60
ATATCATCGA	AGATACGGGG	CGATGCCTAT	ATCGTTCCTC	ATGGAGATCA	TTACCATTAC	120
ATTCCTAAGA	ATGAGTTATC	AGCTAGCGAG	TTGGCTGCTG	CAGAAGCCTT	CCTATCTGGT	180
CGGGAAAATC	TGTCAAATTT	AAGAACCCTAT	CGCCGACAAA	ATAGCGATAA	CACTCCAAGA	240
ACAAACTGGG	TACCTTCTGT	AAGCAATCCA	GGAACCTACAA	ATACTAACAC	AAGCAACAAC	300
AGCAACACTA	ACAGTCAAGC	AAGTCAAAGT	AATGACATTG	ATAGTCTCTT	GAAACAGCTC	360
TACAAACTGC	CTTTGAGTCA	ACGCCATGTA	GAATCTGATG	GCCTTATTTT	CGACCCAGCG	420

CAAATCACAA	GTCGAACCGC	CAGAGGTGTA	GCTGTCCCTC	ATGGTAACCA	TTACCACTTT	480
ATCCCTTATG	AACAAATGTC	TGAATTGGAA	AAACGAATTG	CTCGTATTAT	TCCCCTTCGT	540
TATCGTTCAA	ACCATTGGGT	ACCAGATTCA	AGACCAGAAG	AACCAAGTCC	ACAACCGACT	600
CCAGAACCTA	GTCCAAGTCC	GCAACCTGCA	CCAAATCCTC	AACCAGCTCC	AAGCAATCCA	660
ATTGATGAGA	AATTGGTCAA	AGAAGCTGTT	CGAAAAGTAG	GCGATGGTTA	TGTCTTTGAG	720
GAGAATGGAG	TTTCTCGTTA	TATCCCAGCC	AAGAATCTTT	CAGCAGAAAC	AGCAGCAGGC	780
ATTGATAGCA	AACTGGCCAA	GCAGGAAAGT	TTATCTCATA	AGCTAGGAGC	TAAGAAAAC	840
GACCTCCCAT	CTAGTGATCG	AGAATTTTAC	AATAAGGCTT	ATGACTTACT	AGCAAGAATT	900
CACCAAGATT	TACTTGATAA	TAAAGGTCGA	CAAGTTGATT	TTGAGGCTTT	GGATAACCTG	960
TTGGAACGAC	TCAAGGATGT	CTCAAGTGAT	AAAGTCAAGT	TAGTGGATGA	TATTCTTGCC	1020
TTCTTAGCTC	CGATTTCGTC	TCCAGAACGT	TTAGGAAAAC	CAAATGCGCA	AATTACCTAC	1080
ACTGATGATG	AGATTCAAGT	AGCCAAGTTG	GCAGGCAAGT	ACACAACAGA	AGACGGTTAT	1140
ATCTTTGATC	CTCGTGATAT	AACCAGTGAT	GAGGGGGATG	CCTATGTAAC	TCCACATATG	1200
ACCCATAGCC	ACTGGATTAA	AAAAGATAGT	TTGTCTGAAG	CTGAGAGAGC	GGCAGCCCAG	1260
GCTTATGCTA	AAGAGAAAAG	TTTGACCCCT	CCTTCGACAG	ACCATCAGGA	TTCAGGAAAT	1320
ACTGAGGCAA	AAGGAGCAGA	AGCTATCTAC	AACCGCGTGA	AAGCAGCTAA	GAAGGTGCCA	1380
CTTGATCGTA	TGCCTTACAA	TCTTCAATAT	ACTGTAGAAG	TCAAAAACGG	TAGTTTAAATC	1440
ATACCTCATT	ATGACCATTA	CCATAACATC	AAATTTGAGT	GGTTTGACGA	AGGCCTTTAT	1500
GAGGCACCTA	AGGGGTATAG	TCTTGAGGAT	CTTTTGCGCA	CTGTCAAGTA	CTATGTCGAA	1560
CATCCAAACG	AACGTCCGCA	TTCAGATAAT	GGTTTTGGTA	ACGCTAGTGA	CCATGTTTCGT	1620
AAAAATAAGG	CAGACCAAGA	TAGTAAACCT	GATGAAGATA	AGGAACATGA	TGAAGTAAGT	1680
GAGCCAACTC	ACCCTGAATC	TGATGAAAAA	GAGAATCACG	CTGGTTTAAA	TCCTTCAGCA	1740
GATAATCTTT	ATAAACCAAG	CACTGATACG	GAAGAGACAG	AGGAAGAAGC	TGAAGATACC	1800
ACAGATGAGG	CTGAAATTC	TCAAGTAGAG	AATTCGTGTA	TTAACGCTAA	GATAGCAGAT	1860
GCGGAGGCCT	TGCTAGAAAA	AGTAACAGAT	CCTAGTATTA	GACAAAATGC	TATGGAGACA	1920
TTGACTGGTC	TAAAAAGTAG	TCTTCTTCTC	GGAACGAAAG	ATAATAACAC	TATTTACAGCA	1980
GAAGTAGATA	GTCTCTTGGC	TTTGTTAAAA	GAAAGTCAAC	CGGCTCCTAT	ACAGTAG	2037

(2) INFORMATION FOR SEQ ID NO:2390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2390:

GAGACGAACG	TGAAAAAAAT	TAGCTTATTA	CTAGCCAGTC	TATGTGCCTT	GTTTTTAGTG	60
GCTTGTTCCA	ATCAAAAAACA	GGTAGATGGT	AAACTCAATA	TCGTGACAAC	CTTTTACCCT	120
GTCTATGAAT	TTACCAAGCA	AGTTGCAGGA	GATACGGCTA	ATGTAGAACT	CCTAATCGGT	180
GCTGGGACAG	AACCTCATGA	ATACGAACCA	TCTGCCAAGG	CAGTTGCCAA	AATCCAAGAT	240
GCAGATACCT	TCGTTTATGA	AAATGAAAAC	ATGGAAACAT	GGGTACCTAA	ATTGCTAGAT	300
ACCTTGAGATA	AGAAAAAAGT	GAAAACCATC	AAGGCGACAG	GCGATATGTT	GCTCTTGCCA	360

GGTGGCGAGG	AAGAAGAGGG	AGACCATGAC	CATGGAGAAG	AAGGTCATCA	CCATGAGTTT	420
GACCCCCATG	TTTGGTTATC	ACCAGTTCGT	GCCATTAAAC	TAGTAGAGCA	CATCCGCGAC	480
AGCTTGTCAG	CAGATTATCC	TGATAAAAAA	GAGACCTTTG	AGAAGAATGC	AGCTGCCTAT	540
ATCGAAAAAT	TGCAATCCCT	GGATAAGGCT	TACGCAGAAG	GCTTGTCCTCA	AGCAAAACAA	600
AAGAGCTTTG	TGACTCAACA	CGCAGCCTTT	AACTATCTTG	CCTTGGAATA	TGGACTCAAA	660
CAAGTCGCAA	TCTCAGGCCT	TTCTCCAGAT	GCAGAGCCAT	CAGCTGCTCG	CTTGGCAGAA	720
TTGACAGAGT	ATGTCAAGAA	AAATAAAATC	GCCATATATC	ATTTTGAAGA	AAATGCCCTCA	780
CAAGCCCTTG	CTAACACACT	TTCAAAAAGAA	GCAGGTGTCA	AAACTGATGT	CCTCAATCCT	840
TTAGAAAAGTC	TGACAGAAGA	GGACACCAAG	GATGGAGAAA	ACTACATTTT	CGTGATGGAG	900
AAAAACCTCA	AGGCTTTGAA	ACAAACAACA	GACCAAGAAG	TCCCAGCAAT	CGAACCTGAA	960
AAGGCAGAGG	ATACCAAGAC	AGTCCAAAAT	GGTTACTTCG	AGGATGCAGC	TGTCAAGGAC	1020
CGCACCTTGA	GTGACTATGC	AGGTAAGTGG	CAATCAGTTT	ATCCTTTCCT	TGAAGACGGC	1080
ACGTTTGACC	AAGTCTTTGA	CTACAAGGCT	AAGTTGACTG	GTAAGATGAC	CCAGGCTGAG	1140
TACAAGGCTT	ACTATACAAA	AGGCTATCAG	ACAGATGTGA	CTAAGATTAA	CATTACTGAT	1200
AATACTATGG	AATTTGTTCA	AGGTGGACAA	AGCAAGAAAT	ACACTTACAA	GTATGTCGGT	1260
AAGAAAATTT	TGACTTACAA	GAAAGGCAAT	CGTGGCGTGC	GTTTCCTCTT	TGAAGCCACA	1320
GATGCTGACG	CTGGACAAAT	CAAATATGTT	CAGTTTAGTG	ACCACAATGT	TGCCCCAGTT	1380
AAGGCAGAAC	ATTTCCATAT	CTTTTTTTGGA	GGTACAAGCC	AAGAAGCTCT	ATTTGAAGAA	1440
ATGGATAATT	GGCCAACCTA	CTACCCAGAT	AACCTATCTG	GCCAAGAAAT	CGCCCAAGAA	1500
ATGTTGGCGC	ATTGA					1515

(2) INFORMATION FOR SEQ ID NO:2391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2391:

GGCAGACGCT	TATCCACAGA	GTCTGTCGGG	TGGGCAACAA	CAACGGATTG	CATCGCGCGT	60
GGGTTGGCTA	TGGTACCAGA	TGTTTTGCTC	TTTGACGAAC	CAACTTCAGC	CTTGGATCCT	120
GAAATGGTAG	GTGAGGTAT	GGCTGTTATG	CAAGACCTTG	CCAAGTCAGG	GATGACTATG	180
GTTATCGTAA	CACATGAGAT	GGGATTTGCC	CGTGAGGTGG	CAGATCGTGT	TATCTTTATG	240
GCAGAGCGGT	GTGGTTGTTG	A				261

(2) INFORMATION FOR SEQ ID NO:2392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1359

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2392:

GAGGCTAGCG	TCATGATGAA	GTTTCATATTG	GATATTGTTA	GTACACCAGC	TATTTTAGTA	60
GCTTTAATTG	CAATCTTAGG	ATTAGTTCCT	CAGAAGAAGA	AATTACCTGA	TATTATTAAA	120
GGTGGAATTA	AGACCTTTGT	TGGTTTCCTTA	GTTGTATCTG	GTGGTGCAGG	AATTGTACAA	180
AATTCCTTTAA	ATCCATTTGG	TACCATGTTT	GAGCATGCCT	TTCATTTATC	TGGCGTTGTG	240
CCGAATAATG	AAGCAATTGT	AGCTGTAGCT	TTAACAACAT	ATGGCTCAGC	TACTGCAATG	300
ATTATGTTTG	CAGGCATGGT	GTTCAATATC	TTAATCGCTC	GTTTTACTCG	ATTTAAATAT	360
ATCTTTTTTAA	CAGGGCACCA	CACTCTATAT	ATGGCATGTA	TGATTGCGGT	CATTTTATCA	420
GTTGCTGGCT	TTACTAGCTT	GCCTCTCATC	TTACTAGGAG	GATTAGCACT	CGGTATTATT	480
ATGAGTATTT	CCCCAGCATT	TGTGCAAAAA	TATATGGTTC	AATTAACCTG	AAATGACAAG	540
GTGGCTTTAG	GTCAATTCAG	TTCTTTGGGA	TATTGGTTGA	GTGGTTTTAC	TGGTAGCCTT	600
ATCGGTGACA	AATCAAAAATC	AACAGAGGAC	ATTAAATTTT	CAAAGAGTTT	AGCTTTTTTTA	660
CGTGATAGTA	CTGTTAGTAT	CACTTTATCT	ATGGCAGTTA	TTTACATTAT	TGTAGCTATC	720
TTTGCAGGGT	CAGAATATAT	AGAAAAAGAA	ATCAGTAGTG	GTACAAGTGG	TCTAGTTTAT	780
GCTTTACAAT	TAGCAGGTCA	ATTTGCAGCA	GGGGTATTTG	TTATTTTAGC	AGGTGTTTCGC	840
CTTATTTTGG	GCGAAATTGT	TCCAGCCTTT	AAAGGTATTT	CAGAGCGTCT	TGTACCTAAT	900
TCAAAACCTG	CTTTGGATTG	TCCGATTGTT	TATACTTATG	CACCCAATGC	AGTTCTAATT	960
GGATTTATCT	CTAGTTTAT	TGGTGGTTTA	GTAAGTATGG	CAATTATGAT	TGCTTCAGGA	1020
ACGGTTGTTA	TCTTACCAGG	CGTTGTGCCT	CATTCTTCT	GTGGAGCGAC	TGCAGGTGTC	1080
ATTGGGAATG	CATCTGGTGG	TGTTTCGTGGA	GCCACTATTG	GAGCATTTTT	ACAAGGTATT	1140
TTAATCAGTT	TTCTTCCAGT	CTTTTAAATG	CCAGTTTGG	GAGGACTCGG	TTTCCAAGGA	1200
TCAACTTTCT	CAGATGCAGA	TTTGGTCTA	TCAGGAATTA	TTTTAGGAAT	GTTAAATCAA	1260
TTTGGCTCAC	AAGCAGGCAT	TGTGATTGGT	CTTGTCTTA	TTTTAGCAGT	TATGTTTGGA	1320
GTATCCTTTA	TTAAAAAGCC	ATCTGCAAAG	GAGGAATAA			1359

(2) INFORMATION FOR SEQ ID NO:2393:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2393:

ATGGAAAGCG TTCTTGAAAG CTTGAAACAA GAAAAAGACC ACCTCGAAAA AATCATTAAG	60
GTAGTTACCT CTGGTGGTAA ATTTCTGAGA TTGCCGTATC AAAAAAAGTC ACGCTCGATT	120
AGTGAGAATC TGAAATTGAT TTCTCAAAAT CTTGATAAAT TGAGCGAGCA AGTTCAACAA	180
ACCACGAATC AGCATTCATG A	201

(2) INFORMATION FOR SEQ ID NO:2394:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2394:

CGACTGAGCG TATTGTTGAT GCTTATCTTA AGAGCGAGGC GGTATCATAG AATGTGCTTA	60
ATCTGTCAGA GAATCGAACT CATTAAAGCT GGGCAAAATC CCTACTTTGT CAAAGAGTTG	120
GAAACAGGCT ATCTTGTGAT TGGAGACCAC CAGTATTTTG CAGGATATAG TCTTTTTCTA	180
GCTAAGGAAC ACGTTACCGA ATTGCACCAT TTGAAAAAGG AAACAAGACT CCGTTTTCTC	240
GAAGAAATGA GTCTAGTCCA AGAGGCAGTT GCCAAGGCAT TTGCTGCTGA GAAAATGAAT	300
ATCGAACTGC TAGAAAATGG CGATGCCCAT CTTCATTTGGC ATCTGTTTCC TAGACGAAGA	360
GGTGATATGA ATGGTCACGG TCTCAAGGGA CGTGGGCCAG TTTGGTGGGT CCCTTTGAAG	420
AAATGA	426

(2) INFORMATION FOR SEQ ID NO:2395:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2395:

CAAGCTGGCG	TGGTAGTAGT	AGATAATACA	TCTTATTTCC	GTCAAAATCC	AGATGTTCCCT	60
TTGGTTGTTC	CAGAGGTCAA	TGCTCATGCA	CTTGATGCTC	ACAACGGAAT	CATTGCCTGC	120
CCTAATTGTT	CAACAATCCA	AATGATGGTG	GCTCTTGAGC	GGTTTCGCCA	AAAATGGGGC	180
TTGGAGCGTA	TCATTGTTTT	AAC TTATCAA	GCCAGTATTC	AGGAGCTGGT	ATGGGAGCAA	240
TTCTTGAGAC	ACAACGTGAA	CTTCGTGAAG	TCTTGA			276

(2) INFORMATION FOR SEQ ID NO:2396:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2396:

CTTCCTAGCT	TAGATGGCTC	GCAGCACCGC	CATTTCTCTG	GA CTAAGACA	AGTGAAAATT	60
AATTCTCAAC	TTTCTTATTA	TAACGTTTTT	TTAAGCTTGC	GTCAACTGGA	AATGATCTCC	120
GTTGAATTAG	ACCAATTCCC	TACATCTCTG	ATTACTTTTT	CAGGATATAT	TTTTTCTTAC	180
TGCCGTTTTT	CTTTTTATCC	CAAATTTTCA	TATTACTAA			219

(2) INFORMATION FOR SEQ ID NO:2397:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2397:

GATTATAGCT	TAATGGATAC	AACATTGTTT	TATGGAATAG	TGATTGTCTT	GGCAGTGAGT	60
CCCCTTTTAC	TGTCAAGCTT	TCATTCTATT	CGTCAGCAAA	AGTTGCTTCG	CAAACAGATG	120
GAGCAACGAC	AAGAGTATTT	AGCTTCTTTA	ACATCTGGTG	ATGAAGTGTT	GTTATTGTCT	180
GGAATTCATG	GAAAAATCAT	TTCTATCCAA	GATGACTTGG	TCTCCTTGCA	GATTGCAAAA	240
GGTGTGGTCA	TCTATGTAGA	AAAGGAAAGT	GTAATGGGAA	AGACAAAAGA	ACTGCTTTTT	300
AAGTAG						306

(2) INFORMATION FOR SEQ ID NO:2398:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1383 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2398:

TATAATAGCT	TTATGAATAA	AAAACGAACG	GTGGACCTGA	TACATGGTCC	GATTCTTCCC	60
TCGCTCTTAA	GCTTCACCTT	TCCAATTTTG	CTATCAAATA	TTTTTCAACA	GCTCTATAAC	120
ACTGCTGATG	TCTTGATTGT	TGGACGATTT	CFTGGTCAAG	AATCCTTGGC	TGCAGTAGGA	180
GCGACGACAG	CGATTTTTGA	CCTGATTGTA	GGTTTTACAC	TTGGTGTTGG	CAATGGCATG	240
GGGATTGTCA	TTGCTCGTTA	TTATGGGGCT	CGGAATTTCA	CTAAAATCAA	GGAAGCAGTA	300
GCAGCTACTT	GGATTTTAGG	TGCTCTTTTG	AGCATTCTAG	TTATGTTGCT	GGGCTTTCTT	360
GGCTTGATATC	CTCTCTTGCA	ATACTTAGAT	ACTCCTGCAG	AAATTCTTCC	TCAATCTTAT	420
CAATATATTT	CTATGATTGT	GACCTGTGTA	GGTGTCAGCT	TTGCTTATAA	TCTTTTTGCA	480
GGCTTGTTGC	GGTCTATTGG	TGACAGTCTA	GCAGCCCTGG	GATTTCTGAT	TTTCTCTGCC	540
TTGGTTAATG	TGGTCTGGA	TCTCTATTTT	ATTACGCAAT	TGCATCTGGG	AGTTCAATCC	600
GCAGGACTTG	CTACCATTAT	TTCGCAAGGT	TTATCAGCGG	TTCTCTGCTT	TTATTATATT	660
CGTAAAAGTG	TGCCAGAACT	CTTGCCACAG	TTTAAACATT	TCAAATGGGA	CAAAAGCTTG	720
TACGCAGATC	TCTTGAGCA	AGGTTTGGCT	ATGGGCCTGA	TGAGTTCAAT	TGTATCTATC	780
GGCAGTGTGA	TTTTACAGTC	TTCTGTTAAT	ACATTTGGTG	CAGTGATTAT	TAGTGCCAG	840
ACGGCAGCTC	GACGCATTAT	GACCTTTGCC	CTTCTTCCTA	TGACCGCTAT	TTCTGCATCA	900
ATGACGACCT	TTGCTTCTCA	GAATCTAGGA	GCTAAGCAAC	CTGACCGCAT	TGTTCAAGGT	960
CTTCGAATCG	GCAGTCGTTT	AAGTATATCC	TGGGCAGTTT	TTGTTTGTAT	TTTCCTCTTT	1020

TTTGCCAGTC	CAGCTTTGGT	TTCCTTCTTG	GCTAGTTCGA	CAGATGGTTA	CTTGATAGAA	1080
AATGGAAGTC	TCTATCTGCA	AATCAGTTCA	ACCTTTTATC	CCATTTTGAG	CCTCTTGTTG	1140
ATTTATCGCA	ATTGCTTGCA	GGGCTTGGGG	CAAAAGATCC	TTCCTCTAGT	TTCTAGCTTT	1200
ATTGAACTAA	TCGGAAAAAT	CGTTTTTGTG	GTTTTGATTA	TTCCTTGGGC	AGGATATAAG	1260
GGTGTATACC	TTTGTAACC	TCTTATCTGG	GTTGCCATGA	CAGTTCAACT	GTACTTCTCA	1320
CTATTCCGTC	ATCCCTTGAT	AAAAGAAGGA	AAGGCAATTT	TGGCAACCAA	AGTGCAATCC	1380
TAG						1383

(2) INFORMATION FOR SEQ ID NO:2399:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 888 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...888
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2399:

ATTAACAGCT	TCAGAGCTAC	GAAAGGAAAA	AACTCAATGG	CTACTATTCA	ATGGTTTCCT	60
GGTCACATGT	CTAAAGCTCG	TCGACAGGTG	CAGGAGAATT	TAAAATTTGT	TGATTTTGTG	120
ACGATTTTAG	TAGATGCACG	CTTGCCCTCTA	TCTAGTCAAA	ATCCTATGTT	GACCAAGATT	180
GTTGGTGATA	AACCAAAACT	CTTGATTTTA	AACAAGGCCG	ACTTGGCTGA	TCCAGCAATG	240
ACCAAGGAAT	GGCGTCAGTA	TTTTGAATCA	CAAGGAATCC	AGACGCTAGC	TATCAACTCC	300
AAAGAGCAAG	TGACTGTAAA	AGTTGTAACA	GATGCGGCCA	AGAAGCTCAT	GGCTGATAAG	360
ATTGCTCGCC	AGAAAGAACG	TGGGATTTCAG	ATTGAAACCT	TGCGTACTAT	GATTATCGGG	420
ATTCCAAACG	CTGGTAAATC	AACTCTGATG	AACCGTTTGG	CTGGTAAAAA	GATTGCTGTT	480
GTTGGAAACA	AGCCAGGGGT	CACAAAAGGT	CAACAATGGC	TTAAAACCAA	TAAAGACCTG	540
GAAATCTTGG	ATACACCGGG	GATTCTCTGG	CCTAAGTTTG	AGGATGAAAC	TGTTGCACTT	600
AAGTTGGCAT	TGACTGGAGC	TATCAAGGAT	CAGTTGCTTC	CTATGGATGA	GGTTACCATT	660
TTTGGTATCA	ATTATTTCAA	AGAACATTAT	CCAGAAAAGC	TGGCTGAACG	CTTCAAACAA	720
ATGAAAATTG	AAGAAGAACC	GTCTGTGATT	ATTATGGATA	TGACCCGCGC	CCTCGGTTTC	780
CGTGATGACT	ATGACCGTTT	TTACAGTCTC	TTCGTGAAGG	AAGTTCGTGA	TGGCAAAC TC	840
GGTAACTATA	CCTTAGATAC	ATTGGAAGAC	CTCGATGGCA	ACGATTAA		888

(2) INFORMATION FOR SEQ ID NO:2400:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1959 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2400:

ACATCATTAG	TAAAAGGAGT	TAGATTGATG	AATAAAAGAA	AAGTTAGTTT	AGAAGATTTT	60
TATAAATGGT	ATAGTCTAAA	TAAAGAAGAG	TTATTAAATA	AGGCAACTGT	TGGTGAAAAG	120
TTTAATGATA	AATTAAGAAG	AGAGTTTCTC	CAGGAATGGC	CTTTGGATAG	GATTTTAACA	180
ATGTCAATCG	ATGAATATGT	AATAGGAAAG	GGACAGCAAA	ATAAGTCTTT	ATGCTACGCT	240
CTTGAGAAGG	GAAAATACAA	AAATCTATTT	CTTGGAAATTT	CTGGTGGCTC	AGCTTCAAAA	300
TTTGGTATTT	ATTGGAATAA	AAAAACAAAC	AAATATAAAG	ATCAAGCTAA	TAATGAGATT	360
TCAGAGTTGG	ATCAGCGATT	TTCAAAATTA	AAATCAGATT	TGTATGAAAT	TATCAAAGAA	420
GGTATTCGTT	TTAACTTTGA	AAATCCTATT	TTTGATATGA	AAAGATCAAC	AAATGAATTT	480
ATTGGTCGTT	CTGCTATGGT	GACAAAATTA	CTTTGTATCT	ATACTGAGGG	AGATCCTTTC	540
TTTGGTGTA	ATATTAATAG	TCAGAAAGAA	TTTTGGAACC	ACTTTGTTTC	TCAGACAAAT	600
CAAGGTGGAC	CTTATCTGCA	AAATCATAAA	ATAATTGAAC	TGGTGTCCAA	AACTTATCCT	660
GAGTTGGAGC	CATCGAAAT	AGGAACATG	CTTTTGTAGT	ATTCTAAGCT	TTTTATGGAA	720
AATAAGGAAG	ACAATAGTAC	AATGGATTCA	TCAAACAATT	TTAGTCATCA	ATTAACTCAA	780
TCTCTATTAA	AGTCTCCAAA	CCTTATCCTT	CGTGGTGCTC	CTGGCACAGG	AAAGACTTAT	840
CTTGCTAAAG	AAATTGCCAA	AGAATTAACG	GATGGCAACG	AAGATCAAAT	CGGATTTGTA	900
CAATTTCCACC	CATCATATGA	TTATACGGAT	TTTGTAGAAG	GTTTAAGACC	AGTATCAAAT	960
GGGGATGGAG	CTATTGAGTT	TAGGCTACAG	GACGGTATTT	TTAAAGATTT	TTGTCAGAAA	1020
TCAAAAGAAA	CCCAATTGAT	TGGAGGACAA	GATAATTTTG	ATGAGGCTTG	GGATTCTTAC	1080
TTAGAATATA	TAAATGTTGC	TGAAGAAAAA	GAATATATAA	CAAAAACATC	TTACTTATCT	1140
GTTAATAGTA	GACAAAATTT	GTCAGTAAAT	TATGATAGTG	GTGTTCCAGG	ATGGTCACTA	1200
CCTAGCAAAT	ATGTTTACGA	GTTGTATAAA	GATAAAAATT	ATAATAAGCA	AGAATACTAC	1260
AAAAGTGGTG	GAAAACTGT	CCTAGAAACA	TTGAGAAAGA	GATTTGGTTT	GAAAGACTAT	1320
GTTTCCCCAA	CAGAAATTGA	TACTGATAAG	AAATTCGTTT	TCATCATCGA	TGAAATCAAT	1380
CGTGGGGAGA	TTTCTAAGAT	TTTTGGCGAA	CTCTTTTCT	CTATCGACCC	TGGCTATCGT	1440
GGTGAAAAAG	GAAGTGTTTC	TACCCAATAT	GCAAATCTAC	ACGAAACTGA	TGAAAAGTTC	1500
TATATCCCCG	AAAAATGTTA	CATCATCGGA	ACTATGAATG	ATATTGATCG	TTCAGTGGAT	1560
ACCTTTGATT	TTGCTATGCG	TCGTCGTTTT	CGTTTTGTG	AAGTTACTGC	CGAGGGTCAA	1620
GTTGGCATGT	TGGATAAAGA	GCTGAATATC	CATGCAGAAG	AAGCAAAAAT	TCGTCTAAGA	1680
AACTTGAACG	CTGCTATCGA	AAATGTTTCA	GAATTAAACA	GTCATTATCA	TATTGGACCA	1740
AGTTATTTTC	TTAAGTTGAA	GGATGTAGAT	TTTGACTATG	AATTACTCTG	GTCCGATTAT	1800
ATTAAGCCTC	TCCTAGAAGA	CTACTTGCGA	GGTCTTATG	ATGAGGTTGA	AACTTTGGAA	1860
ACTTTGAAAA	AAGCATTTGA	ACTGACAAAT	AATGAGCAAA	AAGATCAGGC	AGTAGCTGAT	1920
GACAAATGAAA	GCGATGAAAA	CGATGATGCG	GATTACTGA			1959

(2) INFORMATION FOR SEQ ID NO:2401:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 891 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2401:

AATCAATTAG	TCTCAAGCTT	TCTATCAATT	TCTTCTCCAA	AATATGCTAT	AATAATAGCA	60
AAAGATAAAG	AAGGAAGACC	TATGATTAAA	CTACTAGCCT	TGGATATGGA	TGGAACCCCTC	120
CTCAATGAAG	CCAAGGAAAT	CCCACAGGCT	CACATCGCTG	CTATTACCA	AGCCATTGAA	180
AAAGGTGTCA	AACTGGTTC	CTGTACGGGT	CGCCCCCTTT	TCGGTGTCC	CCCCTACTAC	240
AAAAAACTGG	GACTCGACCT	CCAGAATGAG	TATGTGATTG	TTAACAACGG	TTGTTCAACT	300
CACCAGACTA	GCGACTGGGG	CTTGGTTGAC	TGGCAAGAAC	TTAGTCCAGC	TGACATCGAA	360
TACCTCTATG	ACCTTGCTGA	AAAGAGTGAT	GTTCAGTTGA	CACTTTTTGA	CGAGTCACAT	420
TATTTTGTTT	TCGGTGGCAA	ACCCAATCAA	GTTATTGAAA	ATGATGCTAA	ACTAGTATTT	480
TCAGACCTGA	CTGAAATTTT	TCTTGAAGAA	GCGACTAGTG	GAAAGTTACG	GATGTTCCAA	540
GGTATGTTTT	TAGGAACAAA	AGAACAAACA	GACGATTTTG	AGCAGCGTTT	TGCTGAAGAG	600
CTTTGCCAAC	GATTCAGTGG	AGTTCGTTTC	CAGCCTGTCA	TTTATGAAGC	AATGCCGCTT	660
GGAACGACAA	AGGCTACTGC	TCTTTCACGA	CTAGCTGAGA	TTTTGAAGAT	TGATTCCTCA	720
GAGATTATGG	CCATGGGCGA	TGCTAATAAC	GATATCGAAA	TGCTCCAGTT	TGCAGGGCTT	780
GGGATTGCAA	TGGGAAATGC	CAGCGATTAT	GTCAAATCTC	TTGCGGATGC	CGTTACCTCA	840
AGCAACGAAG	AAGACGGCGT	TGCGCGTGCT	ATTGAGAAAT	ATATTCTATA	A	891

(2) INFORMATION FOR SEQ ID NO:2402:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 864 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2402:

CACATGTTAG	TTTTTTCAGA	ATACCAGACT	GGAACAATCG	ACCTTGCCCT	AAGCTTTTAT	60
GGATATGAGG	AATGCACACC	TAATTACTCT	TTTGGTCCAG	CCATTTCGTGA	TACATACGTT	120
CTACATTACA	TTACTAAAAG	ACAAGGAAAA	TTTTATTACA	AGGGTAAAAT	TGTTGATTTA	180
AAAGAAGGAG	ATTTCTTTCT	ATTAAAACCA	GAGGAACTAA	CCTTTTATCA	AGCAGATAGT	240
AAAGAACCTT	GGGCCTACTA	CTGGTTAGGA	ATCACTGGAG	GGAAATCCCC	TGATTATTTT	300

GCTCTTTCTC	AAATTTCTGA	TCAATCCTAT	CTCATCCAAT	CTGAAACTTG	TCATACCCAG	360
ACTACTGCAA	AACTCATCTC	AGACATTGTC	CGCTTCGCTC	AGATTACAAA	ATCAAGTGAA	420
TTAGCTCAAC	TCCATATCAT	GGGACAACTT	CATGAACTGA	TGTTTCATCT	GGGAACTATT	480
GCTCCCAATC	AGAAAAAAAA	GAATATTTCA	TCAACCCACC	AACTCTATCT	TGAATGCAAA	540
CGATTAATTG	ATAGCCACTA	TCCTCAATCA	CTTACAATTC	AAGATTTAGC	AAAAGAACTA	600
TCCGTTTACA	GAAGCTACTT	ATCAAGCGTA	TTCAAAGAAT	TTAATACCTT	ATCACCCAAA	660
GAATACCTAC	TCTACGTTCT	AATGCACCGA	GCTAGACAAC	TTCTCGAAAA	TACCCAAGAG	720
TCCATCAAGG	TAATTGCATA	CTCGGTAGGT	TTTTTCAGATC	CACTCCATTT	TTCGAAAGCT	780
TATAAACAAAT	ACTTTAATCA	GACTCCAAGT	CATACAAGAA	AAGAATACTC	TCAATACCAA	840
CTAGTAAGAA	AGGCAACATT	ATGA				864

(2) INFORMATION FOR SEQ ID NO:2403:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 417 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...417
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2403:

CCAATGTTAG	TACCTAAACG	TGTTAAACAC	CGTCGTGAGT	TCCGTGGAAA	AATGCGCGGT	60
GAAGCAAAAAG	GTGGAAAAGA	AGTAGCATTTC	GGTGAATACG	GTCTTCAAGC	TACAACTAGC	120
CACTGGATCA	CTAACCGCCA	AATCGAAGCT	GCTCGTATCG	CCATGACTCG	TTACATGAAA	180
CGTGGTGGTA	AAGTTTGGAT	TAAAATCTTC	CCACACAAAT	CATACACTGC	TAAAGCTATC	240
GGTGTGCGTA	TGGGATCTGG	TAAAGGGGCA	CCTGAAGGTT	GGGTANCACC	AGTTAAACGT	300
GGTAAAAATGA	TGTTCGAAAT	CGCTGGTGTA	TCTGAAGAGA	TTGCACGTGA	AGCGCTTCGA	360
CTTGCTAGCC	ACAAATTGCC	AGTTAAATGT	AAATTTCGTAA	AACGTGAAGC	AAAATAA	417

(2) INFORMATION FOR SEQ ID NO:2404:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2404:

TCAACTATAG TGAAGTTCAA TATCAAGAAG ATGTTGAAAC AATCCGAAAA GAGGCTGAAA	60
TCATCGAAGG AGAGTAATAT GGGACTCATA AAAACTCTAG CTAAAATTTA TGGTAATTAC	120
TTTTTGACCG TGCAAGGTGT AAAAGTGATG AAAACGATAA AGAAAGCTGA CCATGTCGTT	180
GTTGGTCTGG GCAAACTTTT TATTGCAGAT AAGCTAATGG ATACGGCTCG GTGGCTCATT	240
AAGCCAGAGG AGAGAGAATG A	261

(2) INFORMATION FOR SEQ ID NO:2405:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 276 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2405:

CACATCATAG TTTCTAAAGC ATTGTTAGAG ATTACTTTAA AATCCTCTTA TCAATTTGTT	60
CATATTCTAT TTCAATCTAC TATATATATC CCATCAACTA TGCATCATAA TTTAGGTAAC	120
TCATACTCAA TAAAAATCAA AAAGCAAAC T AGAAAGCTAG GCACAGACTG CTCAAAACAC	180
CGTTTTAAGG TTGTGGATAG AACTGACGAA GTCAGCTCAA AACACTGTTT TGAGGTTGTA	240
GATACGACTC ACATATATAC GACAAGGCAA CGCTGA	276

(2) INFORMATION FOR SEQ ID NO:2406:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2406:

TCTACAATAG TTCAAGTATT AAGTGAGGTG GATAATCTAA ATTTAGTGTG GTATACTATT	60
TTTGTTCATCG GTTACCGATT ACGTTCCTAT GGGTTCGTGA GAGGAGGTGA AACTAATGAG	120
CCTTATACCA GAGCTCGCTC TTACTATTAT AGCAGATGTT ATAGCTGGAA TTATCTTGTA	180
TTTCGTCTGC AAATGGCTAG ATGGTAA	207

(2) INFORMATION FOR SEQ ID NO:2407:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2407:

CAGTGGATAG TTGGCTGCAC CACCATAACT TCTGTAGTCC CCAACCCAAG CATCTTTTGTG	60
GTGGTTACGG ATAAAGCGGG TGATGGCACT GTTGATACCT TTATTGGTGT AGCCACCGTA	120
GGTCAAGTCA GCTGCCCAGT GATGGAAGGT AGAGTCGTAC TCACCACCAT GGCCCCACTC	180
GATCGCAAAG CGCCAGCCTT GTTTGTTAAT TTCTTTAGCA AGAACGTGGG TAGCCCAGGC	240
ACCGTTATCA CCTGA	255

(2) INFORMATION FOR SEQ ID NO:2408:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 396 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2408:

AGAAGAGTAG	TCATGGATAG	GAATATAGAT	CAAGAATTAG	TAAGTATTAT	AATACCAACA	60
CATAATAGGT	ATGAATCTCT	GATTAGAGCT	GTGAAAAGTT	GTTTACATCA	AAGTTATAAA	120
AATATCGAAG	TTATAATTAT	TGATGATAAT	TATAGTAATG	TAAATTTAAG	AAATAAAATT	180
ATCCATCAAT	TTGGCTATAC	CAATCATAGA	ATTAAGTTAA	TTTTAAGTAA	TGAAGATTTA	240
GGTGCAACTA	ATGCCAGAAA	CATAGGTATA	AAAAATTCTA	GAGGTAAGTA	TATATCATTT	300
TTAGACGATG	ATGATGAATA	TATGCCAGAT	CGAATTTTAA	AGTTGATGGC	NTGTTTAAAA	360
ANACCGTGGA	ATGAAGAATG	TAGCTCTAGT	TTATAG			396

(2) INFORMATION FOR SEQ ID NO:2409:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 459 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2409:

GCGGAANTAG	TGGGGGTGGG	GGTGGGTAGG	GCACTGCCAA	CGTTGNNTGG	TATGAACCAA	60
GTTCTCAAAG	TCTTATCTGA	AGTTGGCATT	CAAAAAATCA	TGTTCTTTTT	GANTGTTCTT	120
TTTTATGGAA	ATAACTGTAT	TGACAAAGCCG	GTGATTGAAG	ATACCNTGTT	TGACCCTGTC	180
AACCCCTTATG	CAGAGACAAA	ACTGATGGGC	GAACGAATGA	TTTACTGGAT	GGCCAATCGC	240
TACGACTGGA	AATATGTTAT	TTTCCGTTAC	TTTAATGTTG	CTGGGGCTGA	AATGGATGCT	300
TCAAACGGTC	TGCGTGTGAA	AAATCCAAC	CACATCATTC	CAAATATCAA	CAAGACCGCA	360
TTGGGACAAA	ATGATAGCTT	AAAAATATTT	GGAGATGACT	ACGATACACG	TGACGGTTCA	420
TGTATTCGAG	ATTACATTTA	TGTCTTGGAC	CTTGCATAG			459

(2) INFORMATION FOR SEQ ID NO:2410:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 786 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...786
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2410:

CATGGTTCAG	TTTGTGGGGG	TTCAGCGTCC	ACGCTACAAG	GTAGGGACTT	CCTATCCAGT	60
TATCTGGGTG	GACGTACCGC	TCATGGATAT	CTCGTCCAGC	ATGGTGCGTG	CCTTCCTTGC	120
CCAAGGTCGG	AAACCCAACT	TTCTCCTACC	TCAGCCAGTG	CTAGACTACA	TCGAGAAGGA	180
GGGGCTCTAC	TGATGTCCTA	TCAAGACTAT	ATCAACTGCT	CCCGTGAGGC	TTTGTGGGAA	240
AAAATGGCAG	AGCTTCTACC	TGAGAAACGT	CTAACCCATT	GTCTAGGTGT	GGAGCGTGCC	300
GCTATGGAAT	TAGCTCAGCG	CTTTGGTGTA	GATGTTGAGA	AAGCAAGTCT	AGCAGGTCTT	360
CTTCATGACT	ATGCTAAAAA	GTTGTCAGAT	CAGGAATTTT	TAGACTTGAT	TGACCGTTAC	420
CAGCTAGACC	CTGACCTCAA	AAACTGGGGC	AATAATGTCT	GGCATGGTAT	GGTCGGAATT	480
TACAAAATTC	AGGAAGATTT	GGATTTGCAT	GATTCAGAAA	TCCTGCGAGC	CATTGAAGTC	540
CATACAGTCG	GTGCTGGTCA	AATGACAGAC	CTAGATAAGG	TCATCTACGT	CGCAGACTAT	600
ATCGAGCACA	ATCGAGCCTT	TCCTGGAGTA	GATGTGGCGC	GTGAGATTGC	AAGTCTATCG	660
CTCAATAAGG	CGGTGGCCTA	CGAAACAGCT	CGTACCGTGG	AGTATCTAGC	TCATCAGGGA	720
TTCCCCATCT	ATCCCCAAAC	CCTTGAAACC	TATAACGCCT	TTGTGCACTA	TTTGAAAGAG	780
GAATAA						786

(2) INFORMATION FOR SEQ ID NO:2411:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1074 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1074
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2411:

ATTCTTCCAG	TTCGCCTTCC	TCGCTGCGTT	CGCGCAGCCC	CTGGCGCTCG	GCGTCGACGT	60
GGCGCTCCAG	TTCGGCGAAC	TTCTCCAGTT	GCCGCTGGCG	TTCCAGCAGT	TCTCGCCGGC	120

ACTGCCGCAG	GCGCTCGCGC	TCCCCTTCGA	GGCGCTGCGC	GGTCTCGGCG	CAGTCCTGTT	180
CCAGGCCGGC	TTCCCTTTTCC	CGCAGCAGTC	CTACCTGCTG	CTGCCAGGCT	TCCAGGCGCC	240
GGCGGTCGAG	CATGGCCGCC	TGGCAGGCGA	GAAACAGCCG	TTGCTCTTCG	GCCAGTCGCC	300
AGTCGCGGTA	GTCCCGTTGC	GCCGCCTGGC	GCTCGGTGTG	TTCCTGCGCC	GCGGCGCGAA	360
CCCGTAGCAA	TTGGCGGCCC	TGGGCGCGCT	CGGCCCGGTC	CAGGCGCAGG	CGTCGGACGC	420
GCAACAGCAG	CGCCAGGCTC	ATGCGCAGAG	GCTCCGCAAC	TGCGCGCAGG	CCTGTGCGTA	480
ATCGCTGGTT	TCGTGGGTAC	CCTGGCGCAG	CCACTGGCGG	ATCGCCGCGA	TCTTCTCGAT	540
GGCCTGGTCG	GCTTCGCTGT	CCTGGCCTTT	CTGGTATTCT	CCGATCTTCA	GCAGCAACTC	600
GACTTCCTCG	TACTTCGCCA	GCCATTGCGC	CAAGCGTCCG	GCCGCATGGC	GCTGATCGTC	660
GTCGACGATC	TGGTTCATGA	CCCGGCTCAC	CGAGTGCAGC	ACGTCGATGG	CCGGATAGTG	720
GTTGGCGGCG	GCCAGCTTGC	GCGACAGCAC	GATGTGCCCC	TCGAGAATCG	AGCGGGTCTC	780
GTCGGCCACC	GGCTCGCTCA	TGTCGTCGCC	TTCCACCAGC	ACGGTGTTAG	GCGCGGTGAT	840
CGAGCCCCGC	TCGGATTGCC	CGGCACGCTC	CATCAAGCGT	GGCAGCGCGG	CGAACACCGA	900
TGGCGGATAG	CCGCGGCGGG	TGGGCGGTTT	ACCGGCCGCC	AGGCCGATTT	CGCGCTGGGC	960
CCTGGCGAAG	CGGGTCAGCG	AGTCCATCAG	CAGCAGGACG	CGGCGTCCCT	GGTCGCGGAT	1020
ATACTCGGCG	ATGCTGGTGG	CGACGAAATC	GGAATTGAGC	TTTACACCAC	GTGA	1074

(2) INFORMATION FOR SEQ ID NO:2412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2412:

TATTTTGCAG	TTGTTGGAGG	ACAAATAATG	ACACCAGAAC	AACTTAAAGC	AAGTATTCTC	60
CAAAGAGCGA	TGGAAGGGAA	ATTAGTGCCG	CAAAATCCCA	ATGACGAACC	TGCAAGTGAA	120
TTATTAAAGA	GAATTAAAGC	TGAAAAAGAA	AAACTTATCA	GTGAAGGAAA	AATCAAACGA	180
GATAAAAAGG	AAACTGAGAT	ATTTCTGTGGT	GATGATGGGA	AACATTATGG	GAAGTTTGCT	240
GATGGAAGTA	CTCAAGAAAT	TGATGTTTCCT	TATGATATTC	CTGATACTTG	GGAGTGGGTG	300
AGGATAAAAT	CAATTTATTG	GAATTTTGGG	CAAAATAAGC	CAGAGAAATC	CTTTAGGTAT	360
ATAGATACGT	CTAGTATTGA	TAGAAAAAAG	AACATAATCA	ACTACAAAAA	TCTACAATAT	420
CTTTCACCTG	AACAAGCGCC	TTCCCGTGCC	AGAAAATTAG	TTTCGCAGAA	TAGTGTCTTA	480
TTTTCAACAG	TTAGACCATA	TCTAAAAAAT	ATTGCTGTAG	TTAGAGAACT	TAAAGAGTAT	540
TTGATAGCTA	GTACAGCATT	TATTGTTTTG	GATACTTTAC	TTAACGAAAC	ATATTTGAAA	600
TATTATTTAT	TATCAGATAA	TTTTATCAAT	CGTGTTAATA	ATAAATCTAC	TGGAACAAGT	660
TATCCTGCAA	TCAATGATTA	TAATTTTAAT	CTATTATTAA	TTGCTCTCCC	CCCCTATACC	720
GAACAACAAC	GAATAGTAGA	AGCAATCGAA	TCAGCTTTAG	AAAAAGTAGA	TGAATATGCT	780
GAAAGTTATA	ATAGACTAGA	ACAGCTAGAT	AAAGAATTTT	CAGATAAACT	AAAAAAATCT	840
ATTCTTCAAT	ATGCTATGCA	AGGAAAATTA	GTTGAACAAG	ACCCAAATGA	TGAATCAGTC	900
GAAGTTTAC	TTGAAAAAAT	ACGAGCAGAA	AAACAAAAAC	TCTTTGAAGA	AGGCAAGATT	960

AAAAAGAAAAG	ATTTGGACAT	TTCTATTGTT	TCCCAAGGAG	ATGATAACTC	TTATTATGAG	1020
GAAGTACCTT	GTGAAAATACC	AGAAAAGTTGG	GAATGGGTGA	GGTTAAACGA	TATAACCTCC	1080
TACATTCAAA	GAGGGAAGTC	TCCAAAATAT	TCAAATATTC	CTATATACCC	TGTGATTGCT	1140
CAGAAATGTA	ATCAATGGTC	TGGCTTTTCT	ATTGACTTAG	CAAGATTTAT	TGATCCCGAA	1200
ACAGTTCATA	GTTACCAGAA	AGAAAAGATTA	CTAAGAGATG	GTGATTTAAT	GTGGAATTCA	1260
ACAGGTCTAG	GTACGTTAGG	ACGATTAGCT	ATTTACCATG	AAAATAAAAA	TCCTTATGGC	1320
TGGGCTGTTG	CAGATAGCCA	TGTTACAGTT	ATAAGAGTCT	TATCGGGAGT	TATTAATTGC	1380
CATTTTCATCT	ATAATTTTCT	TTCTCTCCT	ATTGTTTCACT	CAGTTATTGA	AGAAAAAGCG	1440
TCGGGTAGTA	CAAAACAAAA	AGAATTATTA	ACGAAAACCTA	TAAAAGAATA	TTTAATCCCC	1500
CTCCCACCCC	TTCTGAACA	ATCCAGAATC	GTTGATAAAA	TCGAACAATT	TTTCGCCCAT	1560
ATTGACGCAC	TAATTTAG					1578

(2) INFORMATION FOR SEQ ID NO:2413:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1596 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1596
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2413:

TATTTTGCAG	TTGTTGGAGG	ACAAATAATG	ACACCAGAAC	AACTTAAAGC	AAGTATTCTC	60
CAAAGAGCGA	TGGAAGGGAA	ATTAGTGCCG	CAAAATCCCA	ATGACGAACC	TGCAAGTGAA	120
TTATTAAAGA	GAATTAAAGC	TGAAAAAGAA	AAACTTATCA	GTGAAGGAAA	AATCAAACGA	180
GATAAAAAGG	AAACTGAGAT	ATTTCTGTTG	GATGATGGGA	AACATTATGG	GAAGTTTGCT	240
GATGGAAGCA	CTCAAGAAAT	TGATGTTCCCT	TATGATATTC	CTGATACTTG	GGAGTGGGTG	300
AGGTTTTCTA	CATTGGTTGA	AATTGTCAGA	GGTGGCTCTC	CACGACCAAT	CAAAGATTAT	360
CTTACTTCTG	AAGTAGATGG	AATAAATTGG	ATAAAAAATAG	GTGATACTGA	AAAGGGTGAA	420
AAGTATATAA	ATAATGTTAA	AGAAAAAATC	AAAAAATCAG	GGCTTAACAA	AACTAGATTT	480
GTAAAAAAG	GTACATTTTT	GTTAACTAAT	TCTATGAGTT	TTGGTAGACC	TTATATTTTG	540
AATGTTGATG	GTGCAATACA	CGATGGATGG	TTGGCTATTT	CGAACTATGA	AAACTCATTGA	600
AATAAAGATT	ACCTATTCTA	TATTCTTTCA	TCAAATGTAG	TTTATTCTCA	ATTTCTATCT	660
CTAATTAGTG	GAGCTGTTGT	GAAAAACTTG	AATAGTGATA	AAGTTGCTTC	TATTCTTATC	720
CCTCTCCCCC	CACTATCCGA	ACAACAACGC	ATAATAGAAG	CAATCGAATC	AGCTTTAGAA	780
AAAGTAGATG	AATATGCTGA	AAGTTATAAT	AGACTAGAAC	AGCTAGATAA	AGAATTTCCA	840
GATAAACTAA	AAAAATCTAT	TCTTCAATAT	GCTATGCGAG	GAAAATTAGT	TGAACAAGAC	900
CCAAATGATG	AATCAGTCGA	AGTTTTACTT	GAAAAAATAC	GAGCAGAAAA	ACAAAACTC	960
TTTGAAGAAG	GCAAGATTAA	AAAGAAAGAT	TTGGACATTT	CTATTGTTTC	CCAAGGAGAT	1020
GATAACTCTT	ATTATGGGAA	CAAAGACGAA	ACAACCTCTT	ATCCTATATA	TAAAATCCCA	1080
GAAGCATGGA	GATATATTAA	ATTTGCTAGC	CTAGTTAACT	TCAGAATAGG	AAAAACTCCT	1140
CCACGCAGTG	AAGCTACTTT	TTGGGGAAC	GAAATACCTT	GGGTATCTAT	ATCAGATATG	1200
CCTATATCTG	GTTATGTAA	TAATACGAGA	GAATCTATTT	CTAAATTAGC	ATTAAAATCA	1260
AAGAAAAATAG	ACATTTTACC	TAAAGGAAC	TTATTAAATGA	GTTTTAAATT	ATCTATTGGA	1320

AAAGTTGCCA	TATTGGATAT	TCCTGCCACT	CATAATGAAG	CCATTATATC	GATATTCCCC	1380
TATGCTAATA	AAGAAAAATAT	TATCAGAGAT	TACTTAATGA	TATTTTTTGCC	ACTTATCTCT	1440
ACTTTAGGTG	ATTCAAAAAGA	TGCTATCAA	GGGAAAACAT	TAAATAGTAC	CAGTATCTCC	1500
GAATTATTAA	TCCCTATTTC	TAATCATGAA	GAGATGAAAA	GAATCATTTT	CAAAGTTGAT	1560
TTACTTTTTC	AAAAAGTTTC	TCAACTTTTT	GAGTAA			1596

(2) INFORMATION FOR SEQ ID NO:2414:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...225
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2414:

AATATGGCAG	TAAAGATTTC	AGGAGTCCTG	AAAGACGGCA	CAGGAAAACC	GGTACAGAAC	60
TGCACCATTC	AGCTGAAAGC	CAGACGTAAC	AGCACCACGG	TGGTGGTGAA	CACGGTGGGC	120
TCAGAGAATC	CGGATGAAGC	CTGCTTTTTT	ATACTAAGTT	GGCATTATAA	AAAAGCATTC	180
CTTATCAATT	TGTTGCAACG	AACAGGTCAC	TATCAGTCAA	AATAA		225

(2) INFORMATION FOR SEQ ID NO:2415:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 189 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...189
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2415:

TTTTTAGGCT	TATGTATTGC	CTGTATGGGC	GTATCTGTCG	GTGAAGGTTT	ATTGATGACT	60
GGACTGTTTA	AATCAGTAGC	ACGCCAACCA	GATAATGCTT	CTGAGTTTCG	TAGTTTGATG	120
TTTTTAGGTG	TTGCCTTTAT	TGAAGGAACT	TTCTTTGTAA	CTCTTGTCTT	CTCATTTATT	180
ATCAAATAA						189

(2) INFORMATION FOR SEQ ID NO:2416:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1035 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1035
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2416:

AGGCAAGGCT	TCGGAGCAGA	TATTGATGTA	ACAGGCGAAA	TCGTCTTTAA	TACAGGGATG	60
ACCGGCTACC	AAGAATCCAT	TACAGACCAG	TCTTATAATG	GACAAATCTT	GACCTTTACT	120
TATCCTTTGG	TAGGAAATTA	TGGTATTAAT	CGTGATGATT	ATGAATCCAT	TATTCCAAC	180
TGTAAGGGAG	TCGTTGTTTT	TGAAGAAGCG	CGTAGAGCTA	GCAACTGGCG	CAACCAAATG	240
ACCTTGATG	AATTTTTGAA	AGCCAAGAAA	ATTCCAGGGA	TTTCAGGAAT	TGATACGCGT	300
GCTCTTACCA	AGATTATCCG	TAAGCATGGT	ACTATGCGTG	CAACCTTGAC	CCATGTTGGG	360
GACAGTATGG	ACCATGTGAC	GGACCAGCTC	CAAGCAACAG	TTTTACCGAC	AGACAATATC	420
AAACAGGTTT	CTACTAAAAC	GTCCTTATCCA	GCTCCAGGAG	TTGGTTTGAG	CGTGGTGCTA	480
GTGGACTTTG	GTCTCAAGCA	CTCAATCCTA	CGTGAACTTT	CTAAACGCAA	CTGTAACGTG	540
ACAGTTGTTT	CTTATTCGAC	AACGGCTGAA	GAAATTCTCC	ATCTCAATCC	TGATGGAGTT	600
ATGTTGTCAA	ATGGTCCAGG	TAACCCAGAA	GACGTTCCAC	AAGCACTCGA	CATGATTCGC	660
GGTGTACAA	GAAAAATTCC	AATCTTTGGT	ATTTGTATGG	GACACCAACT	CTTTGCAATG	720
GCAAACGGGG	CTAAGACCTA	TAAGATGAAG	TTTGCCACC	GTGGATTCAA	CCATGCGGTA	780
CGTGAAATCG	CAACAGGACG	AGTAGACTTC	ACCAGCCAGA	ACCATGGTTA	TGCAGTCAGC	840
CGCGAGGATT	TGCCAGAGCA	CTTGATTATT	ACCCACGAAG	AAATCAATG	CAAGTCAGTG	900
GAAGGTGTGC	GCCACAGATA	CCAACCTGCT	TTCTCTGTTC	AATACCACCC	AGATGCAGCT	960
CCTGGACCAC	ACGACGCTAG	CTACCTATTT	GACGAGTTTA	TCGAGATGAT	GGAAATTTTT	1020
AAACAATCAA	ACTAA					1035

(2) INFORMATION FOR SEQ ID NO:2417:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 285 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2417:

ACTTGTC AAG	TTTGTAACAA	GACAAATATT	AAAAATAAAA	AAGAGGTATT	CGTTATGAAT	60
ACAAAAAAGA	TGTCACAATT	TGAAATTATG	GATACTGAGA	TGCTTGCTTG	CGTTGAAGGT	120
GGCGGATGCA	ATTGGGGAGA	TTTTGCCAAA	GCAGGTGTTG	GAGGAGGAGT	AGCACGAGGT	180
CTTCAGCTAG	GAATTAAAAC	AAGAACATGG	CAAGGTGCAG	CAACTGGTGC	TGCGGGAGGA	240
GCTATACTTG	GAGGTGTGGC	CTATGCAGCG	ACATGTTGGT	GGTAA		285

(2) INFORMATION FOR SEQ ID NO:2418:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 315 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2418:

TCATTCCAAG	TATTGATGAA	GGTAAAGATT	GCAAGGGCTG	CAAACCCCTGG	TTTCACAATC	60
GGGAAGGCTA	CACTCCAGAA	GGTACGAATC	TCACCACAAC	CGTCGATTTT	AGCTGATTCA	120
AGCAACTCTG	TAGGAATATT	TTCACTAAAT	TGTTTCATGA	GGAAGACACC	GAATGGCCAT	180
CCAATCAAAAG	GCAAGATAAC	TGCCCAGAGA	GTATCGTGGA	TTCCCATGAA	GTTGACGATA	240
CGTACCAATG	GTACAAGGAC	AACTTGTTTT	GGAAGCGCCA	TAGCAGCGAT	AAAGATAGCA	300
AATAGAATGC	GTTGA					315

(2) INFORMATION FOR SEQ ID NO:2419:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1908 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2419:

AAGAAACAAG	TATATACTGT	TTTTGCTGAT	TCTATAAAAG	ATGAATTAGA	CTATACCAAT	60
TTTAAGGAGA	AAGCACAGCT	TGCCTGTGTC	GTATATACTA	TGTGTGGAAT	TGTTGGTGTT	120
GTTGGAAACA	CAAAATGCAAC	TGATATTTTT	ATTCAAGGGC	TTGAAAAGCT	TGAATACCGT	180
GGCTATGATT	CTGCGGGAAT	TTTTGTCCTA	GATGGTGTCTG	ATAACCATTT	GGTGAAGGCG	240
GTTGGTCGTA	TTGCAGAAAT	GTCTGCCAAG	ACAGCTGGTG	TTGAGGGAAC	AACTGGTATC	300
GGACATACTC	GTTGGGCTAC	TCACGGAAAA	CCAAC TGAGG	ACAATGCTCA	CCCACACCGC	360
TCTGAGACAG	AACGTTTTGT	CTTGGTG CAT	AATGGGGTGA	TTGAGAACTA	TC TTGAAATC	420
AAGGAAGAAT	ACCTTG CAGG	TCACCACTTC	AAGGGGCAGA	CAGATACTGA	AATAGCCGTT	480
CATTTGATTG	GAAAATTTGC	GGAAGAAGAA	GGGCTCTCAG	TTCTTGAAGC	CTTTAAAAAA	540
GCTCTTCATA	TTATCCGTGG	TTCATATGCC	TTTGCCTTGA	TTGACTCTGA	AAATCCAGAT	600
GTCATCTATG	TAGCGAAAAA	CAAATCTCCA	CTTTTGATTG	GTCTTGGGGA	AGGCTACAAT	660
ATGGTCTGCT	CAGATGCTAT	GGCTATGATT	CGTGAAACCA	ACCAATACAT	GGAAATTCAT	720
GACCAAGAGT	TGGTAATCGT	CAAGGCTGAT	AGCGTGGAAG	TTCAAGACTA	TGATGGTAAC	780
AGTCGTGAAC	GTGCTAGCTA	TACTGCGGAA	CTTGACTTGT	CAGATATCGG	TAAGGGAACT	840
TATCCTTACT	ACATGCTTAA	GGAAATTGAT	GAGCAACCAA	CTGTTATGCG	TAAACTCATT	900
CAAGCCTACA	CGGATGATGC	TGGTCAAGTA	GTGGTTGCTC	CTGCTATCAT	TAAGGCTGTT	960
CAAGACGCAG	ACCGCATCTA	CATCCTTGCA	GCTGGAACAT	CTTACCATGC	AGGATTTGCT	1020
TCTAAGAAAA	TGTTGGAAGA	ATTGACAGAT	ACACCAGTTG	AACTTGGAAT	CTCATCTGAG	1080
TGGGGCTACG	GTATGCCACT	TCTCAGCAAG	AAACCACTCT	TCATCTTTAT	CAGCCAATCT	1140
GGTGAACAG	CGGATAGTCG	TCAAGTTTTG	GTCAAGGCTA	ATGAAATGGG	AATTCCAAGC	1200
TTAACAGTGA	CAAAATGTTCC	AGGTTCAACC	CTCTCACGTG	AAGCCAAC TA	TACCATGCTC	1260
CTTCACGCAG	GACCTGAAAT	TGCCGTGGCA	TCAACTAAAG	CCTATACAGC	GCAAATCGCA	1320
GCCCTTGCC T	TCCTTGCAAA	AGCAGTCGGA	GAAGCAAATG	GTAATGCTAA	AGCGCAAGCC	1380
TTTGACCTGG	TTCATGAATT	GTCAATCGTA	GCTCAGTCTA	TTGAATCAAC	TCTTTCAGAG	1440
AAAGAAACCA	TTGAAGCCAA	GGTTCGTGAA	CTTCTTGAAA	CAACTCGTAA	CGCCTTTTAC	1500
ATCGGACGTG	GTCAAGATTA	CTACGTAGCC	ATGGAAGCAA	GTCTCAAAC T	CAAAGAGATT	1560
TCTTATATCC	AGTGTGAAGG	TTTTGCGGCA	GGAGAACTCA	AGCACGGAAC	CATTGCC TTG	1620
ATTGAAGAAG	GAACGCCTGT	TTTGGCTCTC	TTGTCAGATC	CAGTTCTTGC	CAACCATACT	1680
CGTGGAATA	TCCAAGAGGT	CGCAGCCCGT	GGTGCCAAAG	TCCTCACTAT	CGCAGAAGAG	1740
AATGTAGCCA	AAGATACCGA	CGATATCGTC	CTTACGACCG	TACATCCATA	CCTCTCACCA	1800
ATTTCAATGG	TCGTACCAAC	GCAATTAGTC	GCTTACTTTG	CAACCCTCCA	CCGTGGCCTC	1860
GATGTGGACA	AACCACGTAA	CCTTGCCAAG	TCAGTAACGG	TAGAATAA		1908

(2) INFORMATION FOR SEQ ID NO:2420:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2420:

AACGGGCTTT	ACTCGTGAAA	TTTCGAATTA	TTTAGTCAAG	ACTCTAGAAG	GTTTTGGTTA	60
CCAGCCAGTT	CGCACAGCTA	AGGGTGGTGT	CAATGTGACC	ATCAAAGGTC	AAAATGATGA	120
GCAACATCGC	TATGTGACTG	CTCATGTGGA	TACGCTGGGT	GCTATTGTTC	GTGCTGTCAA	180
ACCAGATGGT	CGTCTTAAAT	TGGACCGTAT	CGGTGGTTTT	CCTTGGAACA	TGATTGAAGG	240
TGAAAACGTG	ACCGTTCATG	TGGCTAGCAC	AGGTCAAAAG	GTATCAGGAA	CCATCCTCAT	300
CCACCAAAC	TCTTGCCATG	TCTACAAGGA	TGCAGGAAC	GCAGAGCGCA	CGCAGGACAA	360
TATGGAAGTG	CGTTTGGATG	TAAAAGTAAG	CAATGAAAAA	GAAACTCGTG	CTCTTGGGAT	420
TGAGGTCGGT	GATTTTATCA	GCTTCGATCC	ACGAACTGTT	GTGACTGATA	CAGGTTTTTA	480
TCAAGTCTCG	TCATTTGGAT	GA				502

(2) INFORMATION FOR SEQ ID NO:2421:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 435 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2421:

GAGGTAAAAG	TCTTGGCTAA	ACCAACACGT	AAACGTCGTG	TGAAAAAGAA	TATCGAATCT	60
GGTATTGCTC	ATATTCACGC	TACATTTAAT	AACACTATTG	TTATGATTAC	TGATGTGCAT	120
GGTAATGCAA	TTGCTTGGTC	ATCAGCTGGT	GCTCTTGGTT	TCAAAGGTTC	TCGTAAATCT	180
ACACCATTCG	CTGCTCAAAT	GGCTTCTGAA	GCTGCTGCTA	AATCTGCACA	AGAACACGGT	240
CTTAAATCAG	TTGAAGTTAC	TGTAAAAGGT	CCAGGTTCCTG	GTCTGTGAGTC	AGCTATTCGT	300
GCGCTTGCTG	CCGCTGGTCT	TGAAGTAACA	GCAATTCGTG	ATGTGACTCC	AGTGCCCACA	360
CAATGGTGCT	CGTCCTCCAA	AACGTCGCCG	TGTATAATCA	TCGCATTACA	CTGCTTTTTCG	420
TTTAAGAGGG	AGTAA					435

(2) INFORMATION FOR SEQ ID NO:2422:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 582 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...582
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2422:

AGACTGAAAG	TATTTTCTAT	CACTTCTGTG	AAACCAGGAG	AAGGAAAAAC	AACGACTTCC	60
ACCAATATCG	CTCGGGCTTT	TGCGCGTGCA	GGTTACAAAA	CGTTGCTGAT	TGATGCAGAC	120
ATGCGTAACT	CCGTGATGTC	AGGTGTCCTT	AAATCAAGGG	AAAGGATTAC	CGGGCTAACA	180
GAATTTCTAT	CAGGGACTAC	AGACCTGTCA	CAGGGACTTT	GTGATACCAA	TATTGAGAAT	240
CTCTTTGTGA	TTCAGGCTGG	CTCTGTGTCA	CCAAATCCGA	CAGCCCTTCT	TCAAAGTAGG	300
AATTTTCAGTA	CAATGCTTGA	AACCGTGCGT	AAATATTTTG	ACTATATCGT	CGTAGACACT	360
GCTCCTGTCG	GTGTCGTGAT	TGATGCGGCT	ATCATTACGC	AGAAATGTGA	TGCTTCTATT	420
TTAGTGACGA	AGGCAGGCGA	AACAAAGCGA	CGGGATATTC	AAAAAGCGAA	AGAACAGATA	480
GAACAAACTG	GGAAGCCGTG	TTTAGGAGTT	GTGTTGAATA	AATTCGATAC	TTCAGTAGAC	540
GAATACGGTT	CTTATGGAAG	TTATGGGAAA	AAGAAAAAAT	AG		582

(2) INFORMATION FOR SEQ ID NO:2423:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 474 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2423:

AAGAAGAAAG	TAAAAAATTA	CAAAGGAGTA	CCCATGATAC	CGCAAGAAAT	GTGGAATAAA	60
TACAAGCAAA	TCAATCCTTT	GATCGGAGAT	GAAATCGATG	CTTGGGCTTT	TGGAGTTGAA	120
CCAGACCTTT	TAGCGGATTT	GGTGTTTAAA	GGAGAAAAGA	CAGCAACAGC	ATCAGCCTAT	180
GACCTCTATG	TACTAGAAGA	CGAACCCTT	CCCCAAGTAG	GGACCTTCGA	TATCATTTTA	240
GATAGTCAAA	ATCAGTCTGT	CTGCATTGTC	GAAATTACAA	AGGTTTCTGT	TGAACTCTTC	300
AATCAAGTTT	CTGCGCAACA	TGCCTTTAAG	GAAGGTGAGG	GAGACAAATC	ACTTGCCTAT	360
TGGCGCCAGG	TTCATGAGGA	CTTTTTCACA	GACTGTTTGG	GTGAAGTAGG	GCTGACTTTT	420
ACATCTGAAA	GCAAGGTTGT	TTTAGAAGAA	TTTCGCAAGG	TCTACCCACT	GTAG	474

(2) INFORMATION FOR SEQ ID NO:2424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2424:

AAGGAGAAAG	TAAGTATGTC	AAAAGAAATT	AAATTTTCAT	CAGATGCCCCG	TTCAGCCATG	60
GTTTCGTGGTG	TCGATATTCT	TGCAGACACT	GTTAAAAGTAA	CCTTGGGACC	AAAAGGTCGC	120
AATGTCGTTT	TTGAAAAGTC	ATTCGGTTCA	CCCTTGATTA	CCAATGACGG	TGTGACCATT	180
GCCAAAGAAA	TGAATTGGA	AGACCATTTT	GAAAATATGG	GTGCTAAGTT	AGTATCAGAA	240
GTAGCTTCTA	AAACCAATGA	TATCGCAGGT	GACGGAACTA	CGACTGCAAC	AGTCTTGACC	300
CAAGCTATCG	TCCGTGAAGG	AATCAAAAAC	GTCACAGCAG	GTGCAAATCC	AATCGGTATT	360
CGTCGTGGGA	TTGAAACAGC	AGTTGCCGCA	GCAGTTGAAG	CTTTGAAAAA	CAACGCCATC	420
CCTGTTGCCA	ATAAAGAAGC	TATCGCTCAA	GTTGCAGCAG	TATCTTCTCG	TTCTGAAAAA	480
GTTGGTGAGT	ACATCTCTGA	AGCAATGGAA	AAAGTTGGCA	AAGAAGGTGT	CATCACCATC	540
GAAGAGTCAC	GTGGTATGGA	AACAGAGCTT	GAAGTCGTAG	AAGGAATGCA	GTTTGACCGT	600
GGTTACCTTT	CACAGTACAT	GGTGACAGAT	AGCGAAAAAA	TGGTGGCTGA	CCTTGAAAAT	660
CCGTACATTT	TGATTACAGA	CAAGAAAATT	TCCAACATCC	AAGAAATCTT	GCCACTTTTG	720
GAAAGCATTC	TCCAAGAGCA	TTGTTCCATT	TGGGATTATG	CCGGATGA		768

(2) INFORMATION FOR SEQ ID NO:2425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2425:

TGGAGGAAAG	TTATGACCAT	TTTTCCAGAT	GATTTTCTTT	GGGGTGGAGC	TGTTGCAGCT	60
AATCAAGTAG	AGGGAGCATA	TAATGAAGAT	GGTAAGGGCT	TATCAGTTCA	GGATGTGTTA	120
CCCAAAGGTG	GATTAGGAGA	AGCAACAGAA	AATCCTACAG	AAGATAACTT	AAAAATTGATA	180
GGTATTGATT	TTTATCATAA	ATATAAGGAA	GATATATCCT	TGTTTTCTGA	AATGGGCTTT	240
AATGTTTTTC	GTACTTCTAT	TGCATGGAGT	AGAAATTTTC	CAAAAGGAGA	TGAAGAAGAA	300
CCTAACGAAG	CTGGTTTGAA	ATATTATGAT	GAATTGTTTG	ATGAACTACA	TGCTCACGGG	360
ATAGAGCCAC	TTGTAACCTC	TTCACACTAT	GAGACTCCAT	TATATTTAGC	AAGAAAATAT	420
CATGGATGGG	TTGATAGGAG	AATGATTTCAT	TTTTATGAAA	AATTTGCTCG	AACAGTTTTA	480
GAAAGGTATA	AAGATAAAGT	TAAATATTGG	CTTACATTTA	ACGAAGTAAA	CTCTGTTTTG	540
GAATTACCAT	TTACTAGTGG	AGGAATAGAT	ATACCTAAGG	AGAATCTTTC	GAAACAAGAA	600
TTATATCAAG	CTATACATCA	TGAATTAGTC	GCCTCAAGTT	TGGTTACAAA	AATTGCTCGT	660
GAGATTAATT	CAGAGTTTAA	GGTGGGATGT	ATGGTATTAG	CTATGCCAGC	TTATCCAATG	720
ACTCCAAATC	CAAAAGATGT	ATGGGCGACT	CATGAGTATG	AGAATCTAAA	TTATCTATTT	780
TCAGATGTGC	ATGTTAGAGG	TTATTATCCG	AATTATGCAA	AAAGATATTT	TAAGGAAAAT	840
GACATTAACA	TAGAGTTTGC	AGCTGAAGAT	GCAGAGTTAT	TAAAAAATTA	TACTGTAGAT	900
TTTTTATCCT	TTAGCTATTA	CATGAGTGTG	ACTCAATCTG	CTATTCCAAC	ACAGTATAAT	960
TCAGGAGAAG	GGAATATTAT	TGGTGGTTTA	GTAAATCCTT	ATTTAGAGTC	TTCAGAGTGG	1020
GGATGGCAAA	TTGATCCAAT	TGGACTACGT	ATAATTTTAA	ATAGATATTA	TGACCGTTAT	1080
CAAATCCCAT	TATTTATAGT	AGAAAATGGA	TTAGGTGCTA	AAGATCAACT	AATAAAAGAT	1140
GAACTTAATA	ACTTAACCGT	CCAAGATGAT	TATAGAATTC	AGTATATGAA	AGAACATTTA	1200
TTGCAAGTTG	CTGAAGCTCT	ACAGGATGGT	GTTGAAATTA	TGGGCTATAC	GTCTTGGGGA	1260
TGTATTGACT	GTGTTTCTAT	GTCCACTGCA	CAACTTTTCTA	AAAGGTACGG	TCTCATTTAT	1320
GTTGATCGAA	ATGATGATGG	AAATGGCACA	TTCAATCGAT	ATAAGAAAAAT	GTCCTTTACT	1380
TGGTATAAAG	GAGTGATTGA	ATCAAATGGA	GACTCCTTAT	TCAAATAG		1428

(2) INFORMATION FOR SEQ ID NO:2426:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 711 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2426:

AAAGTTGAAG	TAGCTGGAGA	TGGCACAGCA	ACAATCACAT	TCCCAGATGG	TTCAGTAGTG	60
ACGATTCTAG	GAAAAGATAC	AGTTCAACAA	TCTGCGAAAG	GTGAATCTGT	AAC'TCAAGAA	120
GCTACACCAG	AGTATAAGCC	AGAAACTACA	CCAGGTGGAG	ATAAGGGAGG	CAATAC'TGGA	180
AACTCAGATG	CTAATGCGAA	TGCAGGCGGT	GGTAGCCAGG	CGGGTGGATC	AGCTCACACA	240
GGTTCACAAA	ACTCAGCTCA	ATCACAAGCT	TCTAAGCAAT	TAGCTACTGA	AAAAGAATCA	300
GCTAAAAATG	CCATTGAAAA	AGCAGCCAAG	GACAAGCAGG	ATGAAATCAA	AGGCGCACCG	360
CTTTCTGATA	AAGAAAAAGC	AGAACTTTTA	GCAAGAGTGG	AAGCAGAAAA	ACAAGCAGCT	420
CTCAAAGAGA	TTGAAAATGC	GAAAACTATG	GAAGATGTGA	AGGAAGCAGA	AACGATTGGA	480
GTGCAAGCCA	TTGCCATGGT	TACAGTTCCT	AAGAGACCAG	TGGCTCCTAA	GACAACAAGT	540
GCACCGCAAG	CAACTGCAGG	AACAATGCAA	GATGTTACCT	ACCAGTCACC	TGCTGGCAAA	600
CAATTACCTA	ACACAGGTTT	AGCATCAAGT	GCAGCACTTG	CTAGTCTTGG	TCTAGTGGTG	660
GCAACAAGTG	GTTTTGCTTT	GCTAGGAAGA	AAGACTAGAC	GTAAGAAAATA	G	711

(2) INFORMATION FOR SEQ ID NO:2427:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 225 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2427:

TGGGTTGAAG	TAACTCTTGT	TCAAAGTGGT	GTTACGATTT	CAAGAACTCC	TCTCAGCTCT	60
GAGGCCACGG	TAATGATTGA	TGCGACGGAA	GTAAAAATCA	ATCGCCCTAA	AAAAGAATTA	120
GCGAATTATT	CTTGTAAGAA	AATGCCACGC	TATGAAGGCT	CAAGCGATTG	TCACAAGTCA	180
AGGGAGAATT	GTTTCTTTTG	ATATCACTGT	GAAC'TATTGT	CATGA		225

(2) INFORMATION FOR SEQ ID NO:2428:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 987 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2428:

TATAATGAAG	TGTTAGAAAA	ACAGGTTTCA	TTTGCCTGGA	AAGGAAAAAT	TATGTCTGAA	60
AAAAATTTT	ATATTACAAC	GCCGATTTAC	TATCCATCTG	GGAAACTTCA	TATCGGTTCT	120
GCCTACACAA	CTATCGCATG	TGATGTCCTA	GCACGTTACA	AACGCCTGAT	GGGCTACGAT	180
GTATTTTATC	TGACAGGTCT	TGATGAACAT	GGTCAGAAAA	TCCAGCAGAA	AGCGGAAGAA	240
GCTGGTATTA	CACCTCAAGC	CTATGTTGAT	GGAATGGCGG	TTGGAGTTAA	AGAACTCTGG	300
CAATTACTAG	ATATCTCATA	CGATAAATTT	ATCCGTACAA	CTGATGACTA	CCATGAAAAA	360
GTTGTCGCAC	AGGTCTTTGA	ACGCTTACTT	GCTCAAGATG	ATATTTACTT	GGGTGAATAC	420
TCTGGTTGGT	ATTCAGTATC	AGACGAAGAA	TTCTTTACAG	AAAGCCAGCT	GGCAGAAGTT	480
TTCCGTGATG	AAGCTGGAAG	TGTGACTGGT	GGTATTGCTC	CATCAGGTCA	TGAGGTTGAA	540
TGGGTTTCTG	AAGAATCATA	CTTTCTTCGC	CTTAGCAAAT	ACCAAGACCG	TTTGGTCGAA	600
TTTTTCAAAG	CTCATCCTGA	ATTTATCACG	CCAGATGGTC	GCCTTAATGA	AATGCTACGC	660
AACTTCATCG	AGCCAGGTTT	GGAAGATTTG	GCGGTATCTC	GTACACCTT	TACATGGGGA	720
GTGCCTGTCC	CATCAAATCC	AAAACACGTT	GTCTACGTTT	GGATTGATGC	CCTTCTTAAC	780
TATGCGACAG	CTCTTGCTA	CGCTCAAGAC	GAACATGGTA	ACTTTGACAA	GTTCTGGAAT	840
GGAACAGTCT	TCCATATGGT	AGGAAAAGAT	ATCCTTCGCT	TCCACTCTAT	CTACTGGCCA	900
ATCCTTCTTA	TGATGTTGGA	TGTTAAATTA	CCTGATCGTT	TGATTGCCCC	ATGGTTGTTT	960
GTTTCATGAAA	GACGGAAAAA	TGTCTAA				987

(2) INFORMATION FOR SEQ ID NO:2429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2429:

ACTTTCGAAG	TATGCTATAA	TAAAGAAAAAT	AAAAACAAGA	GGTTTATCAT	GACAAAAATTA	60
TATGGAAGCT	TGGAAGCGGG	CGGTACAAAAG	TTTGCTGTG	CTGTCGGTGA	TGAAAACTTT	120
AACGTTGTAG	AAAAACACA	ATTTCCAACA	ACAACTCCAA	TCGAAACAAT	CGATAAAACC	180
ATTGAGTCTT	CTCAAATTC	GATAACCTTT	CTGGTCTTGC	AGTTGGTTCA	TTTGGGCCGA	240

TTGATATTGA CAAAACTCA AAAACTTATG GCTTTATCAC GACGACTCCA AAACCAAAC	300
GGGCAAATGT GGACTTGCTT GGTGCCTTTC GTCGCGCCCT AA	342

(2) INFORMATION FOR SEQ ID NO:2430:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 429 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2430:

TGGACCGAAG TCATCGAGTT CAACGCTCGG TTCGGAGATC CAGAACTCA GCTTATCTTG	60
CCTCGCTTAA CCTCTGACTT TGCTCAAAAT ATCACAGATA TCCTGGATAG CAAGGAGCCA	120
AATATCACGT GGACGGACAA GGGTGTGACT CTGGGTGTGG TTGTCGCATC CAAGGGCTAC	180
CCGCTAGATT ATTCAAAGGG TGTGAGTTG CCAGTCAAAA CCGATGGCGA CATCATTACC	240
TACTATGCAG GGGCTAAGTT TGC GGAAAAT AGCAGAGCAC TGCTCTCAA CCGCGGACGA	300
GTTTATATGC TCGTTACCAC AGCAGATACC GTCAAAGAAG CCAAGCCAG CATCTACCAA	360
GAAGTATCCC AACAAAAAAT AGAAGGACTC TTCTACCGAA CAGATATCGG AAGCAAGGCA	420
ATTAAGTAA	429

(2) INFORMATION FOR SEQ ID NO:2431:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1815 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2431:

GCTCGAGAAG	TGGTGTGGG	TTATGACTTG	TCTGAAGAAG	AAGAACAAAT	CCTCAGCCGC	60
CAGATGAATC	TGGTACTCTC	TTATGAAAAA	GAAAGCTTTG	AAGACCTTCA	TTTATTGGAT	120
TTGCGATTGG	CAACGGTGGA	GCAAACGGCA	TCTAGTAAGC	TGCTCCAGTA	TGTTTCATCGG	180
ACTCAGATGA	GGGAATTGAA	CCACCTCAAA	CCTGTTATCC	GCTACGAAAT	TAAGGATTTC	240
TTGCAGATGG	ATTATGCGAC	CAAGGCTAGT	CTGGATTTGG	TTGAGAATGC	TCGCTCAGGT	300
AAGAAACAAG	GCAGTCTTTT	CTGGCTTTTG	GATGAAACCA	AAACGGCTAT	GGGGATGCGT	360
CTCTTGCGTT	CTTGGATTCA	TCGCCCCCTG	ATTGATAAGG	AACGAATCGT	CCAACGTCAA	420
GAAGTAGTGC	AGGTCTTTCT	CGACCATTTT	TTTGAGCGTA	GTGACTTGAC	AGACAGTCTC	480
AAGGGTGTTT	ATGACATTGA	GCGCTTGGCT	AGTCGTGTTT	CTTTTGGCAA	AACCAATCCA	540
AAGGATCTCT	TGCAGTTGGC	GACTACCTTG	TCTAGTGTGC	CACGGATTCTG	TGCGATTTTA	600
GAAGGGATGG	AGCAACCTAC	TCTAGCCTAT	CTCATCGCAC	AACCTGGATGC	AATCCCTGAG	660
TTGGAGAGTT	TGATTAGCGC	AGCGATTGCT	CCTGAAGCTC	CTCATGTGAT	TACAGATGGG	720
GGAATTATCC	GAAGTGGATT	TGATGAGACT	TTAGACAAGT	ATCGTTGCGT	TCTCAGAGAA	780
GGGACTAGCT	GGATTGCTGA	GATTGAGGCT	AAGGAGCGAG	AAAACCTCTGG	TATCAGCACG	840
CTCAAGATTG	ACTACAATAA	AAAGGATGGC	TACTATTTTC	ATGTGACCAA	TTCGCAACTA	900
GGAAATGTGC	CAGCCCACCT	TTTCCGCAAG	GCGACGCTGA	AAAACCTCAGA	ACGCTTTGGA	960
ACCGAAGAAT	TAGCCCGTAT	CGAGGGAGAT	ATGCTTGAGG	CGCGTGAGAA	GTCAGCCAAC	1020
CTCGAATACG	AAATATTTAT	GCGCATTTCG	GAAGAGGTCG	GCAAGTACAT	CCAGCGTTTA	1080
CAAGCTCTAG	CCCAAGGAAT	TGCGACGGTT	GATGCTTTAC	AGAGTCTGGC	GGTTGTGGCT	1140
GAAACCCAGC	ATTTGATTCG	ACCTGAGTTT	GGTGACGATT	CACAAATTGA	TATCCGGAAA	1200
GGGCGCCATG	CTGTCGTTGA	AAAGGTTATG	GGGGCTCAGA	CCTATATTCC	AAATACGATT	1260
CAGATGGCAG	AAGATACCAG	TATTCAACTG	GTTACAGGGC	CAAACATGAG	TGGGAAGTCT	1320
ACCTATATGC	GTCACTTAGC	CATGACGGCG	GTTATGGCCC	AGCTGGGTTT	CTATGTTCC	1380
GCTGAAAGCG	CCCATTTACC	GATTTTTGAT	GCGATTTTTA	CCCGTATCGG	AGCAGCAGAT	1440
GACTTGTTT	CGGGTCAGTC	AACCTTTATG	GTGGAGATGA	TGGAGGCCAA	TAATGCCATT	1500
TCGCATGCCA	CCAAGAACTC	TCTCATTTCT	TTTGATGAAT	TGGGACGTGG	AACTGCAACT	1560
TATGACGGGA	TGGCTCTTGC	TCAGTCCATC	ATCGAATATA	TCCATGAGCA	CATCGGAGCT	1620
AAGACCTCT	TTGCGACCCA	CTACCATGAG	TTGACTAGTC	TGGAGTCTAG	TTTACAACAC	1680
TTGGTCAATG	TCCACGTGGC	AACTTTGGAG	CAGGATGGGC	AGGTCACCTT	CCTTCACAAG	1740
ATTGAACCGG	GACCAGCTGA	TAAATCTACG	GTATCCATGT	TGCCAAGATT	GCTGGCTTGC	1800
CAGCAGACCT	TTTAG					1815

(2) INFORMATION FOR SEQ ID NO:2432:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...372
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2432:

CTAGGAGAAG	TTATGCGTCT	TATCTATCTG	ATAATTGGTT	TTTTATCACT	GGCCTTGGCT	60
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ATTGTTGGGG	TTGTTTTACC	CTTGTTGCCG	ACAACGCCTT	TCCTTTTGTT	GTCTATTGCT	120
TGTTTCTCCA	GAAGTTCCAA	GCGTTTCGAA	GACTGGCTTT	ATCATACCAA	GCTCTATCAA	180
ACATATGTAG	CTGATTTTCG	CGAGACCAAG	TCTATTACGC	GTGAACGAAA	GAAAAAATC	240
ATCGTCTCTA	TCTACGTCTT	GATGGGAATT	TCTATTTATT	TTGCACCTCT	TTTACCAGTC	300
AAAATCGGTT	TGGGTGCTTT	GACCATCTTT	ATCACTTATT	ATCTCTTCAA	GGTCATTCCA	360
GACAAAGAAT	AG					372

(2) INFORMATION FOR SEQ ID NO:2433:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 255 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...255
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2433:

AAGCTGCGAG	TTGTGAGGCT	CGCTATTATG	TTGCGTGATT	TAGATCTCTA	TAAGGTGATT	60
TTCGAGGGAA	ATTATCGGGC	GACAGCGGGT	AGAGAAGAGA	TGAAAGAGGC	TATTTTGGAA	120
TATCAAGCAA	ATCTGCTGC	CTTAAAAGAT	CTCAAAGAAA	AGGCTAAGAA	TATTTCCAGA	180
GAGTATTCTG	AAGAGCATCT	GTTACAAATC	TGTTGGACT	TTTATGAGAA	ACAAGCCGCT	240
TTAGGGAGAA	AGTAA					255

(2) INFORMATION FOR SEQ ID NO:2434:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2434:

AATAGGCGAG	TGATGGGGAT	CGAACCCACG	CATGCCAGAG	CCACAATCTG	GTGTGTTAAC	60
CACTTCACCA	CACCCGCCAT	AATTCTATTA	ACACGGGCAG	TAGGAATTGA	ACCCACACTG	120
AAGGTTTTGG	AGACCTTAGT	TCTACCTTTA	AACTATGCCC	GTAAAATGGA	AGGGGAGGGA	180
TTCGAACCCC	CGAACCCGAA	GGAGCGGATT	TACAGTCCGC	CGCGTTTAGC	CTCTTCGCTA	240
CCCTTCCAAA	ATATATAA					258

(2) INFORMATION FOR SEQ ID NO:2435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2435:

ATATTTAGAG	TCCATTACAG	GTTCTGGTGG	GAACCTAGGC	CCAGGATTTG	GTGTGATAAT	60
TCCATGATGC	GAAATGAGTT	TCGAGAAAGG	GTGGAGCAAC	TTCTTCAACA	AAAAGAAATA	120
AATGAAAATA	GTGAGTTGAG	TCACCTGTTT	CGTCTTGCTA	TACAAAATTT	AGACAGAAAT	180
GAAAAATACC	AATCGTTCAT	GGCCAATTTG	AGTCAAGGGT	TGTCACTTTA	CCTCATGACG	240
CATCATTACC	AGGCACCTAA	GTCTGTCAAT	GATTTTGGTT	TATGGATTGC	CAAAGCTCCT	300
AGCCAGGAAA	GAGGGAGACT	GGCTTTCTTG	CAGATGCTTG	CTCAAACCCCT	ACAGGGCTTT	360
CGTTAA						366

(2) INFORMATION FOR SEQ ID NO:2436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2436:

GGGGAAGAG	TAATGGATTT	ATTTGGATTT	GGGACGGTTA	TTGTTCAATTT	TTTAATTATT	60
AGTCACAGTT	ACCATTTTAT	TTGTAAAGGT	CAAATAAATA	GAAAAGAATT	ATTCGTTTTT	120
GGTGCTTATA	CATTACTAAC	AGAAATAGTA	TTTGATTTTC	CCTTATATAT	TCTATATTTA	180
GATGGGTAG	GGATTGAAAG	ATTTTTATTT	CCTTTGGGAT	TATATTCCTA	TTTTCGATGG	240
ATGAAACAGT	ATGAGAGGGA	TAGAGGACTA	TTCCTAAGTT	TACTACTATC	TCTTTTATAT	300
GAGAGCACTC	ATAACTTTCT	GTCCGTAAC	TTCTCCTCTA	TAACAGGAGA	TAATTTTGT	360
TTACAATATC	ATTTCCCAT	CTTTTTCGTT	GTGACGGTGT	TAACCTATTT	TGTTACATTA	420
AAAATCATTT	ACTATTTCCA	TTTGGAAC	GCCATTTTGT	ACGAGGACTA	CCTTTATCCT	480
TTCTTGAAAA	AAGTATTTTT	TGCTTTACTA	TTGCTACATA	TTGTATCTTT	CGTTTCAGAT	540
ATGGTAAGTA	CGATTAAACA	TTTGAATAGT	TTTGGAAGTA	TTTTGTCATC	TATTGTCCTT	600
ATCTCTCTCC	TTTTGACCTT	CTTTGCAATG	AATTCCTCATA	AAGTTCAAAT	GGAGAAAGAG	660
ATTGCTTTGA	AGCAGAAGAA	ATTTGAACAG	AAACATTTAC	AGAATTACAC	AGATGAAATT	720
GTTGGTCTGT	ATAATGAAAT	CCGTGGTTTT	CGACATGATT	ATGCTGGAAT	GCTTGTCAGC	780
ATGCAGATGG	CAATTGACAG	TGGTAATTTA	CAGGAAATTG	ACAGAATTTA	CAATGAAGTT	840
TTAGTCAAAG	CAATCATATA	ATTGCGTTCA	GATAAGTACA	CTTACTTTGA	TTTGAACAAC	900
ATAGAAGACT	CAGCTTTACG	AAGTTTGGTT	GCTCAGTCAA	TTGTCTATGC	TCGAAATAAT	960
GGTGTAGAGT	TTACACTGGA	AGTAAAAGAT	ACGATTACCA	AGCTTCCAAT	TGAACATTG	1020
GATTTGGTTC	GTATCATGAG	CGTTTTATTG	AATAATGCTG	TCGAAGGATC	GGCTGATAGC	1080
TATAAAAAGC	AGATGGAAGT	AGCAGTTATT	AAGATGGAAA	CTGAAACAGT	TATTGTGATT	1140
CAGAATTCAT	GTAATAATGAC	GATGACTCCT	TCAGGAGATC	TATTTGCCTT	AGGATTCTCC	1200
ACTAAGGGAA	GAAATCGCGG	AGTCGGATTA	AATAATGTGA	AAGAACTACT	AGATAAGTAC	1260
AACAATATTA	TTTTAGAAAC	AGAGATGGAA	GGCAGTACAT	TTAGACAAAT	CATTAGATTT	1320
AAGAGGGAAT	TTGAATGA					1338

(2) INFORMATION FOR SEQ ID NO:2437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2437:

AAGAGAAGAG	TACGATTAAG	TGCTCTTTTT	TATGGTTGTA	AAAAAGTTCA	TTTGAACAAT	60
TTAAGCAGTG	TAGATAGTGA	GGAGCTGTTT	CAATTCATC	GTGAACGAGG	GAATGCTGAA	120
AACTTTATCA	AAGAAAGGAA	AGCAGGATTC	TTTGGGGATA	AGACAGATAG	TTTCGACCATG	180

ATTAAGAATG AAGTACGTAT GATGATGGGC TGTCTGGCTT ATAATCTCTA CCTCTTTT	240
AAGCAGCTAG CTGGTGATGA AGTAAAGGCC TTGACTATCA AGCGTTTTCG ACGTCTCTTC	300
CTTCATATTG CCGGAAAATA TGTCTCTACT GCTAGACGAC ATATTCTCAA ATTCTCAAGT	360
CTATACGCCT ATTCAAAACA GTTCAAGCC TTATTTGATA CAATCTGCCA GATAAATCTG	420
ATACTCCCTG TTCCATATAG AGCTAGAGGG CAGGGGAAAA CATGCCTAAC AGAATAA	477

(2) INFORMATION FOR SEQ ID NO:2438:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...264
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2438:

ATGGGAAGAG TTGACAGGGC TTCAGTTGAA AGAGTTGACC GACCTGACCT TGTGTTATCA	60
ATTGATTTTA GGTCTTTTGT CAACTATAGT TGGTTTGTA AGAAGTTAAT ATTTGGAGAA	120
GAGGATTGCT ATCTTCTCCA TTTTATGTG CAGAGTTATA GTGGCTTGAT GCTGGGAAAG	180
TACACTGTGA CTGCTAAAAC ATTCCTAGAA GTTGCTTTGA TTTACCTAAT CTATTTATGC	240
AAATTTTATG TTATTTTACT ATAA	264

(2) INFORMATION FOR SEQ ID NO:2439:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1890 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1890
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2439:

GTTGAGAGAG	TAGTTTATAT	GAAAATTGAA	AATAAAAATG	TAAGACGTAA	TTTCTTTTGG	60
GGAGATGGTC	GATTTTATAC	TACTGATATC	GTAAACAAAC	GGGCAGGAGT	AATGATAGAA	120
AATGTTTCGA	AAGAAGAAAT	TACCATTACA	TTGGAGAATG	GTATAAGACT	TTCTTCAAAT	180
CATTTTTCAG	CAATCGTTAG	GGAAGAGGGA	GATACGCGAA	TTCAAGTTTC	TTTTGTTTGT	240
CCTTCCATT	GTTTACGTTT	AATCTTTGAA	TCGAGGGATG	ATGTTCTTTC	GAAGCAATTA	300
GTTTTAGAA	CATCTACTGA	GGTTATTAAA	TCTGTAGAGG	TAGAGAGTTT	TGAGTTTGAA	360
ACAGAAGACA	ATATTTTCTA	TCCGAAAAGA	CAAGATTGTA	TTAAGGAAAT	GGCGAATTTT	420
TCCGGTCATT	ATGTAGAATT	GGGACAACCT	GTTTATGCGA	ATTCTTTATT	CTTAGGAATG	480
GAATTTCCAA	TGTCTGAAAA	CAAGGTAGAT	GGTAGACACT	ATGTATCAAG	ATATTACTTG	540
GGAAGTGTG	TAAATCAAGA	AAAGAGTTTG	TGGTCTTGTA	TTATTGGGGG	AGCATGTTCT	600
TATAAAAAAG	AAGAGATTCA	AGAGGCATTT	TTTGAATATG	TTGAAGGAAT	AGCTCAACCT	660
AGTTATTTCC	GTAAACAGTA	TAATTCCCTG	TATGACCATA	TGACCGATAT	TACAGAGGAA	720
GGTATTTTAA	AAAGTTTTTC	TGAGATTCTG	GATGGATTTG	AAAATCATGG	AGTTCATTTA	780
GATGCTTATG	TTGTTGATGA	TGGTTGGACA	AACTATCAAT	CAGTTTGGGA	ATTCAATCAT	840
AAATCCCAA	ATGGTTTGAG	AAATATTAAA	CATCTTGTA	ATGGATTTGG	TTCAAGCCTA	900
GGATTGTGGA	TTGGTCCCCG	AGGTGGTTAT	AATGGGACAG	AAATCATTAT	GAGTGATTGG	960
TTAGAAGCAC	ATCCAGAGTT	AAATATTGGA	TCTAAAAATT	TGATTTCAA	TGATGTAAAC	1020
GTGGCTGATT	TTAACTATCT	CAATCAAATG	AAGAAAAAGA	TGTTGGAATA	TCAAAAAGAA	1080
TTCGATATCA	GCTATTGGAA	AATTGATGGT	TGGTTACTTC	AACCTGACAA	ACCTGATAAG	1140
AGTGGACCGC	ACGGTATGTA	TACCATGACA	GCGGTTTATG	AGTTCCTAAT	TCAACTGTTG	1200
ATAGATCTAA	GAAAGGAGAG	AGGAGGAAAA	GATTGTTGGT	TAAACTTGAC	TTCTTATGTA	1260
AATCCTAGTC	CATGGTTTTT	ACAGTGGGTC	AATAGTTTAT	GGATTCAAAT	ATCTCAAGAT	1320
GTAGGCTTTA	CAGAGAATGC	AGGTAATGAT	ATCAATCGTA	TGATTACTTA	CCGAGATAGT	1380
CAGTATCAAG	AAATTTTGGA	AAAACGTGAG	ATACAGTTAC	CTATGTGGTC	GCTTTATAAT	1440
CATGAACCAA	TCTATGCTGT	CAGTGCAAAT	ACCTGGTACA	TGGATCATCA	AATGTTTGCA	1500
TCAATACCA	ATTTTGAAAGC	TTATCTATTA	TTTATTTCAA	CAAGAGGGAA	TGCTTTTTGG	1560
GAGTTTCACT	ATTCTTTTGA	TATGTTTGAT	GAAGAACGCT	GGAAAGCCAA	TGCTCGTGCC	1620
GTCAAATGGA	TAGAGGAGAA	TTATCAAACA	CTAAAAATATA	GTAAAAAAT	AGGAGGAAGT	1680
CCTGAAAAAT	TTGAAATTTA	TGGTTATAAG	TGTCACAATC	AGAAGACTTC	TACTGAAATT	1740
CTCTCTCTGA	GAAATCCTGC	TCAGATTAAA	CAAAAAATAA	AAATAGAGAA	TCTTTTCGATA	1800
GAGAATTTTA	CCAGAGTAAT	TGGAGATTTT	ACTATTCAAG	AAGATGAGAT	AGAATTGGCA	1860
CCGTACTCTA	TCGTGATACT	GAAGAAGTAA				1890

(2) INFORMATION FOR SEQ ID NO:2440:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 888 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...888
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2440:

ATAGAGAGAG	TGAATCTTAT	GCTCCAACAA	CTCGTAAATG	GTTTGATTCT	AGGTAGTGTT	60
TACGCGCTGT	TAGCCCTAGG	ATATACCATG	GTTTACGGAA	TTATCAAGCT	CATCAACTTC	120
GGCCATGGTG	ATATTTATAT	GATGGGAGCC	TTTATCGGTT	ATTTCTTGAT	CAATTCCTTC	180
CAAATGAATT	TCTTTGTAGC	GCTTATTGTA	GCTATGCTAG	TGACAGCTAT	TCTTGGTGTC	240
GTGATTGAGT	TTCTTGCTTA	CCGACCTTTG	CGCCACTCTA	CTCGTATTGC	TGTTTTGATT	300
ACGGCTATTG	GGGTTTCTTT	CCTATTGGAG	AATGGAATGG	TCTATCTGGT	TGGTGCCAAT	360
ACCCGTGCCT	TCCCTCAAGC	GATTCAAACA	GTTTCGATATG	ATTTGGGACC	AATTAGCTTA	420
ACAAATGTGC	AGTTAATGAT	TTTGGCCATT	TCCTTGATTT	TGATGATTTT	GTTACAAGTC	480
ATTGTCCAAA	AGACTAAGAT	GGGGAAAGCC	ATGCGTGCAG	TATCAGTAGA	TAGCGACGCG	540
GCACAATTGA	TGGGGATCAA	TGTAAACCGT	ACGATTAGCT	TTACCTTCGC	TTTGGGTTCT	600
GCTCTTGCGG	GTGCGGCTGG	TGTTCTGATT	GCTCTTTATT	ATAACTCTCT	TGAGCCTTTG	660
ATGGGGGTTA	CTCCAGGTCT	TAAATCTTTC	GTTGCCGCAG	TACTTGGTGG	TATCGGAATT	720
ATTCTTGGTG	CGGCTCTTGG	TGGCTTTGTG	ATTGGTCTAT	TGGAAACCTT	TGCGACAGCC	780
TTTGGGATGT	CAGATTTCCG	TGATGCCATT	GTTTATGGAA	TCTTGTTGTT	GATCTTGATT	840
GTCCGCCCAG	CTGGTATCCT	TGTAAGAAT	GTGAAAGAGA	AGGTGTAA		888

(2) INFORMATION FOR SEQ ID NO:2441:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...240
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2441:

TCAGGTGGAG	TGGTTAATGT	TAAAGAGTAT	CCACTATATT	TCTTCTCATA	CTCAATGGAA	60
ATCAAAGAGC	AAACTAGGAA	GCTAGCCGCA	GGCTGCTCAA	AACACTGTTT	TGAGGTTGTG	120
GATAGAACTG	ACGAAGTCAG	TAACCATATA	TACGGTAATG	TGACGCTGAC	GTGGTTTGAA	180
GAGATTTTCG	AAGAGTATTA	TATTTCAAAA	GGCCGAAGTA	AGTTTACTCC	GACCTGTTAG	240

(2) INFORMATION FOR SEQ ID NO:2442:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 942 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2442:

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GAGAAAGGAG TTGGTAGCTT GACTCTTCGT TCACATTCTG AACGGCTAAT GGGGACTACT      60
ATCACTATTT CATTAGTGGA TGAGCAAGCC GATATCTTTC TCCAAAAATC CTTTGACTTG      120
CTCAAAGAGC TTGAATACCG CTTCAACGCC AATAGTCAAG AATCTGAGTT GATGGAAATC      180
AATTATCAAG CAGGAGTATC CCCCCTCACG GTTCATCCAG ACCTGTTTGA GCTGATTTCA      240
CTTGGGTTAG AGCATAGCCT AGCGCTCTCT AGCCACCTCA ATATCAGCAT TGGTCCCTTA      300
ATTCAAACCT GGCGTATCGG TTTTTCAGAT GCCAAGGTCG CCCAGCCTCA AGAAATTGAA      360
TCGGTGCTGC CTCTAATCAA TCCTCATGGT ATCGAGTTAG ATTCTTCTAC TTCTACTGTG      420
TTTTTAAAC AGAAAGGAAT GAAGATCGAT CTAGGTTGTT TAGCCAAAGG ATACAGTGCG      480
GATAAGGTTG CCCAATTTCT TAGGAAAGAG GGGGTGACTT CTGCCTTGAT CAATCTGGGA      540
GGGAATATCC TGACCATTGG AAAAAATCAG GCAAGAGGGG ATAACCCATG GCAAATCGGG      600
ATTCAAGACC CAGCCAATCC TAGGGGAAAT CATTTAATGA CCATCCCTGT TGTCAATAAA      660
TCTGTCGTGA CTTCAGGCAT TTATGAACGT CACCTGACCG TCGATGGACA AGATTACCAT      720
CACATTTTGT ACAGTCAAAC AGGATATCCT GTTGAAACGG AACTAGCGAG TCTAACAATC      780
ATCTCTGATA AATCAGTCGA TGGCGAAATC TGGACGACTC GACTCTTTGG AGAAAGACCT      840
GCTTCTATCC TCTGGCAAAT CGAAAGTTTG GAGGGCATCG AAGTCATCCT CATCGATAAA      900
GAAGGCCACC TAAGCTGTTC TTCAGGAATT CCTACTCTAT AG                               942
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(2) INFORMATION FOR SEQ ID NO:2443:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2443:

```
AAAGGAGGAG TTTTATGAA ATCCTTTAAA GATTTTCGAG AATCTTTAAC AGCTGAAGAT      60
ATGCAAGCTA TCTCTGCTAA AGCTAATGAA GCTACTAAAC AGATTGACCA TACAGACGGA      120
TTGCAACTGG GGAAGGTCAG TGGTTTGACT TCTGTAATAA CTACTATTGA GTTACTTGAG      180
AAGTATCATG AATGGCTTCA TAGCTAA                               207
```

(2) INFORMATION FOR SEQ ID NO:2444:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...375
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2444:

CATTCGGGAG	TGAAACAGTC	TGGGAGACTG	TTTCAGCCTG	AGCCTAGAAA	TTTGAAAGCG	60
AAGCTGTTTA	GCCAAGTCAT	AGTAAGGGCT	AAACATATCC	ATAGTAATGA	TTTTGACGCG	120
ACATCGGACG	GCTCTATCAT	ATTTAAGAAA	GTGATCTCGG	ATGACAGCTT	GTGTTCTACC	180
TTCAAGAACA	GTGATGATAT	CGAGCTTTTC	AAAATCTTGC	GCAATAAAGC	TCATCTCCAT	240
CTCCCGATTG	AAACAGTCAC	TCCCCGGAAT	GTTTCAACGT	CCCAAGACAT	AATCTTAGGC	300
AGATTCTTAA	AATTACACTC	AAAGTGGGAA	TCATTGAGCT	TTCGAATGAC	AGTTGAAGTT	360
GAGATGGAAA	GCTGA					375

(2) INFORMATION FOR SEQ ID NO:2445:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...327
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2445:

CATTCGGGAG	TGAAACAGTC	TGGGAGACTG	TTTCAGCCTG	AGCCTAGAAA	TTTGAAAGCG	60
AAGCTGTTTA	GCCAAGCCAT	AGTAAGGGCT	AAACATATCC	ATAGTAATGA	TTTTGACGCG	120
ACATCGGACG	GCTCTATCGT	AGCGAAGAAA	GTGATTTCGA	ATGATAGCTT	GTGTTCTTCC	180

CTCAAGAACA GTGATGATAT TGAGCTTGTC AAAATCTTGC GCAATAAAGC TCATCTCCAT	240
CTCCCGATTG AAACAGTCAC TACCCGGACT GTTTCACGT CCCAAGACAT AATCTCAGGA	300
AGACAAGAAA AATCATGTTT AAAGTGA	327

(2) INFORMATION FOR SEQ ID NO:2446:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...327
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2446:

CATTCGGGAG TGAAACAGTC TGGGAGACTG TTTCAGCCTG AGCCTAGAAA TTTGAAAGCG	60
AAGCTGTTTA GCCAAGTCAT AGTAAGGGCT AAACATATCC ATAGTAATAA TTTTGACGCG	120
ACATCGGACA GCTCTATCGT AGCGAAGAAA GTGATTTTCA ATGATAGCTT GTGTTCTTCC	180
CTCAAGAACA GTGATGATAT TGAGATTGTT AAAATCTTGC GCAATGAAGC TCATCTCCAT	240
CTCCCGATTG AAACAGTCAC TCCCGGACT GTTTCACGT CCCAGGACAT AATCTCAGGA	300
AGACGCGAAA AATCATGCTC AAAGTGA	327

(2) INFORMATION FOR SEQ ID NO:2447:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...327
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2447:

CATTCGGGAG	TGAAACAGTC	TGGGAGACTG	TTTCAGCCTG	AGCCTAGAAA	TTTGAAAGCG	60
AAGCTGTTTA	GCCAAGCCAT	AGTAAGGGCT	AAACATATCC	ATAGTAATGA	TTTTGACGCG	120
ACATCGGACG	GCTCTATCGT	AGCGAAGAAA	GTGATTTCTGA	ATGATAGCTT	GTGTTCTTCC	180
CTCAAGAACA	GTGATGATAT	TGAGATTGTT	AAAATCTTGC	GCAATGAAGC	TCATCTCCAT	240
CTCCCGATTG	AAACAGTCAC	TCCCCGGACT	GTTTCAACGT	CCCAGGACAT	AATCTCAGGA	300
AGACAAGAAA	AATCATGTTT	AAAGTGA				327

(2) INFORMATION FOR SEQ ID NO:2448:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...327
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2448:

CATTCGGGAG	TGAAACAGTC	TAGGAGACTG	TTTCAGCCTG	AGCCTAGAAA	TTTGAAAGCG	60
AAGCTGTTTA	GCCAAGTCAT	AGTAAGGGCT	AAACATATCC	ATAGTAATGA	TTTTGACGCG	120
ACATCGGACG	GCTCTATCAT	ATTTAAGAAA	GTGATCTCGG	ATGACAGCTT	GTGTTCTACC	180
TTCAAGAACA	GTGATGATAT	CGAGCTTTTC	AAAATTTTGC	GCAATAAAGC	TCATCTCCAT	240
CTCCCGATTG	AAACAGTCAC	TCCCCGGACT	GTTTCAACGT	CCAAGACAT	AATCTTAGGC	300
AGATTCTTAA	AATTACACTC	AAAGTGA				327

(2) INFORMATION FOR SEQ ID NO:2449:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2449:

CATTCGGGAG	TGAAACAGTC	TGGGAGACTG	TTTCAGCCTG	AGCCTAGAAA	TTTGAAAGCG	60
AAGCTGTTTA	GCCAAGTCAT	AGTAAGGACT	AAACATATCC	ATAGTAATAA	TTTTGACGCG	120
ACATCGGACA	ACTCTATCGT	AGCGAAGAAA	GTGATTTTCA	ATGATAGCTT	GTGTTCTACC	180
CTCAAGAACA	GTGATGATAT	TGAGCTTGTT	AAAATCTTGC	GCAATGAAGC	TCATCTTTCC	240
CTTTGTAAAA	GCATACTCAT	CCCAAGACAT	AATCTCAGAA	AGACAAGAAA	AATCATGTTT	300
AAAGTGAAAA	TCATTGAGCT	TACGAATGAC	AGTTGA			336

(2) INFORMATION FOR SEQ ID NO:2450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2450:

AATGGGGGAG	TTTTTTTGAA	GCCATTTAAA	ACAATCGAGG	AACAAATCGC	AACACTAAAA	60
ATCAGAGGGT	TATCCATTAC	AGATGAATCT	AAAGCAGCTA	AGTACCTGCT	AAGTAACAAT	120
TACTACAATA	TTATCAATGG	ATACAGTAAG	TTTTTTTCAAC	ACCCTGGTAC	TGACACTTAT	180
ATTGACGGCG	TCACATTTGA	CGAAGTTTCA	AGTCTCTATA	CATTTGACAA	AGATGTAAAA	240
CGAGCCATTT	TGCAAGCTAT	TCTTGAAGCT	GAACACCATA	TCAAGTCAAT	CACTGCTCAC	300
AGATTCGCCG	AAGCTTACCC	CAGTCAAAAA	TACGCTTATT	TAAACACCAA	TTCTTATGCA	360
GATAATAAAA	TATTAGACGT	GGGATTTATT	GTATCAAAAC	TATCCAAAAT	CATAAACACA	420
AACAAGCGAT	ACAGAGGAAA	TTCAATTTCAC	CACTACGCAC	ATACTCATT	AGATGTCCCA	480
ATCTGGGTAC	TAAGTATTA	TCTAGAGTTT	GGAGATTTAC	GCACGATTAT	TGAAAACCTG	540
CCTAATTTCAC	TCCAAAATGA	AATCGCACGG	GATTTAGTAA	GTTTTATAAG	CACAAACATA	600
CCTGACTTTA	ACGATGTTTT	CCCACCAGAA	ACCTTGATAT	CTTTTCTAAA	AAATATTAAC	660
GAGGTACGAA	ACAAATGCGC	TCACAATAAT	CGCTTATTAA	ACTTCAGATG	CCGTTCTAAT	720
AGTACGTTTT	GGGAAACGAT	TCATAACAAA	GAGATCTTGA	TGGGAGATGA	CAGTAGAAAA	780
ACTGTATATT	CAACAATTAT	TAGCCTTCAA	TGCTTTATTA	GTAAAGCAGC	ATTCAACATT	840
TTGTGGAATA	CTCTTAGAAA	AAAAGTTATC	AACTAGAGA	AAAAGCTGCC	TTCTATAGAC	900
ATCAATGTAA	TCAACCAGTC	TTTAGGTTTT	CCTAATGATT	GGCACCGTAA	TGAACCAAAA	960
GTATAA						966

(2) INFORMATION FOR SEQ ID NO:2451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2451:

GTCTTTTGG	TCTATCTGAT	CATTACTGTA	CACAAGCTTG	GTCGTGTCAT	CGATGAAACA	60
GAAAAGACGA	TTAAAACCTT	GACTTCAGAT	GTGGATGTGA	CCTTGCATCA	CACCAATGAG	120
TTGTTGGCTA	AGGTCAATGT	CTTGGCAGAT	GATATCAATG	TCAAGGTGGC	TACGATTGAT	180
CCACTCTTCA	GTGCTGTTGC	AGATTTATCT	CTATCTGTTT	CAGACCTCAA	TGACCATGCG	240
CGTGTCTTGA	GCAAGAAAGC	TTCATCAGCT	GGTTCAAAAA	CACTCAAGAC	TGGTGCAAGT	300
CTGTCAGCTC	TTCGCTTTC	AAGTAAATTT	TTCAAAAAAT	AA		342

(2) INFORMATION FOR SEQ ID NO:2452:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2452:

CTGTTCTTGG	TAAGGAAGTA	CCTGTATCAT	CAACCAAGTC	TTTTACAGGA	CATTTGCTGG	60
GGGCTGCGGC	GTGCAGTAGA	AGCTATCGTC	ACCATCGAAG	CTATGCGTCA	TAACTTTGTA	120
CCAATGACAG	CTGGGACAAG	TGAAGTATCA	GATTATATCG	AAGCTAATGT	CGTTTATGGA	180
CAAGGCTTGG	AGAAAGAAAT	TCCATACGCT	ATTTCAAATA	CTTTTGTTTT	TGGAGGCCAC	240
AATGCAGTTC	TTGCTTTCAA	ACGTTGGGAG	AATAGATAA			279

(2) INFORMATION FOR SEQ ID NO:2453:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2453:

CTCAGCTTGG TAGAGTACTT GGTTCGGGAC CAAGGTGTCG CAGGTTCGAA TCCTGTCTTC	60
CCGATTCATG GCGGTGTAGC TCAGCTGGCT AGAGCGTCCG GTTCATACCC GGGAGGTCGG	120
GGGTTCGATC CCCTTCGCCG CTATAATGAT CTTGTCGGAC CTTTAGCTCA GCTGGTTAGA	180
GCTCTCGGCT CATAA	195

(2) INFORMATION FOR SEQ ID NO:2454:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2454:

TTAAGATTGG TAATCAAAAA TATAGGGAGG AATGTTTTGA ATAAGAAATA TAACATAGTT	60
CTATTTTGT TGTATATAGT TTATTTATTT GGATATTTTT CAATTTCAAA AACGTTAATT	120
CCTATAATGT GTGTGTTCCA AGTATTCTTG ATAGAACATA TATTTAGAAT TCGAAATAGA	180
ATGATGCAGA TAGGTGAAAT TATAATTATT GTTGCTTCTA TAATATTATT TATTGATAGT	240
ATATTGAGTT TGTA	255

(2) INFORMATION FOR SEQ ID NO:2455:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2455:

AAGAGATTGG	TGTTGAGTGT	CCAAGCTGTC	ATCAGGGACA	AATTATTGAG	CGAAAAACCA	60
AGCGTAATCG	CCTATTCTAT	GGTTGCAATC	GCTATCCAGA	ATGTGAATTT	ACCTCTTGGG	120
ACAAGCCTGT	TGGTCGTGAC	TGTCCAAAAT	GTGGCAACTT	CCTCATGGAG	AAAAAAGTCC	180
GTGGTGGTGG	CAAGCAGGTT	GTTTGTAGCA	AAGGAGATGA	CTCTTCACCA	CGAGTGCNGN	240
GCACAA						246

(2) INFORMATION FOR SEQ ID NO:2456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2448 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2448

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2456:

CCATCACTGG	TCAAGCACAA	GAGTGACCGC	ATCTCCCTCC	ACCAAAAAGA	CTTGGAATC	60
ACCTCTGTAG	AAGTTGCAGG	TCAAGCTCGT	CCATTTACAG	TTGACCATGA	CAATGAAGCC	120
CTTCATATCG	AATTGGCTGA	GGCTGGTCAA	GTTGAATTGG	TTCTTGCCTT	TTCTGGTAAA	180
ATTACAGACA	ACATGACAGG	GATTTACCCT	TCTTATTATA	CAGTTGATGG	AGTCAAGAAG	240
GAGGTCTTGT	CTACTCAGTT	CGAGAGCCAT	TTTGCGCGCG	AAGCTTTCCC	ATGTGTGGAT	300
GAGCCTGAAG	CCAAAGCAAC	TTTTGACCTC	TCTCTTCGCT	TTGACCAAGC	AGAAGGTGAA	360
TTGGCCTTGT	CAAAATGCC	AGAAATCGAT	GTTGAAAACC	GTAAGGAAAC	AGGTATCTGG	420

AAGTTTGAGA	CAACACCTCG	CATGTCTTCT	TACTTGTTGG	CCTTTGTTGC	TGGTGATTG	480
CAAGGGGTGA	CCGCTAAAAC	TAAAAATGGT	ACCCTGGTAG	GTGTCTACTC	AACCAAAGCA	540
CATCCACTTT	CAAATCTTGA	TTTCTCACTG	GATATCGCTG	TTCGCTCTAT	CGAGTTTTAC	600
GAAGATTACT	ATGGAGTTAA	GTATCCAATT	CCTCAATCTC	TCCACATCGC	CCTTCCTGAC	660
TTCTCAGCTG	GTGCTATGGA	AAACTGGGGT	CTTGTGACCT	ACCGTGAAGT	TTACTTGGTT	720
GTCGATGAGA	ACTCTACATT	TGCTAGCCGT	CAACAAGTTG	CCCTTGTTGT	GGCCCATGAA	780
TTGGCTCACC	AATGGTTTGG	GAACCTCGTG	ACTATGAAAT	GGTGGGATGA	CCTTTGGCTC	840
AATGAAAGTT	TCGCTAATAT	GATGGAATAC	GTCTGTGTGG	ATACCATCGA	ACCAAGCTGG	900
AATATCTTTG	AAGATTTCCA	AACAGGTGGA	GTACCTCTTG	CTCTTGAACG	TGACGCTACT	960
GATGGCGTTC	AGTCTGTCCA	CGTCGAAGTT	AAACATCCAG	ATGAAATCAA	TACACTCTTT	1020
GACGGCGCTA	TCGTCTATGC	CAAAGGAAGC	CGTCTCATGC	ACATGCTTCG	CCGTTGGCTA	1080
GGAGATGCTG	ATTTTGCTAA	AGGTTTGCAT	GCCTACTTTG	AAAAACACCA	ATACAGCAAC	1140
ACCATTGGTA	GTGACCTTTG	GGATGCCCTT	GGTCAAGCGT	CAGGACGTGA	TGTCGCAGCC	1200
TTCATGGATT	CTTGGTTGGA	ACAGCCTGGT	TACCCAGTTC	TTACTGTCAA	AGTTGAAAAT	1260
GATGTCTTGA	AGATTTTACA	AAAACAATTG	TTCATCGGTG	AGAACGAAGA	CAAGAACCGT	1320
CTCTGGGTGG	TGCCCCCTCA	TAGCAACTGG	AAAGGCTTGC	CTGATACACT	CGAAACTGAA	1380
AGTATCGAAA	TCCCTGGCTA	CGCAGCTCTT	CTTGCTGAAA	ATGAAGGAGC	TCTTCGTCTC	1440
AACACTGAAA	ATACTGCCCA	CTATATTACC	GACTATCAAG	GAGACTTGTG	AGAAGCTGTT	1500
CTTGCTGAGC	TAGAGACACT	TGATAACACA	AGCAAACGTC	AAATTGTTCA	AGAACGTCGT	1560
TTGTTGGCTG	AGGCAGGGCA	CATTTCTTAT	GCAGACTTGC	TTCCAGTTCT	TGATAAACTT	1620
GCTAAGGAAG	AGTCTTATCT	GGTGGTTTCA	GCTGTTTCTC	AAGTGATTTC	AGCCCTTGAG	1680
CGCTTTATTG	ATGAAGGAAC	GGATGCTGAA	ACAGCCTTCA	AAGGACTGGT	TGCTAAATTG	1740
GCTCGTCATA	ACTATGACCG	TCTTGGTTTT	GAAGCTAAAG	ACGGAGAATC	AGATGAGGAT	1800
GAATTGGTTC	GTCAGCTGGC	TGTTTTCGAT	ATGATTTCGT	CAAATGATGC	AGAAGCTCGT	1860
CAAGTCGCTA	GCCAAATCTT	CGCAACACAC	AAGGAGAATC	TTGCAGAACT	CCCAGCAGCT	1920
ATTCTGTTAC	AAGTTCTGAT	TAATGAGATG	AAACATCATG	AGACTAAAGA	CTTGTTAGCA	1980
CTTTATCTTG	ATACTTATAC	TCACGCAACA	GATGCTGTCT	TTAAACGCCA	GTTGACAGCA	2040
GCTCTTGCA	ACAGTACAGA	TGCGGATAAT	ATCCAAAAC	TGATTACTTC	TTGGAAGGAC	2100
AAATTTGTGG	TCAAACCACA	GGACTTGTCT	GCTTGGTATT	ACCAATTCCT	AGCTCATCAA	2160
GCAACTCAGA	AAACAGCTTG	GTCTTGGGCG	CGTGAAAAC	GGGCTTGGAT	TAAGGCAGCC	2220
CTTGGAGGAG	ATATGAGCTT	TGATAGCTTT	GTTATCCTTC	CTGCTCATGT	ATTTAAGACT	2280
CAGCAACGCT	TGGCGGAATA	CAAGGAGTTC	TTTGAACCGC	AACTTTCTGA	CCTTGCTCTT	2340
AGCCGTAACA	TCGGTATGGG	AATCAAGGAA	ATTGCAGCGC	GTGTTGACTT	GATTAGCCGT	2400
GAAAAAGCTG	CAGTCGAAGC	AGTTGTTCTT	CAATACGGAA	ATGCATAA		2448

(2) INFORMATION FOR SEQ ID NO:2457:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 945 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...945
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2457:

CCAGGACTGG	TATGTTGGGT	TCTTATAGTA	TTTTTGGTGG	CTGTTAACAG	TTTGAGTGAT	60
TATAAGACAG	ATTTTCGTCT	GTTTGAATTC	TCCAAAATAT	TTGGAGATGA	AGAGTATGGT	120
TTCCAGCTTT	CAGTFACTGT	TTTACGTTAT	GGTTATACAT	ACCGTTTGTT	CTCTTTTG TG	180
GTAGACATGC	TTAATCAAGA	TATGGGACGA	AAC TTGGAAG	TTATTCAACG	TCATGGGGCC	240
CTGCTCTTGG	TTGAAAATGG	GCAACTCTTG	TATGTAGAAT	TGCCTAAAGA	AGGGGTCAAT	300
GTTCATGATT	TCTTTGAGAC	AAGCAAGGTC	AGAGAAACCT	TGTTGATTGC	GACTCGTAAC	360
GAAGGTAAAA	CCAAGGAATT	CCGAGCTATC	TTTGATAAGT	TAGGCTACGA	TGTGGAAAAT	420
CTTAATGACT	ACCCTGACCT	GCCTGAAGTA	GCAGAAACAG	GTATGACCTT	TGAAGAAAAT	480
GCCCCGCTTA	AGGCAGAAAC	CATTTCTCAA	TTAACGGGCA	AGATGGTTTT	GGCAGATGAT	540
TCTGGTCTCA	AAGTCGATGT	CCTTGGTGGC	TTACCAGGCG	TCTGGTCAGC	TCGTTTCGCA	600
GGTGTGGGAG	CAACTGACCG	TGAAAATAAT	GCCAAACTCT	TGCACGAATT	GGCCATGGTC	660
TTTGAACTCA	AGGACCGCTC	GGCTCAGTTC	CACACAACCC	TAGTCGTAGC	CAGCCCAAAT	720
AAGGAAAGTT	TAGTGTTGAA	CACCAGACCT	GGTCAGGTTA	TATTAAC TTT	GAAACCTAAG	780
GGTGAAAATG	GCTTTGGCTA	TGATCCCCTC	TTCTTGTAG	GAGAGACAGG	TGAGTCATCA	840
GCTGAATTAA	CCCTGGAAGA	AAAAAATAGT	CAATCTCACC	GTGCCTTAGC	CGTTAAGAAA	900
CTTTTGGAGG	TATTTCCATC	ATGGCAAAGC	AAACCATCAT	TGTAA		945

(2) INFORMATION FOR SEQ ID NO:2458:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 207 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...207
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2458:

TTCTTGCTGG	TGGGCAAGGA	ACTCGTCTCG	GTAAACTCAC	TCAAAGCATC	GCAAAACCAG	60
CTGTGCAATT	TGGGGGGCGC	TACCGTATCA	TTGACTTTGC	CCTATCAAAC	TGTGCCAACT	120
CAGGGATTCA	TAATGTTGGG	GTCGTTACAC	AGTATCAACC	ACTTGCTCTC	AACAACCATA	180
TTGGGAATGG	TTCAAGCTGG	GGACTAG				207

(2) INFORMATION FOR SEQ ID NO:2459:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 657 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2459:

GATAGTATGG	TCAAAGTAGC	AACCCAGACA	CCGATTATCA	GTCTCTTCTT	GCTGATTTTA	60
TCCTTGAAA	CATCTTTCAT	TCCTTCGATT	GCTCTGAATC	TTTCGGTAGT	CGCATTTTGT	120
ATTCTCTTTA	TGCTCTATTA	CCGTCGATTT	AAAATGTTAG	CTTGGATGAT	CATACTTGCC	180
ATTTTACCAT	CTTTTGCCAA	CTACTGGGCA	GTTTCAGTTAC	ACGGAGATGC	TTCACAGGCA	240
GTCATGCTTG	GAACGAGGGC	CTTTGTGACA	GTTTGTATCG	GCCTTGTCCT	TGTTTCCTCT	300
ATTTCACTAA	AAGAGCTTCT	CTTGTACTTG	GCTCAAAAGG	GGCTATCACG	CTCTTGGTCC	360
TATGCCTTGA	TTGTGGTATT	CAATTCCCTT	CCTCTCATTC	AGCAAGAAAT	CAAGTCCCTC	420
AAAGAAGCTT	GCCTATTACG	TGGTCAAGAA	CTGTATTTTT	GGTCGCCCTT	GATTTACAGT	480
AAGGTTCTGA	TGACAGTCTT	TAGGTGGCGC	CATCTTTACC	TGAGAGCTCT	GTCTGCTCAT	540
GGATATGACG	AACATGCACA	GTTGAAGAAT	AGCTATCGGA	CTTTTATATAT	TCCTAAAAAA	600
ACAAAATTAA	TCTACCTGCT	TTTCTTTTTA	TTGCTTCAAA	CCAGTCTATT	TTTATAA	657

(2) INFORMATION FOR SEQ ID NO:2460:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 660 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2460:

AGCACCATGG	TTGGCGAAAT	ATTATGCCAC	GTCCAGAACA	TCCTAGGAAA	GCAGACGCTC	60
AAACCATTGT	CGCGTCTAAA	AATAAAATCT	CAATTCAAGA	AGGCAAGAAA	GCGCTTTAAA	120
TATAGTAGAC	GTTTTCGTAA	GGTTCGCTTG	ATGTACCAAG	ATGAGGCTGG	TTTCAGTAGA	180
ATCAGTAAAC	TGGGATCTTG	TTGGTCTCCA	ATAGGAGTAG	ATCCACATGT	CCATAGTCAC	240
TATATACGAG	AATTTGCTA	TTGTTATGGA	GCTGTTGATG	CCTATACAGG	CGAATCATTT	300
TTCTTAATAG	CTGCTAGATG	TAATACTGAG	TGGATGAACG	CCTTTTTAGA	AGAGCTTTCA	360
CAAGCTTATC	CAGATGATTA	TCTTTTACTC	GTTATGGACA	ATGCTATATG	GCATAAATCA	420
AGTATCTTAA	AGATTCCGAC	TAATATTGGT	TTTGCATTTA	TTCCCTCCATA	CACACCAGAG	480
ATGAACCCCA	TTGAACAAAGT	GTGGAAAGAG	ATTTCGTAAAC	GTGGATTTAA	GAATAAAGCC	540
TTTCGAATTT	TGGAAGATGT	CATGAATCAA	CTCCAAGATG	TCATACAAGG	ATTGGAGAAG	600

GAGGTGATAA AGTCCATCGT TAATCGGAGA TGGACTAGAA TGCTTTTGA AAGCAGATGA 660

(2) INFORMATION FOR SEQ ID NO:2461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2461:

AGCGCCATGG TTGGCGAAAT ATTATGCCAC GTCCAGAACA TCCTAGGAAA ACAGACGCTC	60
AAACCATTTGT CGCGTCTAAA AATAAAATCT CAATTCAAGA AGAAAAGAAA GCGCTTTAAA	120
ACCAGTAGAC GTTTTCATAA GGTTCGCTTG ATGTACCAAG ATGAGGCTGG TTTCGGTAGA	180
ATCAGTAAAC TGGGATCTTG TTGGTCTCCA ATAGGAGTAG GTCCACATGT CCATAGTCAC	240
TATATACGAG AATTTCGCTA TTGTTATGGA CCCATACAGG CGAATCATTT TTCTTAA	297

(2) INFORMATION FOR SEQ ID NO:2462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2462:

AGCGCCATGG TTGGCGAAAT ATTATGCCAC GTCCAGAACA TCCTAAGAAA GCAGACGCTC	60
AAACCATTTGT CGCGTCTAAA AATAAAATCT CAATTCAAGA AGAAAAGAAA GCGCTTTAAA	120
ACCAGTAGAC GTTTTCATAA GGTTCGCTCG ATGTACCAAG ATGAGGCTGG TTTCGGTAGA	180

ATCAGTAAAC	TGGGATCTTG	TTGGTCTCCA	ATAGGAGTAG	GTCCACATGT	CCATAGTCAC	240
TATATACGAG	AATTTCGCTA	TTGTTATGGA	GCTGTTGATG	CCCATACAGG	CGAATCATTT	300
TTCTTAAGAG	CTGGTGGATG	TAATACTGAG	TGGATGAACG	CCTTTT'TAGA	AGAGCTTTCA	360
CAAGCTTATC	CAGATGATTA	TCTTTTACTC	GTTATGGACA	ATGCTATATG	GCATAAATCA	420
AGTACCTTAA	AAATTCCGAC	TAATATTGGC	TTTGCATTTA	TTCTTCCATA	CACACCAGAG	480
ATAAACCCCG	TTGAACAAGT	GTGGAAAGAG	ATTTCGTAAAC	GTGGATT'TAA	GAATAAAGCC	540
TTTCGAACTT	TGGAAGATGT	CATGAATCAA	CTTCAAGATA	TCATACAAGG	ACTGGAGAAG	600
GAGGTGATAA	AGCCCATCGT	TAATCGGAGA	TGGACTAGAA	TGCTTTT'TGA	AAGCAGATGA	660

(2) INFORMATION FOR SEQ ID NO:2463:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 189 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...189
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2463:

GCTTTAATGG	TGCCCCTGCA	AAGTTTGATA	TTCGTGCTTG	GAGTCCAGAC	CATACTAAAA	60
TGGGCAAAGG	GATTACTCTC	TCAAATGAAG	AATTTCAAAC	GATGGTGGAT	GCCTTTTAAAG	120
GCAACTAATA	CTCTTCGAAA	ATCTCTTCAA	ACCGCATCAG	CTTTGCCTTG	CCGTATGTAT	180
GGTTACTGA						189

(2) INFORMATION FOR SEQ ID NO:2464:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3789 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...3789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2464:

GAAAAAATGG	TCTACAGCAT	CCGTTCCCTC	AAAAATGGAA	CTGGTTCTGT	CCTTATCGGT	60
GCAAGCCTTG	TCTTGCTTGC	CATGGCTACA	CCAACTATCT	CATCCGACGA	AAGTACACCA	120
ACCACTAACG	AACCCAACAA	CAGAAATACA	ACCATCCTTG	CCCAACCTCT	TACTGATACA	180
GCAGCTGGCT	CTGGTAAGAA	CGAAAGTGAT	ATTTCTTCAC	CTAGAAATGC	AAACGCTTCC	240
CTAGAGAAAA	CAGAAGAAAA	ACCTGCTGCA	AGCCCAGCCG	ATCCAGCACC	ACAAACTGGA	300
CAAGATCGTT	CAAGTGAGCC	AACTACTTCT	ACTAGTCCAG	TAACAACCTGA	AACTAAGGCA	360
GAAGAGCCCA	TCGAAGATAA	CTACTTCCGT	ATCCATGTCA	AAAAACTTCC	TGAAGAAAAC	420
AAGGATGCTC	AAGGACTATG	GACTTGGGAC	GATGTTGAAA	AACCATCTGA	AAACTGGCCA	480
AACGGAGCTT	TGTCCTTCAA	GGATGCCAAG	AAAGATGACT	ACGGCTATTA	CCTAGATGTC	540
AAATTAAAGG	GAGAACAAGC	CAAGAAAATT	AGCTTCCTCA	TCAACAATAC	AGCTGGAAAA	600
AATCTAACCG	GCGATAAATC	TGTAGAAAAA	CTAGTTCCAA	AAATGAACGA	AGCTTGGTTA	660
GACCAAGATT	ACAAGGTTTT	CTCTTACGAG	CCACAGCCTG	CAGGAACGTG	TCGCGTCAAC	720
TACTACCGCA	CAGATGGCAA	CTATGACAAG	AAATCTCTCT	GGTACTGGGG	AGATGTAAAA	780
AATCCAAGTA	GCGCTCAATG	GCCTGACGGA	ACAGACTTTA	CGGCTACAGG	CAAATATGGC	840
CGCTATATCG	ACATTCCCTCT	TAATGAAGCC	GCAAGAGAAT	TTGGATTTTT	ATTACTAGAT	900
GAGAGCAAAC	AAGGAGACGA	CGTGAAAATC	CGTAAAGAAA	ATTATAAGTT	CACAGATTTG	960
AAAAATCATA	GCCAAATTTT	CCTAAAAGAC	GATGATGAAT	CGATTTACAC	AAATCCATAC	1020
TATGTCCATG	ATATCCGTAT	GACAGGAGCC	CAACACGTAG	GCACTTCTAG	CATTGAAAGT	1080
AGCTTTTCAA	CACCTGTCCG	TGCTAAAAAA	GAAGATATCC	TCAAACACTC	CAACATCACT	1140
AATCACCTAG	GAAACAAGGT	AACTATTACC	GATGTTGCAA	TCGATGAAGC	TGGTAAGAAA	1200
GTGACCTACA	GCGGAGATT	CTCTGACACA	AAACATCCCT	ATACTGTTAG	CTACAATTCC	1260
GACCAATTCA	CTACCAAAAC	AAGCTGGCGC	CTGAAAGATG	AGACATACAG	CTATGATGGC	1320
AAACTGGGAG	CTGACCTAAA	AGAAGAAGGA	AAACAAGTTG	ATTTGACCC	TTGGTCACCA	1380
AGTGCTGATA	AGGTTTCTGT	TGTTGTCTAC	GACAAGAATG	ACCCTGACAA	AGTAGTTGGA	1440
ACTGTGCTC	TCGAAAAAGG	GGAAAGAGGA	ACTTGGAAC	AAACTCTAGA	CAGCACAAAC	1500
AAACTCGGAA	TCACAGATTT	CACCTGGCTAC	TATTATCAAT	ACCAAATCGA	GCGTCAAGGT	1560
AAACTGTTC	TTGCACTCGA	TCCTTACGCT	AAATCTCTTG	CTGCTTGGAA	TAGCGACGAT	1620
GCCAAGATTG	ACGATGCCCA	TAAAGTGGCT	AAAGCCGCC	TTGTAGATCC	AGCTAAACTC	1680
GGACCTCAAG	ACTTGACTTA	TGGTAAGATT	CACAATTTCA	AGACTCGTGA	AGACGCCGTT	1740
ATCTACGAAG	CTCATGTGCG	TGACTTCACT	TCAGATCCTG	CCATTGCAAA	AGACTTGACC	1800
AAACCATTTG	GGACTTTTGA	AGCCTTCATT	GAAAAACTAG	ACTATCTCAA	AGACTTGGGT	1860
GTAACCCATA	TCCAGCTCCT	TCCAGTCTTG	TCTTACTACT	TTGTCAATGA	ATTGAAAAAC	1920
CATGAACGCT	TGCTGACTA	TGCTTCAAGC	AACAGCAACT	ACAACCTGGG	ATATGACCCT	1980
CAAACTACT	TCTCCTTGAC	TGGTATGTAC	TCAAGCGATC	CTAAGAATCC	AGAAAAACGA	2040
ATCGCAGAA	TTAAAAACCT	CATCAACGAA	ATCCACAAAC	GTGGTATGGG	AGCTATCCTA	2100
GATGTCGTTT	ATAACCACAC	AGCCAAAGTC	GATATCTTTG	AAGACCTAGA	GCCAAACTAC	2160
TACCACTTTA	TGGATGCCGA	TGGCACACCT	CGAAGTAGCT	TTGGTGGTGG	ACGCTTGGGG	2220
ACAACCCACC	ATATGACCAA	ACGGCTCCTA	GTTGACTCTA	TCAAATACCT	AGTTGATACC	2280
TACAAAGTGG	ATGGCTTCCG	CTTCGATATG	ATGGGAGACC	ATGACGCCGC	TTCTATCGAA	2340
GAAGCTTACA	AGGCTGCACG	CGCCCTCAAT	CCAAATCTAA	TCATGTTAGG	CGAAGGTTGG	2400
AGAACCTATG	CCGGTGATGA	AAACATGCCT	ACTAAAGCTG	CTGACCAAGA	TTGGATGAAA	2460
CATACCGATA	CTGTGCTGT	CTTTTCAGAT	GACATCCGTA	ACAACCTCAA	ATCTGGTTAT	2520
CCAAACGAAG	GTCAACCTGC	CTTTATCACA	GGTGGCAAGC	GTGATGTCAA	CACCATCTTT	2580
AAAAATCTCA	TTGCTCAACC	AACTAACTTT	GAAGCTGACA	GCCCTGGAGA	TGTCATCCAA	2640
TACATCGCAG	CCCATGATAA	CTTGACCCCTC	TTTGACATCA	TTGCCCAGTC	TATCAAAAAA	2700
GACCCAAGCA	AGGCTGAGAA	CTATGCTGAA	ATCCACCGTC	GTTTACGACT	TGGAAATCTC	2760
ATGGTCTTGA	CAGCTCAAGG	AACTCCATTT	ATCCACTCCG	GTCAGGAATA	TGGACGTACT	2820
AAACAATTCC	GTGACCCAGC	CTACAAGACT	CCAGTAGCAG	AGGATAAGGT	TCCAAACAAA	2880
TCTCACTTGT	TGCGTGATAA	GGACGGCAAC	CCATTTGACT	ATCCTTACTT	CATCCATGAT	2940
TCTTACGATT	CTAGCGACGC	AGTCAACAAG	TTTGACTGGA	CTAAGGCTAC	AGATGGTAAA	3000
ACTTATCCTG	AAAAATGTCAA	GAGCCGTGAC	TATATGAAAG	GTTTGATTGC	CCTTCGTCAA	3060
TCTACAGATG	CCTTCCGACT	TAAGAGTCTC	CAAGATATCA	AAGACCGTGT	CCACCTCATC	3120

ACTGTCCCAG	GCCAAAATGG	TGTGGAAAAA	GAGGATGTAG	TGATTGGCTA	CCAAATCACT	3180
GCTCCAAACG	GCGATATCTA	CGCAGTCTTT	GTCAATGCGG	ATGAAAAAGC	TCGCGAATTT	3240
AATTTGGGAA	CTGCCTTTGC	ACATCTAAGA	AATGCGGAAG	TTTTGGCAGA	TGAAAACCAA	3300
GCAGGATCAG	TCGGAATTGC	CAACCCGAAA	GGACTTGAAT	GGACTGAAAA	AGGCTTGAAA	3360
TTGAATGCCC	TTACAGCTAC	TGTTCTTTCGA	GTCTCTCAA	ATGGAAC TAG	CCCTGAGTCA	3420
ACTGCAGAAG	AGAAACCAGA	CTCAACCCCT	TCCAAGCCTG	AACATCAAGA	CCCAGCTCCA	3480
GAAGCTAGAC	CTGATTCTAC	TAAACCAGAT	GCCAAAGTAG	CTGATGCGGA	AAATAAACCT	3540
AGCCAAGCTA	CAGCTGATTG	ACAAGCTGAA	CAACCAGCAC	AAGAAGCACA	AGCATCATCT	3600
GTAAAAGAAG	CGGTTCAAAA	CGAATCGGTA	GAAAACTCTA	GCAAGAAAAA	TATACCTGCA	3660
ACCCAGATA	GACAAGCTGA	ACTTCCAAAT	ACAGGAATCA	AAAACGAAAA	CAAAC TCCTA	3720
TTTGCAGGAA	TCAGCCTCCT	TGCGCTCCTT	GGTCTCGGTT	TCTTACTAAA	AAATAAAAAA	3780
GAGAACTAA						3789

(2) INFORMATION FOR SEQ ID NO:2465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2465:

GGAGAAATGG	TTGAAGCCAT	GCGAGCAGGC	CAATTTCTTC	ATCTGCGTGT	ACCAGACGAT	60
GCCCATCTCT	TACGTCTGCC	TATTTCAATT	TCGTCTATTG	ACAAGGCAAA	CAAGCAGTGT	120
CACCTCATTT	ATCGGATTGA	GGGAGCTGGG	ACTGCAATTT	TTTCAACCTT	AAGTCAGGGA	180
GACACTCTTG	ATGTGATGGG	GCCTCAGGGA	AATGGTTTTG	ACTTGTCTGA	CCTTGATGAG	240
CAGAATCAGG	TTCTCCTTGT	TGGTGGTGGG	ATTGGTGTTT	CACCCTTGCT	TGAGGTGGCC	300
AAGGAATTGC	ATGAACGTGG	AGTGAAAGTA	GTGACAGTCC	TCGGTTTTGC	TAATAAGGAT	360
GCTGTTATTT	TGAAAACGGA	ATTGGCTCAG	TATGGTCATG	TCTTTGTAAC	GACAGATGAT	420
GGTTCTTATG	GCATCAAGGG	AAATGTTTCC	GTTGTTATCA	ATGATTTAAA	CAGTCAGTTT	480
GATGCTGTNT	ACTCGTGTGG	GGCTCCATTA	ATGATGAAGT	ATATCAATCA	AACCTTTGAT	540
GATCACCCAA	GAGCCTATTT	ATCTCTGGAA	TCTCGTATGG	CTTGTGGGAT	GGGAGCTTGC	600
TATGCCTGTG	TTCTAAAAGT	ACCAGAAAAC	GAGACGGTCA	GCCAACGCGT	CTGTGAAGAT	660
GGTCCTGTTT	TCCGCACAGG	AACAGTTGTA	TTATAA			696

(2) INFORMATION FOR SEQ ID NO:2466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1303
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2466:

CCAGATGGTT	ATGTGGTCGT	ACTGCATAGC	AAGGATAGGA	GGTAGGATGG	AAAGTTTACT	60
TATTCTATTA	TTAATTGCCA	ACCTAGCTGG	TCTCTTTCTG	ATTTGGCAAA	GGCAGGATAG	120
GCAGGAGAAA	CACTTAAGTA	AGAGCTTGGA	GGATCAGGCA	GATCATTTGT	CAGACCAGTT	180
GGATTACCGC	TTTGACCAAG	CCAGACAAGC	CAGCCAGTTA	GACCAAAAAG	ATTTGGAAGT	240
GGCTGTCAGC	GACCGTTTGC	AAGAAGTGCG	GATTGAATTG	CACCAAGGCC	TGACCCAAGT	300
CCGTCAAGAA	ATGACAGATA	ATCTCCTCCA	AACTAGAGAT	AAGACAGACC	AACGTCCTCA	360
AGCCTTGCA	GAATCAAAATG	AGCAACGTTT	GGAACAAATG	CGCCAGACGG	TCGAGGAAAA	420
ACTAGAAAAG	ACCTTGCA	CACGCTTACA	GGCTTCCTTT	GAGACAGTTT	CTAAACAAC	480
GGAGTCTGTC	AATCGTGGTC	TTGGAGAAAT	GCAGACAGTT	GCCCCTGATG	TCGGAGCTCT	540
TAACAAGGTT	CTCTCTGGAA	CCAAGACGCG	AGGGATTCTG	GGAGAATTGC	AACTGGGGCA	600
AATTATTGAA	GACATCATGA	CACCTGCCCCA	GTACGAACGA	GAATACGCAA	CGGTTGAAAA	660
CTCTAGTGAA	CGAGTGGAGT	ATGCCATCAA	GTTACCCGGA	CAAGGCGACC	AAGAATACGT	720
CTATCTTCCA	ATTGACTCTA	AGTTTCCACT	GGCAGATTAT	TACCGCTTGG	AAGAAGCCTA	780
TGAGACAGGT	GACAAGGATG	AGATTGAACG	CTGTCGTAAG	TCACTCCTAG	CAAGCGTCAA	840
GCGCTTTGCC	AAGGATATCA	AGAGCAAGTA	CATAGCACCG	CCTCGGACAA	CCAACTTTGG	900
AATCTTGTTT	GTTCCGACAG	AAGGTCTTTA	TTCAGAGATT	GTGCGCAATC	CGGTCTTCTT	960
TGATGATTTG	AGACGGGAAG	AACAGATTAT	TGTTGCAGGA	CCAAGTACCC	TATCAGCCCT	1020
TCTTAACTCC	CTATCAGTTG	GTTTCAAGAC	CCTTAATATC	CAAAAGAGTG	CCGACCATAT	1080
CAGCAAGACT	CTTGCCAGTG	TCTACACCGA	GTTTGGCAAG	TTTGGTGGTA	TTCTGGTTCA	1140
GGCACAAAAA	CATCTCCAAC	ATGCCTCTGG	CAATATTGAT	GAATTATTAA	ACCGTCGTAC	1200
CATAGCTATC	GAGCGGACGC	TCCGTCACAT	TGAGTTGTCA	GAAGGTGAGC	CTGCGCTTGA	1260
TCTACTCTAT	TTTCAAGAAA	ATGAGGAAGA	ATATGAAGAT	TAG		1303

(2) INFORMATION FOR SEQ ID NO:2467:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*